

DETECTION OF GENETIC POLYMORPHISMS

The present invention claims priority to Japanese Patent Application Ser. Nos. 2000-399,443 filed December 27, 2000, 2001-135,256 filed May 2, 2001, 2001-256,862
5 filed August 27, 2001, and 2001-(awaiting serial number) filed December 2001, each of
which was filed with the Commissioner of the Japanese Patent Office. Right of priority
under 35 U.S.C. 119 is claimed from these Japanese patent applications under the Paris
Convention for the Protection of Industrial Property. The present invention also claims
priority to PCT application (awaiting serial number) filed December 27, 2001 in the
10 Japanese receiving office. Each of these applications are herein incorporated by
reference in their entireties.

FIELD OF THE INVENTION

The present invention relates to genetic polymorphism data, compositions and
15 methods for detecting genetic polymorphisms, methods for evaluating drugs using
genetic polymorphisms and screening methods for drugs.

BACKGROUND

Human beings come in all shapes and sizes, and over three billion genetic codes
20 are located in somewhat different sites in each human being. Individual DNA sequence
variations in the human genome are known to directly cause specific diseases or
conditions, to predispose certain individuals to specific diseases or conditions, and to
affect responses of individuals to treatments such as drugs. Such variations also
modulate the severity or progression of many diseases. Additionally, DNA sequences
25 vary between populations. Therefore, determining DNA sequence variations in the
human genome is useful for making accurate diagnoses, for finding suitable therapies,
and for understanding the relationship between genome variations and environmental
factors in the pathogenesis of diseases, the prevalence of conditions and the efficacy of
therapies.

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
NDUFA9	18	(intron 4 1090)	atcattgctgttttaaagtt T/C aagtagtgtaatttcagta	6806
NDUFA9	19	(intron 4 1188)	aaccaatcctttttttttt A/T tcttccagaaactttgattt	6807
NDUFA9	20	(intron 5 161)	gggtgtgtgtgatgttttga C/T gttttgattgattgcttct	6808
NDUFA9	21	(intron 5 373)	ctttctcacccttgcaactg C/T agtgggttttgtgccactctt	6809
NDUFA9	22	(intron 5 457)	gccagggaagatgcctattc A/C cacagtgttatgtctccttt	6810
NDUFA9	23	(intron 5 3113)	gattttttctccttcttcaat G/A taagcttcccttaaaataaa	6811
NDUFA9	24	(intron 5 3339)	tctaaactcaaaacaggttt G/A tttggttattgtttaggctg	6812
NDUFA9	25	(intron 6 414)	tatagttttgccttttccag G/C atattacatatatggttaga	6813
NDUFA9	26	(intron 6 518)	ctttcattttctttcatagc T/C tgatagctcatttctttata	6814
NDUFA9	27	(intron 7 974)	ggattatgcgtacttggaaa A/G tactttggatagcgggtgatta	6815
NDUFA9	28	(intron 8 368)	acattaattttgatggagta T/G cacaatgcctccagaggctg	6816
NDUFA9	29	(intron 8 954)	gcatgcaatcagttatatag T/C ctatagataagaattacaattc	6817
NDUFA9	30	(intron 8 1253)	tcctcttgaattgttagata G/T gtatctacacatttctcatc	6818
NDUFA9	31	(intron 8 11608)	gaaaagatagatgtataaat G/A accaaaaattcgtgaagaaa	6819
NDUFA9	32	(intron 8 11930)	ctacaaatatattctaaatg C/T gtaatcattggataagtacaa	6820
NDUFA9	33	(intron 9 1998)	tggttttcaagcctttaaac G/A gctgtggaaccctgtgctca	6821
NDUFA9	34	(intron 9 2238)	ccagctacttggaggctga A/G gttggaggatcacttgagcc	6822
NDUFA9	35	(intron 9 2885)	acagcgtctgtcttctctgc A/G gttctcataggctagcttac	6823
NDUFA9	36	(intron 10 801)	tacactaaagtgtctcttac G/A tttatacttgagaagtgttt	6824
NDUFA9	37	(intron 10 910)	tgcagactttcaggtgggta G/C gatgagggttgctgctgct	6825
NDUFA9	38	(intron 10 1180)	aaaactgagtcagaacgccc G/A tgctcagaaaaacagggcgct	6826
NDUFA9	39	(3' flanking region 554)	gtgccagcacttaggaatta T/G gaccttctaatagaagtcttt	6827
NDUFA9	40	(5' flanking region (-1129) - (-1128))	taaacagtaggggcaagata (TC) gagtggaaacagccaagatt	6828
NDUFA9	40	(5' flanking region (-1129) - (-1128))	taaacagtaggggcaagata gagtggaaacagccaagatt	6829
NDUFA9	41	(5' flanking region -341)	tggtttct c/g ttctccacttt T/Δ cccctgttcttctgtccc c/	6830
NDUFA9	42	(intron 4 594)	attcaactttttatcccccc T/Δ aatgattaacatagtgatt	6831
NDUFA9	43	(intron 10 356-375)	taacttctctctaactgtctt GAAGAACTGTTGACAGTT/Δ	6832
NDUFA9	44	(intron 10 379-381)	cttctctttttctttaacct	6833
NDUFA9	44	(intron 10 379-381)	gaaactgttgacagtttctt CCT/Δ tctttctttaacctactcca	6833
NDUFA9	45	(intron 10 384-387)	tggtgacagttttcttctctt TTTCT/Δ ttaacctactccagtcagg	6834
NDUFA9	46	(intron 10 436-437)	ccattttctccctataaatg (TCTTTTAAATG) ctcttttcaaggt	6835
NDUFA9	46	(intron 10 436-437)	ccattttctccctataaatg ctcttttcaaggt	6836
NDUFA9	47	(intron 10 495-496)	gccacatccaatggtcagtt (TTCAGGCCCTT) ctccagacctatgtca	6837
NDUFA9	47	(intron 10 495-496)	gccacatccaatggtcagtt ctccagacctatgtca	6838
NDUFA9	48	(intron 10 519-520)	gacctcatgtcatgtgctg (GGCCTG) tgcatttgcttctagggagg	6839
NDUFA9	48	(intron 10 519-520)	gacctcatgtcatgtgctg tgcatttgcttctagggagg	6840
NDUFA9	49	(intron 10 558-559)	gatgcaaaaataaaaataaaa (A) tactataccaataccacatc	6841
NDUFA9	49	(intron 10 558-559)	gatgcaaaaataaaaataaaa tactataccaataccacatc	6842
NDUFA10	1	(5' flanking region -1734)	tgcaccttgaactgtttact T/C tctgttaaccatttaccctt	6843
NDUFA10	2	(5' flanking region -1492)	aaaacatccacgcaaacagg T/C tgtgagaagttacgtctgcg	6844
NDUFA10	3	(intron 3 370)	aagactgtgcatgtgccaatg C/A agacagagatgtggatgcca	6845
NDUFA10	4	(intron 3 2485)	ttgttattttcttttctctg G/A aatgcagtgatcagttgaca	6846
NDUFA10	5	(intron 4 236)	ctgtgaaagcagattggagc C/T ctggacctcaaacacacgca	6847
NDUFA10	6	(intron 4 1742)	tgctggcatctgctgtagtct C/T tgctgaagtctgaggactgg	6848
NDUFA10	7	(intron 4 2090)	ggctgggggaaagcagatca T/C gttggctaaaggacaggtgg	6849
NDUFA10	8	(intron 4 3054)	cagctgattatactactgaa A/C cgggataaatg c/t agcttgat	6850
NDUFA10	9	(intron 4 3066)	ctactgaa a/c cgggataaatg C/T agcttgatgattttcagctg	6851
NDUFA10	10	(intron 4 3377)	gtcacagtttaaatgctgct G/A ttttactctgtgtaagtagc	6852
NDUFA10	11	(intron 5 46)	aagcatctctattttgaatg T/C agatcagcactaaaagccct	6853
NDUFA10	12	(intron 8 1465)	gcaacgcccagtttctggta C/T aggcctcatatccagcgtgc	6854
NDUFA10	13	(intron 8 1809)	cctggaggcacaaggtggc C/A ggggcactcaacttccctct	6855
NDUFA10	14	(intron 8 11226)	gttggtgactgtgtggggc A/G tctcacctctcgggctgca	6856
NDUFA10	15	(intron 8 11319)	atcttgcccttccctctgccc G/A tctgtttcaggcttgaactct	6857
NDUFA10	16	(intron 8 11386)	ccataatcctagcttgaacc C/T tcttttttccctgctgaccc	6858
NDUFA10	17	(intron 8 13361)	ccaggccactgattgttttc G/A cattttctagcattttctta	6859
NDUFA10	18	(intron 9 183)	ttctgtgtggaagctgat G/A aagtcctcagatgacagccc	6860
NDUFA10	19	(intron 9 8028)	gaggacattccacagaactg G/A tgactattagagcagaaggt	6861
NDUFA10	20	(intron 9 10742)	ctggaggagaggggtggagc C/G agttcagccagcactggggt	6862
NDUFA10	21	(intron 9 13908)	cacattgttatgtaaccaag C/T ct g/t gaattgcagtgtaaga	6863
NDUFA10	22	(intron 9 13911)	attgttatgtaaccaag c/t ct G/T gaattgcagtgtaagaact	6864
NDUFA10	23	(intron 9 14064)	tcttgactattagaaccct A/G tcagataaaattttaaaacag	6865
NDUFA10	24	(intron 9 14184)	tggttttggttgggaacagc G/A agagatacagaaccgacggt	6866
NDUFA10	25	(intron 9 16487)	cttgaagctgatcggtccct C/A cttgaagctgatcggtccct	6867
NDUFA10	26	(intron 9 16779)	gccagacgtgactgcttttag G/A ttctctatgacattcagacc	6868
NDUFA10	27	(intron 9 17663)	ttccaaatcaccacagaact T/G tgcatgattttgaagctcct	6869
NDUFA10	28	(5' flanking region (-1668) - (-1659))	gtaaaattgttttaactaga (C) 9-11 ttcttaaccaaggtataaa	6870

function. Analysis of genetic polymorphisms such as SNPs allows for the selection of drugs and the development of treatment protocols tailored to each individual patient (so-called "personalized" medical treatments). Instead of the using trial-and-error methods of matching patients with the right drugs, doctors may, for example, be able to analyze a patient's genetic profile and prescribe the best available drug therapy from the beginning. Not only would this take the guesswork out of finding the right drug, it would reduce the likelihood of adverse reactions, thus increasing safety.

SUMMARY OF THE INVENTION

The present invention identifies genetic polymorphisms relating to genes associated with drug metabolism. In some embodiments, the present invention provides methods for determining variations in sequences and genes associated with drug-metabolizing enzymes. In preferred embodiments, the present invention provides methods for collecting genetic polymorphism data for use in evaluating the effectiveness and safety of a drug based on the data, and screening drugs using the data. In some preferred embodiments, the polymorphisms of the present invention are used to evaluate a causal relationship between the genetic make-up of a patient and a response to an administered drug.

The present invention relates to genes encoding enzymes associated with drug metabolism (drug metabolizing enzymes, or DMEs). In particular, the present invention relates to sequence variations associated with variations in DMEs. In some embodiments, variations occur in coding regions of DMEs, such as may alter a function of the DMEs, (*e.g.*, by increasing or decreasing its level of activity, or shifting its activity to an alternative target or function). In other embodiments, the variations occur in non-coding regions of the genome, such as may alter expression of a DME (*e.g.*, increasing or decreasing the amount of an enzyme produced in a cell) or processing of an RNA transcript encoding a DME (*e.g.*, by altering splicing).

In some embodiments, the present invention provides methods for detecting DME-related sequence variations. In some preferred embodiments, the methods of the

present invention are used to create a profile of DME-related polymorphisms in a test subject.

In other embodiments, the present invention provides isolated nucleic acid sequences encoding variant DMEs. For example, the present invention provides a recombinant DNA vector comprising DNA having a nucleotide sequence encoding a variant DME, the nucleotide sequence comprising a sequence including, but not limited to, SEQ ID NOS:1-3360 and 3361-7669, and substantially similar sequences. In a preferred embodiment, the invention provides a host cell transformed with a recombinant DNA vector comprising DNA having a nucleotide sequence encoding a variant DME.

The invention is not limited by the nature of the host cell employed. The art is well aware of expression vectors suitable for the expression of nucleotide sequences encoding variant DMEs that can be expressed in a variety of prokaryotic and eukaryotic host cells. In some preferred embodiments, the host cell is a eukaryotic cell grown in culture, such as for use in *in vitro* drug screening (*e.g.*, by monitoring the expression of genes associated with the pathways targeted by a particular test drug). In other preferred embodiments, the host cell is *in vivo*.

The present invention provides systems and methods for detection of polymorphisms associated with genes encoding enzymes associated with drug metabolism. The present invention is not limited in the nature of the detection assay used for detection or identification of such polymorphisms. Such detection assays include, but are not limited to, hybridization methods and array technologies (*e.g.*, technologies available from Aclara BioSciences, Haywood, CA; Affymetrix, Santa Clara, CA; Agilent Technologies, Inc., Palo Alto, CA; Aviva Biosciences Corp., San Diego, CA; Caliper Technologies Corp., Palo Alto, CA; Celera, Rockville, MD; CuraGen Corp., New Haven, CT; Hyseq Inc., Sunnyvale, CA; Illumina, Inc., San Diego, CA; Incyte Genomics, Palo Alto, CA; Motorola BioChip Systems; Nanogen, San Diego, CA; Orchid BioSciences, Inc., Princeton, NJ; Applera Corp., Foster City, CA; Rosetta Inpharmatics, Kirkland, WA; and Sequenom, San Diego, CA); polymerase chain reaction-based methods (*e.g.*, TAQMAN, Applera Corp., GENECODE system, EraGen, Middleton, WI); branched hybridization methods; enzyme mismatch cleavage methods; NASBA;

sandwich hybridization methods; methods employing molecular beacons; ligase chain reactions, and the like.

Methods of the present invention find application in improving the drug discovery and approval processes. For example, the costs and risks of drug development may be reduced if only those persons capable of responding to a drug are selected for clinical trials. In addition, previously failed drug candidates may be revived as they are matched with more appropriate patient populations. Decreases in the number of adverse drug reactions, the number of failed drug trials, the time it takes to get a drug approved, the length of time patients are on medication, the number of medications patients must take to find an effective therapy, and an increase in the range of possible drug targets will promote a net decrease in the cost of health care.

Thus, in some embodiments, the present invention provides a method of identifying individuals having a polymorphism, comprising providing nucleic acid from a subject; and detecting the presence of at least one polymorphism in said nucleic acid, said at least one polymorphism including, but not limited to, polymorphisms found in SEQ ID Nos:1-3360 and 3361-7669. In some embodiments, the method further provides the step of providing a prognosis (e.g., a genotype relative risk or a population attributable risk) to the subject based on the presence or absence of the at least one polymorphism. In some embodiments, the detecting step is carried out using a detection assay including, but not limited to, a hybridization assay, a TAQMAN assay, an invasive cleavage assay, use of mass spectroscopy, a microarray, a polymerase chain reaction, a rolling circle extension assay, a sequencing assay, a hybridization assay employing a probe complementary to a polymorphism, a bead array assay, a primer extension assay, an enzyme mismatch cleavage assay, a branched hybridization assay, a NASBA assay, a molecular beacon assay, a cycling probe assay, a ligase chain reaction assay, and a sandwich hybridization assay.

The present invention also provides a nucleic acid (e.g., a gene, a probe, a primer, etc.) comprising a sequence selected from the group consisting of SEQ ID NO:1-3360 and 3361-7669 or complements thereof. In some embodiments, the nucleic acid molecule comprises a label. In some embodiments, the nucleic acid is attached to a solid

support (e.g., as part of a microarray). The present invention also provides vectors comprising the nucleic acid and host cell comprising the vector, as well as polypeptide encoded by the nucleic acid. Methods of producing and purifying polypeptides are well known in the art.

5 The present invention further provides kits for detecting a polymorphism, comprising at least one reagent that specifically detects a polymorphism in a sequence including, but not limited to, SEQ ID Nos:1-3360 and 3361-7669. In some embodiments, the kit further comprising instructions for determining whether the subject is at increased risk of having a drug metabolism disorder. In some embodiments, the at least one
10 reagent comprises a nucleic acid probe. The kits can be configured for a variety of uses including, but not limited to, use as an in vitro diagnostic detection assay, an analyte specific reagent detection assay, and a research-use-only detection assay.

 The present invention also provides a method for screening subjects for genetic markers associated with drug metabolizing enzyme(s), comprising: a) providing a
15 biological sample comprising a nucleic acid from a subject; b) testing the nucleic acid for a polymorphism in a genetic marker associated with a drug metabolizing enzyme, said genetic marker comprising one or more nucleotide polymorphisms designated by n, said n selected from a base substitution, an insertion, or a deletion found in a sequence selected from the group consisting of SEQ ID Nos:1-3360 and 3361-7669. The present
20 invention is not limited by the source of the nucleic acid. In some embodiments, the biological sample comprises blood, saliva, amniotic fluid, and tissue. In some embodiments, the subject is a human. In some preferred embodiments, the nucleic acid comprises DNA and/or RNA.

 The present invention further provides a composition comprising an array of
25 detection assays, said array comprising a plurality of drug metabolizing enzyme nucleotide polymorphism detection assays, one or more of said detection assays being capable of detecting one or more nucleotide polymorphisms designated by n in SEQ ID Nos:1-3360 and 3361-7669, wherein n represents a base substitution, insertion, or deletion compared to a wild-type sequence.

The present invention also provides a composition comprising a detection probe for determining the presence or absence of a single nucleotide polymorphism in a gene encoding a drug metabolizing enzyme, said gene comprising a sequence selected from the group consisting of SEQ ID Nos:1-3360 and 3361-7669.

5 The present invention further provides a method of determining the effectiveness of or side-effect of a drug or treatment protocol, comprising; a) administering a drug or treatment protocol to one or more subjects; b) obtaining nucleic acid from said one or more subjects; c) using a detection assay to detect the presence of at least one polymorphism in said nucleic acid from said one or more of subjects, said at least one
10 polymorphism selected from the group consisting of polymorphisms found in SEQ ID Nos:1-3360 and 3361-7669; and d) assigning an effectiveness rating, side-effect rating, or score for said drug or treatment protocol based upon a result of one or more said detection assays (*See e.g.*, Toxicology Testing Handbook: Principles, Applications, and Data Interpretation, ed. Jacobson-Kram and Keller, 2001, herein incorporated by
15 reference in its entirety).

The present invention also provides a method of prescribing a drug or treatment protocol for a subject, comprising; providing nucleic acid from said subject; using a detection assay to detect the presence of at least one polymorphism in the nucleic acid, said at least one polymorphism selected from the group consisting of polymorphisms
20 found in SEQ ID Nos:1-3360 and 3361-7669; and, prescribing said drug or treatment protocol based upon the result of said detection assay.

The present invention further provides a method for generating assay data comprising; obtaining a sample from a subject containing nucleic acid; transferring said sample to a laboratory; and receiving data from said laboratory, wherein said data
25 corresponds to the presence of at least one polymorphism in said nucleic acid, said at least one polymorphism selected from the group consisting of polymorphisms found in SEQ ID Nos:1-3360 and 3361-7669. The present further provides data sets generated by this method.

DEFINITIONS

To facilitate an understanding of the present invention, a number of terms and phrases are defined below:

As used herein, the terms "complementary" or "complementarity" are used in reference to polynucleotides (*i.e.*, a sequence of nucleotides such as an oligonucleotide or a target nucleic acid) related by the base-pairing rules. For example, for the sequence "5'-A-G-T-3'," is complementary to the sequence "3'-T-C-A-5'." Complementarity may be "partial," in which only some of the nucleic acids' bases are matched according to the base pairing rules. Or, there may be "complete" or "total" complementarity between the nucleic acids. The degree of complementarity between nucleic acid strands has significant effects on the efficiency and strength of hybridization between nucleic acid strands. This is of particular importance in amplification reactions, as well as detection methods that depend upon binding between nucleic acids. Either term may also be used in reference to individual nucleotides, especially within the context of polynucleotides. For example, a particular nucleotide within an oligonucleotide may be noted for its complementarity, or lack thereof, to a nucleotide within another nucleic acid strand, in contrast or comparison to the complementarity between the rest of the oligonucleotide and the nucleic acid strand. Nucleotide analogs used to form non-standard base pairs, whether with another nucleotide analog (e.g., an IsoC/IsoG base pair), or with a naturally occurring nucleotide (e.g., as described in U.S. Patent 5,912,340, herein incorporated by reference in its entirety) are also considered to be complementary to a base pairing partner within the meaning this definition.

The term "homology" and "homologous" refers to a degree of identity. There may be partial homology or complete homology. A partially homologous sequence is one that is less than 100% identical to another sequence.

As used herein, the term "hybridization" is used in reference to the pairing of complementary nucleic acids. Hybridization and the strength of hybridization (*i.e.*, the strength of the association between the nucleic acids) is influenced by such factors as the degree of complementary between the nucleic acids, stringency of the conditions involved, and the T_m of the formed hybrid. "Hybridization" methods involve the

annealing of one nucleic acid to another, complementary nucleic acid, *i.e.*, a nucleic acid having a complementary nucleotide sequence. The ability of two polymers of nucleic acid containing complementary sequences to find each other and anneal through base pairing interaction is a well-recognized phenomenon. The initial observations of the "hybridization" process by Marmur and Lane, Proc. Natl. Acad. Sci. USA 46:453 (1960) and Doty et al., Proc. Natl. Acad. Sci. USA 46:461 (1960) have been followed by the refinement of this process into an essential tool of modern biology.

With regard to complementarity, it is important for some diagnostic applications to determine whether the hybridization represents complete or partial complementarity.

For example, where it is desired to detect simply the presence or absence of a foreign DNA sequence, it is only important that the hybridization method ensures hybridization when the relevant sequence is present; conditions can be selected where both partially complementary probes and completely complementary probes will hybridize. Other diagnostic applications, however, may require that the hybridization method distinguish between partial and complete complementarity. It may be of interest to detect genetic polymorphisms. For example, human hemoglobin is composed, in part, of four polypeptide chains. Two of these chains are identical chains of 141 amino acids (alpha chains) and two of these chains are identical chains of 146 amino acids (beta chains). The gene encoding the beta chain is known to exhibit polymorphism. The normal allele encodes a beta chain having glutamic acid at the sixth position. The mutant allele encodes a beta chain having valine at the sixth position. This difference in amino acids has a profound (most profound when the individual is homozygous for the mutant allele) physiological impact known clinically as sickle cell anemia. It is well known that the genetic basis of the amino acid change involves a single base difference between the normal allele DNA sequence and the mutant allele DNA sequence.

The complement of a nucleic acid sequence as used herein refers to an oligonucleotide which, when aligned with the nucleic acid sequence such that the 5' end of one sequence is paired with the 3' end of the other, is in "antiparallel association." Certain bases not commonly found in natural nucleic acids may be included in the nucleic acids of the present invention and include, for example, inosine and 7-deazaguanine.

Complementarity need not be perfect; stable duplexes may contain mismatched base pairs or unmatched bases. Those skilled in the art of nucleic acid technology can determine duplex stability empirically considering a number of variables including, for example, the length of the oligonucleotide, base composition and sequence of the oligonucleotide, ionic strength and incidence of mismatched base pairs.

As used herein, the term " T_m " is used in reference to the "melting temperature." The melting temperature is the temperature at which a population of double-stranded nucleic acid molecules becomes half dissociated into single strands. Several equations for calculating the T_m of nucleic acids are well known in the art. As indicated by standard references, a simple estimate of the T_m value may be calculated by the equation: $T_m = 81.5 + 0.41(\% G + C)$, when a nucleic acid is in aqueous solution at 1 M NaCl (*see e.g.*, Anderson and Young, Quantitative Filter Hybridization, in Nucleic Acid Hybridization (1985). Other references (*e.g.*, Allawi, H.T. & SantaLucia, J., Jr. Thermodynamics and NMR of internal G.T mismatches in DNA. Biochemistry 36, 10581-94 (1997) include more sophisticated computations which take structural and environmental, as well as sequence characteristics into account for the calculation of T_m .

As used herein the term "stringency" is used in reference to the conditions of temperature, ionic strength, and the presence of other compounds, under which nucleic acid hybridizations are conducted. With "high stringency" conditions, nucleic acid base pairing will occur only between nucleic acid fragments that have a high frequency of complementary base sequences. Thus, conditions of "weak" or "low" stringency are often required when it is desired that nucleic acids that are not completely complementary to one another be hybridized or annealed together.

"High stringency conditions" when used in reference to nucleic acid hybridization comprise conditions equivalent to binding or hybridization at 42 C in a solution consisting of 5X SSPE (43.8 g/l NaCl, 6.9 g/l NaH_2PO_4 H_2O and 1.85 g/l EDTA, pH adjusted to 7.4 with NaOH), 0.5% SDS, 5X Denhardt's reagent and 100 $\mu\text{g/ml}$ denatured salmon sperm DNA followed by washing in a solution comprising 0.1X SSPE, 1.0% SDS at 42 C when a probe of about 500 nucleotides in length is employed.

"Medium stringency conditions" when used in reference to nucleic acid hybridization comprise conditions equivalent to binding or hybridization at 42 C in a solution consisting of 5X SSPE (43.8 g/l NaCl, 6.9 g/l NaH₂PO₄ H₂O and 1.85 g/l EDTA, pH adjusted to 7.4 with NaOH), 0.5% SDS, 5X Denhardt's reagent and 100 µg/ml denatured salmon sperm DNA followed by washing in a solution comprising 1.0X SSPE, 1.0% SDS at 42 C when a probe of about 500 nucleotides in length is employed.

"Low stringency conditions" comprise conditions equivalent to binding or hybridization at 42 C in a solution consisting of 5X SSPE (43.8 g/l NaCl, 6.9 g/l NaH₂PO₄ H₂O and 1.85 g/l EDTA, pH adjusted to 7.4 with NaOH), 0.1% SDS, 5X

Denhardt's reagent [50X Denhardt's contains per 500 ml: 5 g Ficoll (Type 400, Pharmacia), 5 g BSA (Fraction V; Sigma)] and 100 g/ml denatured salmon sperm DNA followed by washing in a solution comprising 5X SSPE, 0.1% SDS at 42 C when a probe of about 500 nucleotides in length is employed.

The term "gene" refers to a DNA sequence that comprises control and coding sequences necessary for the production of an RNA having a non-coding function (*e.g.*, a ribosomal or transfer RNA), a polypeptide or a precursor. The RNA or polypeptide can be encoded by a full-length coding sequence or by any portion of the coding sequence so long as the desired activity or function is retained.

The term "wild-type" refers to a gene or a gene product that has the characteristics of that gene or gene product when isolated from a naturally occurring source. A wild-type gene is that which is most frequently observed in a population and is thus arbitrarily designated the "normal" or "wild-type" form of the gene. In contrast, the term "modified," "mutant," or "polymorphic" refers to a gene or gene product that displays modifications in sequence and or functional properties (*i.e.*, altered characteristics) when compared to the wild-type gene or gene product. It is noted that naturally-occurring mutants can be isolated; these are identified by the fact that they have altered characteristics when compared to the wild-type gene or gene product.

The term "oligonucleotide" as used herein is defined as a molecule comprising two or more deoxyribonucleotides or ribonucleotides, preferably at least 5 nucleotides, more preferably at least about 10-15 nucleotides and more preferably at least about 15 to

30 nucleotides. The exact size will depend on many factors, which in turn depend on the ultimate function or use of the oligonucleotide. The oligonucleotide may be generated in any manner, including chemical synthesis, DNA replication, reverse transcription, PCR, or a combination thereof.

5 Because mononucleotides are reacted to make oligonucleotides in a manner such that the 5' phosphate of one mononucleotide pentose ring is attached to the 3' oxygen of its neighbor in one direction via a phosphodiester linkage, an end of an oligonucleotide is referred to as the "5' end" if its 5' phosphate is not linked to the 3' oxygen of a mononucleotide pentose ring and as the "3' end" if its 3' oxygen is not linked to a 5' phosphate of a subsequent mononucleotide pentose ring. As used herein, a nucleic acid sequence, even if internal to a larger oligonucleotide, also may be said to have 5' and 3' ends. A first region along a nucleic acid strand is said to be upstream of another region if the 3' end of the first region is before the 5' end of the second region when moving along a strand of nucleic acid in a 5' to 3' direction.

10 15 When two different, non-overlapping oligonucleotides anneal to different regions of the same linear complementary nucleic acid sequence, and the 3' end of one oligonucleotide points towards the 5' end of the other, the former may be called the "upstream" oligonucleotide and the latter the "downstream" oligonucleotide. Similarly, when two overlapping oligonucleotides are hybridized to the same linear complementary nucleic acid sequence, with the first oligonucleotide positioned such that its 5' end is upstream of the 5' end of the second oligonucleotide, and the 3' end of the first oligonucleotide is upstream of the 3' end of the second oligonucleotide, the first oligonucleotide may be called the "upstream" oligonucleotide and the second oligonucleotide may be called the "downstream" oligonucleotide.

20 25 The term "primer" refers to an oligonucleotide that is capable of acting as a point of initiation of synthesis when placed under conditions in which primer extension is initiated. An oligonucleotide "primer" may occur naturally, as in a purified restriction digest or may be produced synthetically.

30 A primer is selected to be "substantially" complementary to a strand of specific sequence of the template. A primer must be sufficiently complementary to hybridize

with a template strand for primer elongation to occur. A primer sequence need not reflect the exact sequence of the template. For example, a non-complementary nucleotide fragment may be attached to the 5' end of the primer, with the remainder of the primer sequence being substantially complementary to the strand. Non-complementary bases or longer sequences can be interspersed into the primer, provided that the primer sequence has sufficient complementarity with the sequence of the template to hybridize and thereby form a template primer complex for synthesis of the extension product of the primer.

The term "label" as used herein refers to any atom or molecule that can be used to provide a detectable (preferably quantifiable) effect, and that can be attached to a nucleic acid or protein. Labels include but are not limited to dyes; radiolabels such as ^{32}P ; binding moieties such as biotin; haptens such as digoxigenin; luminogenic, phosphorescent or fluorogenic moieties; and fluorescent dyes alone or in combination with moieties that can suppress or shift emission spectra by fluorescence resonance energy transfer (FRET). Labels may provide signals detectable by fluorescence, radioactivity, colorimetry, gravimetry, X-ray diffraction or absorption, magnetism, enzymatic activity, and the like. A label may be a charged moiety (positive or negative charge) or alternatively, may be charge neutral. Labels can include or consist of nucleic acid or protein sequence, so long as the sequence comprising the label is detectable.

The term "signal" as used herein refers to any detectable effect, such as would be caused or provided by a label or an assay reaction.

As used herein, the term "detector" refers to a system or component of a system, e.g., an instrument (e.g. a camera, fluorimeter, charge-coupled device, scintillation counter, etc.) or a reactive medium (X-ray or camera film, pH indicator, etc.), that can convey to a user or to another component of a system (e.g., a computer or controller) the presence of a signal or effect. A detector can be a photometric or spectrophotometric system, which can detect ultraviolet, visible or infrared light, including fluorescence or chemiluminescence; a radiation detection system; a spectroscopic system such as nuclear magnetic resonance spectroscopy, mass spectrometry or surface enhanced Raman

spectrometry; a system such as gel or capillary electrophoresis or gel exclusion chromatography; or other detection systems known in the art, or combinations thereof.

The term "sequence variation" as used herein refers to differences in nucleic acid sequence between two nucleic acids. For example, a wild-type structural gene and a mutant form of this wild-type structural gene may vary in sequence by the presence of single base substitutions and/or deletions or insertions of one or more nucleotides. These two forms of the structural gene are said to vary in sequence from one another. A second mutant form of the structural gene may exist. This second mutant form is said to vary in sequence from both the wild-type gene and the first mutant form of the gene.

The term "nucleotide analog" as used herein refers to modified or non-naturally occurring nucleotides such as 7-deaza purines (*i.e.*, 7-deaza-dATP and 7-deaza-dGTP). Nucleotide analogs include base analogs and comprise modified forms of deoxyribonucleotides as well as ribonucleotides.

The term "polymorphism" refers to the coexistence of more than one form of a gene or portion thereof. A portion of a gene of which there are at least two different forms, *i.e.*, two different nucleotide sequences, is referred to as a "polymorphic region of a gene". A polymorphic region can be a single nucleotide, the identity of which differs in different alleles. A polymorphic region can also be several nucleotides long.

A "polymorphic gene" refers to a gene having at least one polymorphic region.

The term "polymorphic locus" is a locus present in a population that shows variation between members of the population (*e.g.*, the most common allele has a frequency of less than 0.95). In contrast, a "monomorphic locus" is a genetic locus at little or no variations seen between members of the population (generally taken to be a locus at which the most common allele exceeds a frequency of 0.95 in the gene pool of the population).

A "non-human animal" of the invention can include mammals such as rodents, non-human primates, sheep, goats, horses, dogs, cows, chickens, amphibians, reptiles, etc. Preferred non-human animals are selected from the rodent family including rat and mouse, most preferably mouse, though transgenic amphibians, such as members of the *Xenopus* genus, and transgenic chickens can also provide important tools for

understanding and identifying drugs that can affect processes, *e.g.*, embryogenesis and tissue formation.

The term "operably linked" is intended to mean that the promoter is associated with the nucleic acid in such a manner as to facilitate transcription of the nucleic acid from the promoter.

The terms "protein", "polypeptide" and "peptide" are used interchangeably herein when referring to a gene product.

The term "recombinant protein" refers to a polypeptide which is produced by recombinant DNA techniques, wherein generally, DNA encoding the polypeptide is inserted into a suitable expression vector which is in turn used to transform a host cell to produce the heterologous protein.

A "regulatory element", also termed herein "regulatory sequence" is intended to include elements which are capable of modulating transcription from a basic promoter and include elements such as enhancers and silencers. The term "enhancer", also referred to herein as "enhancer element", is intended to include regulatory elements capable of increasing, stimulating, or enhancing transcription from a basic promoter. The term "silencer", also referred to herein as "silencer element" is intended to include regulatory elements capable of decreasing, inhibiting, or repressing transcription from a basic promoter. Regulatory elements are typically present in 5' flanking regions of genes.

However, regulatory elements have also been shown to be present in other regions of a gene, in particular in introns. Regulatory elements may also be present downstream of coding regions. Thus, it is possible that DME genes have regulatory elements located in introns, exons, coding regions, and 3' flanking sequences. Such regulatory elements are also intended to be encompassed by the present invention and polymorphisms in such elements can be identified by any of the assays that can be used to identify polymorphisms in regulatory elements in 5' flanking regions of genes.

The term "regulatory element" further encompasses "tissue specific" regulatory elements, *i.e.*, regulatory elements that affect expression of a DME gene preferentially in specific cells (*e.g.*, cells of a specific tissue). Gene expression occurs preferentially in a specific cell if expression in this cell type is significantly higher than expression in other

cell types. The term "regulatory element" also encompasses non-tissue specific regulatory elements, i.e., regulatory elements that are active in most cell types. Furthermore, a regulatory element can be a constitutive regulatory element, i.e., a regulatory element that constitutively regulates transcription, as opposed to a regulatory element that is inducible, i.e., a regulatory element which is active primarily in response to a stimulus. A stimulus can be, e.g., a molecule, such as a hormone, cytokine, heavy metal, phorbol ester, cyclic AMP (cAMP), or retinoic acid.

As used herein, the term "transfection" means the introduction of a nucleic acid, e.g., an expression vector, into a recipient cell by nucleic acid-mediated gene transfer.

The term "transduction" is generally used herein when the transfection with a nucleic acid is by viral delivery of the nucleic acid. "Transformation", as used herein, refers to a process in which a cell's genotype is changed as a result of the cellular uptake of exogenous DNA or RNA, and, for example, the transformed cell expresses a recombinant form of a polypeptide or, in the case of anti-sense expression from the transferred gene, the expression of a naturally-occurring form of the recombinant protein is disrupted.

As used herein, the term "transgene" refers to a nucleic acid sequence that has been introduced into a cell. Daughter cells deriving from a cell in which a transgene has been introduced are also said to contain the transgene (unless it has been deleted). A transgene can encode, e.g., a polypeptide, or an antisense transcript, partly or entirely heterologous, i.e., foreign, to the transgenic animal or cell into which it is introduced, or, is homologous to an endogenous gene of the transgenic animal or cell into which it is introduced, but which is designed to be inserted, or is inserted, into the animal's genome in such a way as to alter the genome of the cell into which it is inserted (e.g., it is inserted at a location which differs from that of the natural gene or its insertion results in a knockout). Alternatively, a transgene can also be present in an episome. A transgene can include one or more transcriptional regulatory sequence and any other nucleic acid, (e.g. intron), that may be necessary for optimal expression of a selected nucleic acid.

A "transgenic animal" refers to any animal, preferably a non-human animal, e.g. a mammal, bird or an amphibian, in which one or more of the cells of the animal contain heterologous nucleic acid introduced by way of human intervention, such as by

transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by microinjection or by infection with a recombinant virus. The term genetic manipulation does not include classical cross-breeding, or in vitro fertilization, but rather is directed to the introduction of a recombinant DNA molecule. This molecule may be integrated within a chromosome, or it may be extrachromosomally replicating DNA. In the typical transgenic animals described herein, the transgene causes cells to express a recombinant form of one of a protein, e.g. either agonistic or antagonistic forms. However, transgenic animals in which the recombinant gene is silent are also contemplated. Moreover, "transgenic animal" also includes those recombinant animals in which gene disruption of one or more genes is caused by human intervention, including both recombination and antisense techniques.

The term "treating" as used herein is intended to encompass curing as well as ameliorating at least one symptom of the condition or disease.

The term "sample" in the present specification and claims is used in its broadest sense. On the one hand it is meant to include a biological (*e.g.*, human) specimen. On the other hand, a sample may include a specimen of synthetic origin.

Biological samples may be animal, including human, fluid, solid (*e.g.*, stool) or tissue, as well as liquid and solid food and feed products and ingredients such as dairy items, vegetables, meat and meat by-products, and waste. Biological samples may be obtained from all of the various families of domestic animals, as well as feral or wild animals, including, but not limited to, such animals as ungulates, bear, fish, lagamorphs, rodents, etc.

The term "source of target nucleic acid" refers to any sample that contains or is suspected to contain nucleic acids (RNA or DNA). Particularly preferred sources of target nucleic acids are biological samples including, but not limited to blood, saliva, cerebral spinal fluid, pleural fluid, milk, lymph, sputum and semen.

The term "polymerization means" or "polymerization agent" refers to any agent capable of facilitating the addition of nucleoside triphosphates to an oligonucleotide.

Preferred polymerization means comprise DNA and RNA polymerases.

The term "ligation means" or "ligation agent" refers to any agent capable of facilitating the ligation (i.e., the formation of a phosphodiester bond between a 3'-OH and a 5' P located at the termini of two strands of nucleic acid). Preferred ligation means comprise DNA ligases and RNA ligases.

5 The term "reactant" is used herein in its broadest sense. The reactant can comprise, for example, an enzymatic reactant, a chemical reactant or light (e.g., ultraviolet light, particularly short wavelength ultraviolet light is known to break oligonucleotide chains). Any agent capable of reacting with an oligonucleotide to either shorten (i.e., cleave) or elongate the oligonucleotide is encompassed within the term
10 "reactant."

The term "nucleic acid sequence" as used herein refers to an oligonucleotide, nucleotide or polynucleotide, and fragments or portions thereof, and to DNA or RNA of genomic or synthetic origin that may be single or double stranded, and represent the sense or antisense strand. Similarly, "amino acid sequence" as used herein refers to
15 peptide or protein sequence.

The term "peptide nucleic acid" ("PNA") as used herein refers to a molecule comprising bases or base analogs such as would be found in natural nucleic acid, but attached to a peptide backbone rather than the sugar-phosphate backbone typical of nucleic acids. The attachment of the bases to the peptide is such as to allow the bases to
20 base pair with complementary bases of nucleic acid in a manner similar to that of an oligonucleotide. These small molecules, also designated anti gene agents, stop transcript elongation by binding to their complementary strand of nucleic acid (Nielsen, *et al.* Anticancer Drug Des. 8:53 63 [1993]).

As used herein, the terms "purified" or "substantially purified" refer to
25 molecules, either nucleic or amino acid sequences, that are removed from their natural environment, isolated or separated, and are at least 60% free, preferably 75% free, and most preferably 90% free from other components with which they are naturally associated. An "isolated polynucleotide" or "isolated oligonucleotide" is therefore a substantially purified polynucleotide.

population, the percentage likelihood of an allele being present in an individual having one or more particular characteristics, etc.

The term "cleavage structure" as used herein, refers to a structure that is formed by the interaction of at least one probe oligonucleotide and a target nucleic acid, forming a structure comprising a duplex, the resulting structure being cleavable by a cleavage agent, including but not limited to an enzyme. The cleavage structure is a substrate for specific cleavage by the cleavage means in contrast to a nucleic acid molecule that is a substrate for non-specific cleavage by agents such as phosphodiesterases that cleave nucleic acid molecules without regard to secondary structure (*i.e.*, no formation of a duplexed structure is required).

DESCRIPTION OF THE DRAWINGS

Figure 1 shows sample embodiments of TAQMAN probes.

Figure 2 represents one embodiment of the TAQMAN PCR method.

Figure 3 shows examples of probes labeled with fluorescent dyes.

Figure 4 shows a sample embodiment of an invasive cleavage structure, *e.g.*, for an INVADER assay.

Figure 5 shows one embodiment of a FRET probe, *e.g.*, for an INVADER assay.

Figure 6 shows one embodiment of an INVADER assay.

Figure 7 shows a diagram of an INVADER assay probe in which the allele does not match the probe.

Figure 8 shows one embodiment of allele identification using a ligation reaction.

Figure 9 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily B member 2 (ABCB2) gene.

Figure 10 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily B member 4 (ABCB4) gene.

Figure 11 shows a drawing of the structure of and SNP position in the microsomal epoxide hydrogenase 1 (EPHX1) gene.

Figure 12 shows a drawing of the structure of and SNP position in the cytoplasmic epoxide hydrogenase 2 (EPHX2) gene.

Figure 13 shows a drawing of the structure of and SNP position in the guanidinoacetate-N-methyltransferase (GAMT) gene.

Figure 14 shows a drawing of the structure of and SNP position in the nicotinamide-N-methyltransferase (NNMT) gene.

5 Figure 15 shows a drawing of the structure of and SNP position in the phenylethanolamine-N-methyltransferase (PNMT) gene.

Figure 16 shows a drawing of the structure of and SNP position in the phosphatidylethanolamine-N-methyltransferase (PEMT) gene.

10 Figure 17 shows a drawing of the structure of and SNP position in the glutathione-S-methyltransferase 3 (GSTM3) gene.

Figure 18 shows a drawing of the structure of and SNP position in the aldehyde dehydrogenase 5 (ALDH5) gene.

Figure 19 shows a drawing of the structure of and SNP position in the transglutaminase (TGM1) gene.

15 Figure 20 shows a drawing of the structure of and SNP position in the gamma glutamyltransferase (GGT1) gene.

Figure 21 shows a drawing of the structure of and SNP position in the NAD(P)H: quinone oxidettransferase (NQ01) gene.

20 Figure 22 shows a drawing of the structure of and SNP position in the p53-induced gene 3 (PIG3) of a quinone oxide transferase homologue.

Figure 23 shows a drawing of the structure of and SNP position in the NRH: quinone oxide transferase 2 (NQ02) gene.

Figure 24 shows a drawing of the structure of and SNP position in the sulfotransferase 1A1 (SULT1A1/STP1) gene.

25 Figure 25 shows a drawing of the structure of and SNP position in the sulfotransferase 1A2 (SULT1A2/STP2) gene.

Figure 26 shows a drawing of the structure of and SNP position in the sulfotransferase-related protein 3 (SULTX3) gene.

30 Figure 27 shows a drawing of the structure of and SNP position in the tyrosyl protein sulfotransferase (TPST1) gene.

Figure 28 shows a drawing of the structure of and SNP position in the tyrosyl protein sulfotransferase (TPST2) gene.

Figure 29 shows a drawing of the structure of and SNP position in the sulfotransferase 1A3 (SULT1A3/ STM/HAST) gene.

5 Figure 30 shows a drawing of the structure of and SNP position in the cerebroside transferase (CST) gene.

Figure 31 shows a drawing of the structure of and SNP position in the sulfotransferase 1C1 (SULT1C1) gene.

10 Figure 32 shows a drawing of the structure of and SNP position in the sulfotransferase 1C2 (SULT1C2) gene.

Figure 33 shows a drawing of the structure of and SNP position in the thyroid hormone sulfotransferase (ST1B2) gene.

Figure 34 shows a drawing of the structure of and SNP position in the hydrocarbon sulfotransferase 2 (CHST2) gene.

15 Figure 35 shows a drawing of the structure of and SNP position in the sulfotransferase 2A1 (SULT2A1) gene.

Figure 36 shows a drawing of the structure of and SNP position in the sulfotransferase 2B1 (SULT2B1) gene.

20 Figure 37 shows a drawing of the structure of and SNP position in the hydrocarbon sulfotransferase 4 (CHST4) gene.

Figure 38 shows a drawing of the structure of and SNP position in the hydrocarbon sulfotransferase 5 (CHST5) gene.

Figure 39 shows a drawing of the structure of and SNP position in the HNK-sulfotransferase (NHK-1ST) gene.

25 Figure 40 shows a drawing of the structure of and SNP position in the estrogen sulfotransferase (STE) gene.

Figure 41 shows a drawing of the structure of and SNP position in the alcohol dehydrogenase 1 (ADH1) gene.

30 Figure 42 shows a drawing of the structure of and SNP position in the alcohol dehydrogenase 2 (ADH2) gene.

Figure 43 shows a drawing of the structure of and SNP position in the alcohol dehydrogenase 3 (ADH3) gene.

Figure 44 shows a drawing of the structure of and SNP position in the alcohol dehydrogenase 6 (ADH6) gene.

5 Figure 45 shows a drawing of the structure of and SNP position in the alcohol dehydrogenase 7 (ADH7) gene.

Figure 46 shows a drawing of the structure of and SNP position in the short-chained alcohol dehydrogenase family (HEP27) gene.

10 Figure 47 shows a drawing of the structure of and SNP position in the L1 intracellular adhesion molecule (L1CAM) gene.

Figure 48 shows a drawing of the structure of and SNP position in the arylalkylamine-N-acetyltransferase (AANAT) gene.

Figure 49 shows a drawing of the structure of and SNP position in the N-actyltransferase homologue (ARD1) gene of *Saccharomyces cerevisiae*.

15 Figure 50 shows a drawing of the structure of and SNP position in the N-actyltransferase 1 (NAT1) gene.

Figure 51 shows a drawing of the structure of and SNP position in the N-actyltransferase 2 (NAT2) gene.

20 Figure 52 shows a drawing of the structure of and SNP position in the granzyme A (GZMA) gene.

Figure 53 shows a drawing of the structure of and SNP position in the granzyme B (GZMB) gene.

Figure 54 shows a drawing of the structure of and SNP position in the esterase D-formylglutathione hydrolase (ESD) gene.

25 Figure 55 shows a drawing of the structure of and SNP position in the dolichyl-diphosphooligosaccharide-protein glycosyltransferase (DDOST) gene.

Figure 56 shows a drawing of the structure of and SNP position in the microsomal glutathione-S-transferase (MGST1) gene.

30 Figure 57 shows a drawing of the structure of and SNP position in the alcohol dehydrogenase 5 (ADH5) gene.

Figure 58 shows a drawing of the structure of and SNP position in the glutathione-S-transferase M1 (GSTM1) gene.

Figure 59 shows a drawing of the structure of and SNP position in the glutathione-S-transferase M2 (GSTM2) gene.

5 Figure 60 shows a drawing of the structure of and SNP position in the glutathione-S-transferase M4 (GSTM4) gene.

Figure 61 shows a drawing of the structure of and SNP position in the glutathione-S-transferase Z1 (GSTZ1) gene.

10 Figure 62 shows a drawing of the structure of and SNP position in the glutathione-S-transferase P (GSTZPi) gene.

Figure 63 shows a drawing of the structure of and SNP position in the glutathione-S-transferase q1 (GSTT1) gene.

Figure 64 shows a drawing of the structure of and SNP position in the microsomal glutathione-S-transferase 1L1 (MGST1L1) gene.

15 Figure 65 shows a drawing of the structure of and SNP position in the microsomal glutathione-S-transferase 2 (MGST2) gene.

Figure 66 shows a drawing of the structure of and SNP position in the microsomal glutathione-S-transferase 3 (MGST3) gene.

20 Figure 67 shows a drawing of the structure of and SNP position in the glutathione-S-transferase A1 (GSTA1) gene.

Figure 68 shows a drawing of the structure of and SNP position in the glutathione-S-transferase A4 (GSTA4) gene.

Figure 69 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxide reductase 1a subcomplex 1 (NDUFA1) gene.

25 Figure 70 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxide reductase 1a subcomplex 2 (NDUFA2) gene.

Figure 71 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxide reductase 1a subcomplex 3 (NDUFA3) gene.

30 Figure 72 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxide reductase 1a subcomplex 5 (NDUFA5) gene.

Figure 73 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase 1a subcomplex 6 (NDUFA6) gene.

Figure 74 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase 1a subcomplex 7 (NDUFA7) gene.

5 Figure 75 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase 1a subcomplex 8 (NDUFA8) gene.

Figure 76 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase 1a/b subcomplex 1 (NDUFAB1) gene.

10 Figure 77 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase 1a subcomplex 9 (NDUFA9) gene.

Figure 78 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase Fe-S protein 1 (NDUFS1) gene.

Figure 79 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase Fe-S protein 3 (NDUFS3) gene.

15 Figure 80 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase Fe-S protein 4 (NDUFS4) gene.

Figure 81 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase Fe-S protein 5 (NDUFS5) gene.

20 Figure 82 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase Fe-S protein 6 (NDUFS6) gene.

Figure 83 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase Fe-S protein 8 (NDUFS8) gene.

Figure 84 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase 1b subcomplex 3 (NDUFB3) gene.

25 Figure 85 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase 1b subcomplex 5 (NDUFB5) gene.

Figure 86 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase 1b subcomplex 7 (NDUFB7) gene.

30 Figure 87 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily A member 1 (ABCA1) gene.

Figure 88 shows a drawing of the structure of and SNP position in the catechol-O-methyltransferase (COMT) gene.

Figure 89 shows a drawing of the structure of and SNP position in the vitamin-N-transferase (HNMT) gene.

5 Figure 90 shows a drawing of the structure of and SNP position in the cytochrome P450 subfamily 1 (aromatic compound-induced) polypeptide 1 (CYP1A1) gene.

Figure 91 shows a drawing of the structure of and SNP position in the cytochrome P450 subfamily 1 (aromatic compound-induced) polypeptide 2 (CYP1A2) gene.

10 Figure 92 shows a drawing of the structure of and SNP position in the cytochrome P450 subfamily 1 (dioxin-induced) polypeptide 1 (CYP1B1) gene.

Figure 93 shows a drawing of the structure of and SNP position in the arylacetamide deacylase (AADAC) gene.

Figure 94 shows a drawing of the structure of and SNP position in the neuropathy target esterase (NTE) gene.

15 Figure 95 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily C (CFTR/MRP) member 2 (MRP2) gene.

Figure 96 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily B member 1 (ABCB1) gene.

20 Figure 97 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily B member 3 (ABCB3) gene.

Figure 98 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily B member 7 (ABCB7) gene.

Figure 99 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily B member 8 (ABCB8) gene.

25 Figure 100 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily B member 9 (ABCB9) gene.

Figure 101 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily B member 10 (ABCB10) gene.

30 Figure 102 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily B member 11 (ABCB11) gene.

Figure 103 shows a drawing of the structure of and SNP position in the cytochrome P450 subfamily IVB polypeptide 1 (CYP4B1) gene.

Figure 104 shows a drawing of the structure of and SNP position in the cytochrome P450 subfamily XXVIIA polypeptide 1 (CYP27A1) gene.

5 Figure 105 shows a drawing of the structure of and SNP position in the cytochrome P450 subfamily IVF polypeptide 1 (CYP4F2) gene.

Figure 106 shows a drawing of the structure of and SNP position in the cytochrome P450 subfamily 4F polypeptide 3 (CYP4F3) gene.

10 Figure 107 shows a drawing of the structure of and SNP position in the cytochrome P450 subfamily 4F polypeptide 8 (CYP4F8) gene.

Figure 108 shows a drawing of the structure of and SNP position in the aldehyde dehydrogenase 1 (ALDH1) gene.

Figure 109 shows a drawing of the structure of and SNP position in the aldehyde dehydrogenase 2 (ALDH2) gene.

15 Figure 110 shows a drawing of the structure of and SNP position in the aldehyde dehydrogenase 7 (ALDH7) gene.

Figure 111 shows a drawing of the structure of and SNP position in the aldehyde dehydrogenase 8 (ALDH8) gene.

20 Figure 112 shows a drawing of the structure of and SNP position in the aldehyde dehydrogenase 9 (ALDH9) gene.

Figure 113 shows a drawing of the structure of and SNP position in the aldehyde dehydrogenase 10 (ALDH10) gene.

Figure 114 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily C member 7 (ABCC7) gene.

25 Figure 115 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily C member 8 (ABCC8) gene.

Figure 116 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily C member 9 (ABCC9) gene.

30 Figure 117 shows a drawing of the structure of and SNP position in the carboxylesterase 1 (CES1) gene.

Figure 118 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily A member 4 (ABCC4) gene.

Figure 119 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily A member 7 (ABCC7) gene.

5 Figure 120 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily G member 1 (ABCG1) gene.

Figure 121 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily G member 2 (ABCG2) gene.

10 Figure 122 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily G member 4 (ABCG4) gene.

Figure 123 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily E member 1 (ABCE1) gene.

Figure 124 shows a drawing of the structure of and SNP position in the carbohydrate sulfotransferase 1 (CHST1) gene.

15 Figure 125 shows a drawing of the structure of and SNP position in the carbohydrate sulfotransferase 3 (CHST3) gene.

Figure 126 shows a drawing of the structure of and SNP position in the NADH:ubiquinone dehydrogenase flavoprotein 1 (NDUFV1) gene.

20 Figure 127 shows a drawing of the structure of and SNP position in the NADH:ubiquinone dehydrogenase flavoprotein 2 (NDUFV2) gene.

Figure 128 shows a drawing of the structure of and SNP position in the NADH:ubiquinone dehydrogenase flavoprotein 3 (NDUFV3) gene.

Figure 129 shows a drawing of the structure of and SNP position in the NADH:ubiquinone oxidoreductase A10 (NDUFA10) gene.

25 Figure 130 shows a drawing of the structure of and SNP position in the high-mobility group protein 17-like 1 (HMG17L1) gene.

Figure 131 shows a drawing of the structure of and SNP position in the UDP glycosyl transferase 2 family polypeptide A1 (UGT2A1) gene.

30 Figure 132 shows a drawing of the structure of and SNP position in the human organic anion transporter polypeptide 1 (hOATP1) gene.

Figure 133 shows a drawing of the structure of and SNP position in the human organic anion transporter polypeptide 2 (hOATP2) gene.

Figure 134 shows a drawing of the structure of and SNP position in the human organic anion transporter polypeptide 8 (hOATP8) gene.

5 Figure 135 shows a drawing of the structure of and SNP position in the human organic anion transporter 1 (hOAT1) gene.

Figure 136 shows a drawing of the structure of and SNP position in the human organic anion transporter 2 (hOAT2) gene.

10 Figure 137 shows a drawing of the structure of and SNP position in the human organic anion transporter 3 (hOAT3) gene.

Figure 138 shows a drawing of the structure of and SNP position in the aldehyde dehydrogenase 1 family member A2 (ALDH1A2) gene.

Figure 139 shows a drawing of the structure of and SNP position in the aldehyde dehydrogenase 1 family member A3 (ALDH1A3) gene.

15 Figure 140 shows a drawing of the structure of and SNP position in the formyltetrahydroforate dehydrogenase (FTHFD/ALDH1L1) gene.

Figure 141 shows a drawing of the structure of and SNP position in the cytochrome P450 subfamily IIIA (aromatic compound-induced) polypeptide 4 (CYP3A4) gene.

20 Figure 142 shows graph of the results of typing performed on two different groups of subjects using the INVADER assay method.

Figure 143 shows a summary of genetic information.

Figure 144A shows a structure of ATP-binding cassette subfamily A member 1 (ABCA1) gene and the SNP location therein.

25 Accession No.: AF275948.1 and AL359846.11

Figure 144B shows a structure of ATP-binding cassette subfamily A member 1 (ABCA1) gene and the SNP location therein. (continuation of Figure 144A)

Accession No.: AF275948.1 and AL359846.11

30 Figure 145 shows a structure of ATP-binding cassette subfamily A member 4 (ABCA4) gene and the SNP location therein.

Accession No.: NT_019258.1

Figure 146 shows a structure of ATP-binding cassette subfamily A member 7 (ABCA7) gene and the SNP location therein.

Accession No.: NT_025194.1

5 Figure 147 shows a structure of ATP-binding cassette subfamily A member 8 (ABCA8) gene and the SNP location therein.

Accession No.: AC005922.1 and AC015844.5

Figure 148 shows a structure of ATP-binding cassette subfamily B member 1 (ABCB1) gene and the SNP location therein.

10 Accession No.: AC002457.1 and AC005068.1

Figure 149 shows a structure of ATP-binding cassette subfamily B member 4 (ABCB4) gene and the SNP location therein.

Accession No.: AC079591.1, AC079303.3 and AC005045.2

15 Figure 150 shows a structure of ATP-binding cassette subfamily B member 7 (ABCB7) gene and the SNP location therein.

Accession No.: AL360179.3 and AC002417.1

Figure 151 shows a structure of ATP-binding cassette subfamily B member 8 (ABCB8) gene and the SNP location therein.

Accession No.: AC010973.4

20 Figure 152 shows a structure of ATP-binding cassette subfamily B member 9 (ABCB9) gene and the SNP location therein.

Accession No.: AC026362.9 and AC073857.10

Figure 153 shows a structure of ATP-binding cassette subfamily B member 10 (ABCB10) gene and the SNP location therein.

25 Accession No.: AL121990.9

Figure 154 shows a structure of ATP-binding cassette subfamily B member 11 (ABCB11) gene and the SNP location therein.

Accession No.: AC008177.3 and AC069137.3

30 Figure 155 shows a structure of ATP-binding cassette subfamily C member 1 (ABCC1) gene and the SNP location therein.

Accession No.: AC026452.5 and AC025778.4

Figure 156 shows a structure of ATP-binding cassette subfamily C member 2 (ABCC2) gene and the SNP location therein.

Accession No.: AL392107.4

5 Figure 157 shows a structure of ATP-binding cassette subfamily C member 3 (ABCC3) gene and the SNP location therein.

Accession No.: AC004590.1 and AC005921.3

Figure 158A shows a structure of ATP-binding cassette subfamily C member 4 (ABCC4) gene and the SNP location therein.

10 Accession No.: AL356257.11, AL157818.12 and AL139381.12

Figure 158B shows a structure of ATP-binding cassette subfamily C member 4 (ABCC4) gene and the SNP location therein. (continuation of Figure 158A)

Accession No.: AL356257.11, AL157818.12, and AL139381.12

15 Figure 159 shows a structure of ATP-binding cassette subfamily C member 5 (ABCC5) gene and the SNP location therein.

Accession No.: AC068644.5

Figure 160 shows a structure of ATP-binding cassette subfamily C member 7 (ABCC7) gene and the SNP location therein.

Accession No.: AC000111.1 and AC000061.1

20 Figure 161 shows a structure of ATP-binding cassette subfamily C member 8 (ABCC8) gene and the SNP location therein.

Accession No.: AC000406.1

Figure 162 shows a structure of ATP-binding cassette subfamily C member 9 (ABCC9) gene and the SNP location therein.

25 Accession No.: AC084806.9 and AC008250.23

Figure 163 shows a structure of ATP-binding cassette subfamily D member 1 (ABCD1) gene and the SNP location therein.

Accession No.: U52111.2

30 Figure 164 shows a structure of ATP-binding cassette subfamily D member 3 (ABCD3) gene and the SNP location therein.

Accession No.: NT_019284.3

Figure 165 shows a structure of ATP-binding cassette subfamily D member 4 (ABCD4) gene and the SNP location therein.

Accession No.: AC005519.3

5 Figure 166 shows a structure of ATP-binding cassette subfamily G member 1 (ABCG1) gene and the SNP location therein.

Accession No.: AP001746.1

Figure 167 shows a structure of ATP-binding cassette subfamily G member 2 (ABCG2) gene and the SNP location therein.

10 Accession No.: NT_022959.2

Figure 168 shows a structure of ATP-binding cassette subfamily G member 4 (ABCG4) gene and the SNP location therein.

Accession No.: AP001315.3

15 Figure 169 shows a structure of ATP-binding cassette subfamily G member 5 (ABCG5) gene and the SNP location therein.

Accession No.: AC084265.2 and AC011242.8

Figure 170 shows a structure of ATP-binding cassette subfamily G member 8 (ABCG8) gene and the SNP location therein.

Accession No.: AC084265.2

20 Figure 171 shows a structure of ATP-binding cassette subfamily E member 1 (ABCE1) gene and the SNP location therein.

Accession No.: NT_006296.2

Figure 172 shows a structure of ATP-binding cassette subfamily F member 1 (ABCF1) gene and the SNP location therein.

25 Accession No.: NT_007592.3

Figure 173 shows a structure of organic anion transporter 1 (OAT1) gene and the SNP location therein.

Accession No.: AP001858.3, AJ249369.1, and AP000438.4

30 Figure 174 shows a structure of organic anion transporter 2 (OAT2) gene and the SNP location therein.

Accession No.: AC26532.3

Figure 175 shows a structure of organic anion transporter 3 (OAT3) gene and the SNP location therein.

Accession No.: AP001858.3

5 Figure 176 shows a structure of organic anion transporter polypeptide 1 (OATP1) gene and the SNP location therein.

Accession No.: AC022224.22

Figure 177 shows a structure of organic anion transporter polypeptide 2 (OATP2) gene and the SNP location therein.

10 Accession No.: NT_024399.2

Figure 178 shows a structure of organic anion transporter polypeptide 8 (OATP8) gene and the SNP location therein.

Accession No.: NT_024399.2

15 Figure 179 shows a structure of transporter 1 ATP-binding cassette subfamily B (TAP1) gene and the SNP location therein.

Accession No.: X66401.1

Figure 180 shows a structure of transporter 2 ATP-binding cassette subfamily B (TAP2) gene and the SNP location therein.

Accession No.: X66401.1

20 Figure 181 shows a structure of SLC22A4 solute carrier family 22 (organic cation transporter) member 4 (OCTN1) gene and the SNP location therein.

Accession No.: AC008599.6

Figure 182 shows a structure of SLC22A5 solute carrier family 22 (organic cation transporter) member 5 (OCTN2) gene and the SNP location therein.

25 Accession No.: AC023861.3

Figure 183 shows a structure of SLC22A1 solute carrier family 22 (organic cation transporter) member 1 (OCT1) gene and the SNP location therein.

Accession No.: AL35625.5

30 Figure 184 shows a structure of SLC22A2 solute carrier family 22 (organic cation transporter) member 2 (OCT2) gene and the SNP location therein.

Accession No.: AL162582.18

Figure 185 shows a structure of SLC10A2 solute carrier family 10 (sodium/bile acid cotransporter family) member 2 (NTCP) gene and the SNP location therein.

Accession No.: AL157789.6

5 Figure 186 shows a structure of SLC15A1 solute carrier family 15 (oligopeptide transporter) member 1 (PEPT1) gene and the SNP location therein.

Accession No.: AL353574.8 and AL391670.6

Figure 187 shows a structure of microsomal epoxide hydrolase 1 (EPHX1) gene and the SNP location therein.

10 Accession No.: AC058782.8

Figure 188 shows a structure of cytoplasmic epoxide hydrolase (EPHX2) gene and the SNP location therein.

Accession No.: AC010856.3

15 Figure 189 shows a structure of catechol-O-methyl transferase (COMT) gene and the SNP location therein.

Accession No.: AC000080.2

Figure 190 shows a structure of guanidinoacetate N-methyl transferase (GAMT) gene and the SNP location therein.

Accession No.: NT_000879.1

20 Figure 191 shows a structure of phenyl ethanolamine N-methyl transferase (PNMT) gene and the SNP location therein.

Accession No.: AC040933.3

Figure 192 shows a structure of histamine N-methyl transferase (HNMT) gene and the SNP location therein.

25 Accession No.: AC019304.3

Figure 193 shows a structure of nicotinamide N-methyl transferase (NNMT) gene and the SNP location therein.

Accession No.: AC019290.3

30 Figure 194 shows a structure of phosphatidylethanolamine N-methyl transferase (PEMT) gene and the SNP location therein.

Accession No.: AC020558.3

Figure 195 shows a structure of aldehyde dehydrogenase 1 family member A1 (ALDH1A1) gene and the SNP location therein.

Accession No.: AC009284.2 and AL162416.3

5 Figure 196 shows a structure of aldehyde dehydrogenase 1 family member A2 (ALDH1A2) gene and the SNP location therein.

Accession No.: AC025431.7 and AC012653.8

Figure 197 shows a structure of aldehyde dehydrogenase 1 family member A3 (ALDH1A3) gene and the SNP location therein.

10 Accession No.: AC015712.7

Figure 198 shows a structure of aldehyde dehydrogenase 1 family member B1 (ALDH1B1) gene and the SNP location therein.

Accession No.: AL135785.9

15 Figure 199A shows a structure of formyl tetrahydrofolate dehydrogenase (ALDH1L1) gene and the SNP location therein.

Accession No.: AC079848.6

Figure 199B shows a structure of formyl tetrahydrofolate dehydrogenase (ALDH1L1) gene and the SNP location therein. (continuation of Figure 199A)

Accession No.: AC079848.6

20 Figure 200 shows a structure of aldehyde dehydrogenase 2 (ALDH2) gene and the SNP location therein.

Accession No.: AC002996.1 and AC003029.2

Figure 201 shows a structure of aldehyde dehydrogenase 3 family member A1 (ALDH3A1) gene and the SNP location therein.

25 Accession No.: AC005722.1

Figure 202 shows a structure of aldehyde dehydrogenase 3 family member A2 (ALDH3A2) gene and the SNP location therein.

Accession No.: AC005722.1

30 Figure 203 shows a structure of aldehyde dehydrogenase 3 family member B1 (ALDH3B1) gene and the SNP location therein.

Accession No.: AC004923.2

Figure 204 shows a structure of aldehyde dehydrogenase 3 family member B2 (ALDH3B2) gene and the SNP location therein.

Accession No.: AC021987.3

5 Figure 205 shows a structure of aldehyde dehydrogenase 5 family member A1 (ALDH5A1) gene and the SNP location therein.

Accession No.: AL031230.1

Figure 206 shows a structure of aldehyde dehydrogenase 6 family member A1 (ALDH6A1) gene and the SNP location therein.

10 Accession No.: AC005484.2

Figure 207 shows a structure of aldehyde dehydrogenase 8 family member A1 (ALDH8A1) gene and the SNP location therein.

Accession No.: AL445190.9 and AL021939.1

15 Figure 208 shows a structure of aldehyde dehydrogenase 9 family member A1 (ALDH9A1) gene and the SNP location therein.

Accession No.: AL451074.4

Figure 209 shows a structure of alcohol dehydrogenase 1 (ADH1) gene and the SNP location therein.

Accession No.: AP002027.1

20 Figure 210 shows a structure of alcohol dehydrogenase 2 (ADH2) gene and the SNP location therein.

Accession No.: AP002027.1

Figure 211 shows a structure of alcohol dehydrogenase 3 (ADH3) gene and the SNP location therein.

25 Accession No.: AP002027.1

Figure 212 shows a structure of alcohol dehydrogenase 4 (ADH4) gene and the SNP location therein.

Accession No.: AP002026.1

30 Figure 213 shows a structure of alcohol dehydrogenase 5 (ADH5) gene and the SNP location therein.

Accession No.: AC019131.4

Figure 214 shows a structure of alcohol dehydrogenase 6 (ADH6) gene and the SNP location therein.

Accession No.: AP002026.1

5 Figure 215 shows a structure of alcohol dehydrogenase 7 (ADH7) gene and the SNP location therein.

Accession No.: AC027065.3

Figure 216 shows a structure of short-chain alcohol dehydrogenase family gene (HEP27) and the SNP location therein.

10 Accession No.: AL135999.3

Figure 217 shows a structure of UDP glycosyltransferase 1 family polypeptide A1 (UGT1A1) and the SNP location therein.

Accession No.: AC006985.2

15 Figure 218 shows a structure of UDP glycosyltransferase 2 family polypeptide A1 (UGT2A1) and the SNP location therein.

Accession No.: AC011254.3

Figure 219 shows a structure of UDP glycosyltransferase 2 family polypeptide B15 (UGT2B15) and the SNP location therein.

Accession No.: AC019173.4

20 Figure 220 shows a structure of UDP glycosyltransferase 8 (UGT8) and the SNP location therein.

Accession No.: U31353.1

Figure 221 shows a structure of glutathione S transferase A1 (GSTA1) gene and the SNP location therein.

25 Accession No.: AC021133.4

Figure 222 shows a structure of glutathione S transferase A4 (GSTA4) gene and the SNP location therein.

Accession No.: AC025085.4

30 Figure 223 shows a structure of glutathione S transferase M1 (GSTM1) gene and the SNP location therein.

Accession No.: AC000032.7

Figure 224 shows a structure of glutathione S transferase M2 (GSTM2) gene and the SNP location therein.

Accession No.: AC000031.5

5 Figure 225 shows a structure of glutathione S transferase Z1 (GSTZ1) gene and the SNP location therein.

Accession No.: AC007954.7

Figure 226 shows a structure of glutathione S transferase Pi (GSTPi) gene and the SNP location therein.

10 Accession No.: X08058.1 and M24485.1

Figure 227 shows a structure of glutathione S transferase T1 (GSTT1) gene and the SNP location therein.

Accession No.: AF240786.1 and AP000351.3

15 Figure 228 shows a structure of microsomal glutathione S transferase 1 (MGST1) gene and the SNP location therein.

Accession No.: AC007528.5

Figure 229 shows a structure of microsomal glutathione S transferase 1-like 1 (MGST1L1) gene and the SNP location therein.

Accession No.: AC007936.2

20 Figure 230 shows a structure of microsomal glutathione S transferase T2 (MGST2) gene and the SNP location therein.

Accession No.: AC019049.4

Figure 231 shows a structure of microsomal glutathione S transferase T3 (MGST3) gene and the SNP location therein.

25 Accession No.: AC064827.2

Figure 232 shows a structure of sulfotransferase 1A1 (SULT1A1/STP1) gene and the SNP location therein.

Accession No.: U52852.2

30 Figure 233 shows a structure of sulfotransferase 1A2 (SULT1A2/STP2) gene and the SNP location therein.

Accession No.: U33886.1, U34804.1 and AC020765.5

Figure 234 shows a structure of sulfotransferase 1A3 (SULT1A3/STM/HAST) gene and the SNP location therein

Accession No.: L34160.1 and AC012645.4

5 Figure 235 shows a structure of sulfotransferase 1C1 (SULT1C1) gene and the SNP location therein.

Accession No.: AC019100.4

Figure 236 shows a structure of sulfotransferase 1C2 (SULT1C2) gene and the SNP location therein.

10 Accession No.: AF186263.1

Figure 237 shows a structure of sulfotransferase 2A1 (SULT2A1) gene and the SNP location therein.

Accession No.: AC024582.4, AC008745.5, NT_011190.1, and AC024582.4

15 Figure 238 shows a structure of sulfotransferase 2B1 (SULT2B1) gene and the SNP location therein.

Accession No.: AC040922.2 and AC008403.6

Figure 239 shows a structure of sulfotransferase-associated protein 3 (SULTX3) gene and the SNP location therein.

Accession No.: Z97055.1

20 Figure 240 shows a structure of tyrosyl protein sulfotransferase 1 (TPST1) gene and the SNP location therein.

Accession No.: AC026281.5

Figure 241 shows a structure of tyrosyl protein sulfotransferase 2 (TPST2) gene and the SNP location therein.

25 Accession No.: Z95115.1

Figure 242 shows a structure of cerebroside sulfotransferase (CST) gene and the SNP location therein.

Accession No.: AC005006.2

30 Figure 243 shows a structure of thyroid hormone sulfotransferase (ST1B2) gene and the SNP location therein.

Accession No.: AC027059.2

Figure 244 shows a structure of carbohydrate sulfotransferase 1 (CHST1) gene and the SNP location therein.

Accession No.: NT_008982.1

5 Figure 245 shows a structure of carbohydrate sulfotransferase 2 (CHST2) gene and the SNP location therein.

Accession No.: AC055737.10

Figure 246 shows a structure of carbohydrate sulfotransferase 3 (CHST3) gene and the SNP location therein.

10 Accession No.: AC073370.3

Figure 247 shows a structure of carbohydrate sulfotransferase 4 (CHST4) gene and the SNP location therein.

Accession No.: AC010547.5

15 Figure 248 shows a structure of carbohydrate sulfotransferase 5 (CHST5) gene and the SNP location therein.

Accession No.: AC025287.3

Figure 249 shows a structure of HNK-sulfotransferase (HNK-1ST) gene and the SNP location therein.

Accession No.: AC012493.4

20 Figure 250 shows a structure of estrogen sulfotransferase (STE) gene and the SNP location therein.

Accession No.: AC074273.1

Figure 251 shows a structure of NAD (P)H: quinone oxidoreductase 1 (NQO1) gene and the SNP location therein.

25 Accession No.: M81596.1

Figure 252 shows a structure of NRH: quinone oxidoreductase 2 (NQO2) gene and the SNP location therein.

Accession No.: AB050248.1

30 Figure 253 shows a structure of p53-inducible gene 3 (PIG3) in a quinone oxidoreductase homolog and the SNP location therein.

Accession No.: AC008073.3

Figure 254 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 1 (NDUFA1) gene and the SNP location therein.

Accession No.: AC002477.1

- 5 Figure 255 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 2 (NDUFA2) gene and the SNP location therein.

Accession No.: AB054976.1

Figure 256 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 3 (NDUFA3) gene and the SNP location therein.

- 10 Accession No.: AC009968.6

Figure 257 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 5 (NDUFA5) gene and the SNP location therein.

Accession No.: AC073323.5

- 15 Figure 258 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 6 (NDUFA6) gene and the SNP location therein.

Accession No.: AL021878.1

Figure 259 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 7 (NDUFA7) gene and the SNP location therein.

Accession No.: AC010323.6

- 20 Figure 260 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 8 (NDUFA8) gene and the SNP location therein.

Accession No.: AL162423.10

Figure 261 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 9 (NDUFA9) gene and the SNP location therein.

- 25 Accession No.: AC005832.1

Figure 262 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 10 (NDUFA10) gene and the SNP location therein.

Accession No.: AC013469.8

- 30 Figure 263 shows a structure of NADH-dehydrogenase(ubiquinone)1 α / β -subcomplex 1 (NDUFAB1) gene and the SNP location therein.

Accession No.: AC008870.6

Figure 264 shows a structure of NADH-dehydrogenase(ubiquinone)1 β -subcomplex 3 (NDUFB3) gene and the SNP location therein.

Accession No.: AC007272.3

5 Figure 265 shows a structure of NADH-dehydrogenase(ubiquinone)1 β -subcomplex 5 (NDUFB5) gene and the SNP location therein.

Accession No.: AC068361.2

Figure 266 shows a structure of NADH-dehydrogenase(ubiquinone)1 β -subcomplex 7 (NDUFB7) gene and the SNP location therein.

10 Accession No.: AC010527.4

Figure 267 shows a structure of NADH-dehydrogenase(ubiquinone)Fe-S protein 1 (NDUFS1) gene and the SNP location therein.

Accession No.: AC007383.4

15 Figure 268 shows a structure of NADH-dehydrogenase(ubiquinone)Fe-S protein 3 (NDUFS3) gene and the SNP location therein.

Accession No.: AC067943.4

Figure 269 shows a structure of NADH-dehydrogenase(ubiquinone)Fe-S protein 4 (NDUFS4) gene and the SNP location therein.

Accession No.: AC024569.3

20 Figure 270 shows a structure of NADH-dehydrogenase(ubiquinone)Fe-S protein 5 (NDUFS5) gene and the SNP location therein.

Accession No.: AL139015.5

Figure 271 shows a structure of NADH-dehydrogenase(ubiquinone)Fe-S protein 6 (NDUFS6) gene and the SNP location therein.

25 Accession No.: AC026443.2

Figure 272 shows a structure of NADH-dehydrogenase(ubiquinone)Fe-S protein 8 (NDUFS8) gene and the SNP location therein.

Accession No.: AC034259.2

30 Figure 273 shows a structure of NADH-dehydrogenase(ubiquinone)flavoprotein 1 (NDUFV1) gene and the SNP location therein.

Accession No.: NT_009304.2

Figure 274 shows a structure of NADH-dehydrogenase(ubiquinone)flavoprotein 2 (NDUFV2) gene and the SNP location therein.

Accession No.: NT_011024.2

5 Figure 275 shows a structure of NADH-dehydrogenase(ubiquinone)flavoprotein 3 (NDUFV3) gene and the SNP location therein.

Accession No.: AP001748.1

Figure 276 shows a structure of gamma-glutamyl transferase 1 (GGT1) gene and the SNP location therein.

10 Accession No.: D87002.1

Figure 277 shows a structure of transglutaminase 1 (TGM1) gene and the SNP location therein.

Accession No.: M98447.1

15 Figure 278 shows a structure of cytochrome P450 subfamily 1 (aromatic compound-inducible) polypeptide 1 (CYP1A1) gene and the SNP location therein.

Accession No.: X04300.1 and AC020705.4

Figure 279 shows a structure of cytochrome P450 subfamily 1 (aromatic compound-inducible) polypeptide 2 (CYP1A2) gene and the SNP location therein.

Accession No.: AC020705.4

20 Figure 280 shows a structure of cytochrome P450 subfamily 1 (dioxin-inducible) polypeptide 1 (CYP1B1) gene and the SNP location therein.

Accession No.: AC009229.4

Figure 281 shows a structure of cytochrome P450 subfamily 3A (aromatic compound-inducible) polypeptide 4 (CYP3A4) gene and the SNP location therein.

25 Accession No.: AF280107.1

Figure 282 shows a structure of cytochrome P450 subfamily 3A (aromatic compound-inducible) polypeptide 5 (CYP3A5) gene and the SNP location therein.

Accession No.: AC005020.5

30 Figure 283 shows a structure of cytochrome P450 subfamily 3A polypeptide 7 (CYP3A7) gene and the SNP location therein.

Accession No.: AF280107.1

Figure 284 shows a structure of cytochrome P450 polypeptide 43 (CYP3A43) gene and the SNP location therein.

Accession No.: AC011904.3

5 Figure 285 shows a structure of cytochrome P450 subfamily IVB polypeptide 1 (CYP4B1) gene and the SNP location therein.

Accession No.: AL356793.10

Figure 286 shows a structure of cytochrome P450 subfamily IVF polypeptide 2 (CYP4F2) gene and the SNP location therein.

10 Accession No.: AC005336.1

Figure 287 shows a structure of cytochrome P450 subfamily IVF polypeptide 3 (CYP4F3) gene and the SNP location therein.

Accession No.: AD000685.1

15 Figure 288 shows a structure of cytochrome P450 subfamily IVF polypeptide 8 (CYP4F8) gene and the SNP location therein.

Accession No.: AC068845.3

Figure 289 shows a structure of cytochrome P450 subfamily XXVIA polypeptide 1 (CYP27A1) gene and the SNP location therein.

Accession No.: AC009974.7

20 Figure 290 shows a structure of cytochrome P450 subfamily XXVIIB polypeptide 1 (CYP27B1) gene and the SNP location therein.

Accession No.: AC025165.27

Figure 291 shows a structure of allylacetamide deacetylase (AADAC) gene and the SNP location therein.

25 Accession No.: AC068647.4

Figure 292 shows a structure of carboxyl esterase 1 (CES1) gene and the SNP location therein

Accession No.: AC007602.4

30 Figure 293 shows a structure of carboxyl esterase 2 (CES2) gene and the SNP location therein

Accession No.: AC027131.4

Figure 294 shows a structure of granzyme A (GZMA) gene and the SNP location therein.

Accession No.: AC091977.1

5 Figure 295 shows a structure of granzyme B (GZMB) gene and the SNP location therein.

Accession No.: AL136018.3

Figure 296 shows a structure of esterase D/formylglutathione hydrolase (ESD) gene and the SNP location therein.

10 Accession No.: AL136958.9

Figure 297A shows a structure of carboxyl ester lipase (bile salt-stimulated lipase) (CEL) gene and the SNP location therein.

Accession No.: AL138750.8, AL162417.20 and AF072711.1

15 Figure 297B shows a structure of carboxyl ester lipase (bile salt-stimulated lipase) (CEL) gene and the SNP location therein. (continuation of Figure 297A)

Accession No.: AL138750. , AL162417.20 and AF072711.1

Figure 298 shows a structure of interleukin 17 (cytotoxic T lymphocyte-associated serine esterase 8) (IL17) gene and the SNP location therein.

Accession No.: AL355513.11

20 Figure 299 shows a structure of ubiquitin carboxyl terminal esterase L3 (ubiquitin thiol esterase) (UCHL3) gene and the SNP location therein.

Accession No.: AL137244.28

Figure 300 shows a structure of dolichyl-diphosphooligosaccharide-protein glycosyltransferase (DDOST) gene and the SNP location therein.

25 Accession No.: D89060

Figure 301 shows a structure of neuropathy target esterase (NTE) gene and the SNP location therein.

Accession No.: AC021153

30 Figure 302 shows a structure of L1 cell adhesion molecule (L1CAM) gene and the SNP location therein.

Accession No.: U52112

Figure 303 shows a structure of arylalkylamine N-acetyltransferase (AANAT) gene and the SNP location therein.

Accession No.: U40391

5 Figure 304 shows a structure of N-acetyltransferase homolog (ARD1) gene of *Saccharomyces cerevisiae* and the SNP location therein.

Accession No.: U52112

Figure 305 shows a structure of N-acetyltransferase (NAT1) gene and the SNP location therein.

10 Accession No.: X17059

Figure 306 shows a structure of N-acetyltransferase 2 (NAT2) gene and the SNP location therein.

Accession No.: D10870

15 Figure 307 shows a structure of ATP-binding cassette subfamily B member 2 (ABCB2) gene and the SNP location therein.

Accession No.: X66401

Figure 308 shows a structure of ATP-binding cassette subfamily B member 3 (ABCB3) gene and the SNP location therein.

Accession No.: X66401

20 Figure 309 shows a structure of glutathione S transferase M3 (GSTM3) gene and the SNP location therein.

Accession No.: AF043105.1

Figure 310 shows a structure of glutathione S transferase M4 (GSTM4) gene and the SNP location therein.

25 Accession No.: M96233.1

Figure 311 shows a structure of aldehyde dehydrogenase 7 (ALDH7) gene and the SNP location therein.

Accession No.: AC004923

30 Figure 312 shows a structure of high-mobility group protein 17-like 1 (HMG17L1) gene and the SNP location therein.

Accession No.: Z97055.1

Figure 313 shows a printed representation of submissions from Laboratory for Genotyping, The SNP Research Center, The Institute of Physical and Chemical Research (RIKEN) on the IMS-JST JSNP database website

5

GENERAL DESCRIPTION OF THE INVENTION

The present invention provides a method of analysis of drug metabolizing enzymes by analysis of SNPs associated with their encoding genes. In some embodiments, the method of the present invention can be used in the selection of drugs based on, *e.g.*, particular characteristics of an individual patient or on characteristics of a target disease.

In some embodiments, the present invention provides a method for detecting a genetic polymorphism associated with a DME, wherein an oligonucleotide probe and/or oligonucleotide primer is created so as to include the genetic polymorphism site from genetic polymorphism data in a gene for encoding a drug metabolizing enzyme or so as to include the genetic polymorphism site in an amplified fragment when the gene encoding the drug metabolizing enzyme has been amplified, and wherein at least one genetic polymorphism in a gene for encoding the target drug metabolizing enzyme is detected using the oligonucleotide probe and/or oligonucleotide primer thus obtained.

The present invention further provides methods for evaluating a drug, wherein the effectiveness and safety of a drug metabolized by the drug metabolizing enzyme are evaluated based on the results obtained by the detection method.

In some embodiments, the present invention provides a method for screening a drug, wherein the drug to be used is selected based on the results obtained in the evaluation method. In other embodiments, the present invention provides a method for screening a drug, wherein the genetic polymorphism data associated with the gene encoding a DME in a control subject is compared to the genetic polymorphism data associated with the same gene in a test subject, and wherein a drug to be used is selected from the results of an analysis of the effectiveness and/or safety of the drugs metabolized by the drug metabolizing enzyme.

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
PEMT	80	intron 5 - 6636	ttttctctctcaccttttg T/C gttcagaggcagaggtgtgc	5515
PEMT	81	intron 5 - 6448	gttggggccaggtctctgacag G/A accctcgggaccagctcctg	5516
PEMT	82	intron 5 - 5218	ggagccctggctgaagaagc C/G ttacgaccaaggcctggagg	5517
PEMT	83	intron 5 - 4824	ggacagggccgggggttgagc G/A gctgcatgaaggaggagg	5518
PEMT	84	intron 5 - 4249	tcaccagagtgatttctctcg C/A ggcaggtgcctggggtagcc	5519
PEMT	85	intron 5 - 4230	gaggcaggtgcctggggttag C/T cactgggagggtccatgag	5520
PEMT	86	intron 5 - 4182	ggagagtaagggtggggggg G/A cacttaggacagggaagctg	5521
PEMT	87	intron 5 - 3369	ccaggtggggcggtgtgcct G/C tggcctggtgtgtggccag	5522
PEMT	88	intron 5 - 2625	cagggaagctgggcccgtgaa C/T gagctgggcttttggccac	5523
PEMT	89	intron 5 - 1200	attattgtgagcatgggaag A/T gcacatttgggtcacacatgt	5524
PEMT	90	intron 6 + 606	gcctggctagacgccaccca A/G tgaccctgatgatggcagca	5525
PEMT	91	intron 6 + 1229	tttggtccaggaaagggggac G/A gcagccaggagcgtctggtat	5526
PEMT	92	intron 7 + 716	atggagatgtgctcccccg C/G gggtcagaggacctgcggtc	5527
PEMT	93	intron 7 + 1537	ctctgggggacgcataagcc G/A cctccagaggacatcagcca	5528
PEMT	94	intron 7 + 1718	gggcttcacagtgcttgagc T/C ccccggtatgtaggaccca	5529
PEMT	95	intron 7 + 2695	ggctttgggggacctggac C/T catttctagaaaacagcctt	5530
PEMT	96	intron 8 + 140	ccagggctccaggtcagag C/T ggccatggttagcttacaatg	5531
PEMT	97	3'flanking + 179	tacttaggagcgctcagggg C/T tcacctggccatggccatgg	5532
PEMT	98	3'flanking + 394	gatgacactgtcattcctaa A/G tgaatggcctgtgtgctgacc	5533
ALDH1A1	1	intron 1 + 564	cattattttctcagccaagt T/C tgttgccattggagcagatg	5534
ALDH1A1	2	intron 1 + 710	gtcttgagagtaactctgaa C/T ttgctctgtttcacactgct	5535
ALDH1A1	3	intron 1 - 3868	ccctttttatatccagaata C/G agcctaaactcttctctctg	5536
ALDH1A1	4	intron 2 + 2933	taagtatgctatactatatt T/C gatagataactatactata	5537
ALDH1A1	5	intron 2 - 1646	caatgtgattaaactgaatgc C/T gcaaatatgcactgtatatg	5538
ALDH1A1	6	exon 3 + 54	caggcttttcagattggatc C/T ccgtggcgtactatggatgc	5539
ALDH1A1	7	intron 3 + 157	taggccccttaacattgaac T/G attctcaaatagtaactctgc	5540
ALDH1A1	8	intron 3 + 339	tgagctctctagatgatat G/A ttaggttttattcaagcattt	5541
ALDH1A1	9	intron 3 + 655	agcagtttagatgagtcagag C/A ataatatagttggggagg	5542
ALDH1A1	10	intron 3 + 735	gaagccaatttaacataaac C/A aataccaagatcaggtttca	5543
ALDH1A1	11	intron 3 + 863	gcaagtatgggtaatacaag G/A accatttattactcaaatat	5544
ALDH1A1	12	intron 3 + 1757	agatgacaagatttcttcta T/A ttcaaaaattccctagcaca	5545
ALDH1A1	13	intron 5 + 90	ttctctaaacagatggatg C/A ttatgtatttggtaaatgtg	5546
ALDH1A1	14	intron 6 + 213	caggaagccaacacaaagg T/C ttgggtgtcaaacagtcact	5547
ALDH1A1	15	intron 6 + 1323	ttttgaattaaattcttata C/T tgaattcttttaacttttta	5548
ALDH1A1	16	intron 7 + 638	gcaaaagaaagtgggtggaag C/A atactgtaccatgcacaaaa	5549
ALDH1A1	17	intron 9 + (1462-1463)	aatggaattctatgtttttt (T) gttgtgattatttatctatc	5550
ALDH1A1	17	intron 9 + (1462-1463)	aatggaattctatgtttttt gttgtgattatttatctatc	5551
ALDH1A1	18	intron 9 + 1757	tgatctagaatttagtttct A/G taaatgaatagaatccagtg	5552
ALDH1A1	19	intron 12 - 1383	aatcccacttattactctcc T/G gagagcttcaagtcctata	5553
ALDH1A1	20	3'flanking + 40	ttttaagtacaagttttggt T/C acagtgattttctctgttca	5554
ALDH1A2	1	5'flanking - 716	cagggtactctattctgagc C/G cgaggcgaggggagactcgca	5555
ALDH1A2	2	intron 1 + 314	cggtcccgactgcgcgggg G/Δ aaggcgtcggaaccgcttag	5556
ALDH1A2	3	intron 1 + (664-675)	ttttgaactgaagaacttac (T)11-13 ataacgaactgtgacatctt	5557
ALDH1A2	4	intron 1 + 1370	gcattgcagcttagaagtttt A/G ttttatgaggggtctctaac	5558
ALDH1A2	5	intron 1 + 1557	ggtagcttttttcagaattta A/Δ ttgggaagctcttccagttc	5559
ALDH1A2	6	intron 1 + 1934	tcagctcttttagtgagactt C/G taaattttctaaagacaagca	5560
ALDH1A2	7	intron 1 + (1971-1980)	agcatgtgggacaagcagta (T)9-11 aaactgtgaagcagagaagct	5561
ALDH1A2	8	intron 1 + 2295	tactgtaagacaatatgtta T/C tgtttttgtcttctgtaaac	5562
ALDH1A2	9	intron 1 + 2387	ttgggacccacatagatgta C/T tacttaaaataaatgaccag	5563
ALDH1A2	10	intron 1 + 2841	aggaatgtgcttttttaaac T/Δ agatggtgttagtcaaggag	5564
ALDH1A2	11	intron 1 + 3035	gacttttataattttgtata A/G ctgatattataggaatacac	5565
ALDH1A2	12	intron 1 + 3319	aaagagttatgtttttttt T/Δ ctgcatctgatattatagg	5566
ALDH1A2	13	intron 1 + 3474	ttgtctttttatttattcat T/C taaactctgtttttctgggg	5567
ALDH1A2	14	intron 1 + 4186	ccctccaaacctttaactaa G/C attgtctgttttgggtcataa	5568
ALDH1A2	15	intron 1 + 4222	cataaattgtcagtcacaaact A/G catgttaaatagaggacttca	5569
ALDH1A2	16	intron 1 + 4254	aggacttcaggttttttttt T/Δ aaatacttttccataactat	5570
ALDH1A2	17	intron 1 + 4397	ccctccactacatgggctt A/G tgttaccatgtggaattatc	5571
ALDH1A2	18	intron 1 + 5935	aactccaggttgcaaataga T/C gtttctggtatttttaagtag	5572
ALDH1A2	19	intron 1 + 6206	ttttgaaagccctctagca T/G ttctttaatttctttattga	5573
ALDH1A2	20	intron 1 + 9559	agataaattgatgaattatt C/T actctgtgtgctgtgatagat	5574
ALDH1A2	21	intron 1 + (9631-9632)	taaaaagaatttctaaaaga (AAGA) ccttttttttgaataactct	5575
ALDH1A2	21	intron 1 + (9631-9632)	taaaaagaatttctaaaaga ccttttttttgaataactct	5576
ALDH1A2	22	intron 1 + 12731	ctgaaatagaacacttttcag T/A gtacctgtgcagagcagtgaa	5577
ALDH1A2	23	intron 1 + 13442	cagtgctcataaagatccagc G/A gaaatcaaaatgtttcatat	5578
ALDH1A2	24	intron 1 + (14173-14176)	tctaaaaataaataaata AAAA/Δ gagaaaattaagtttaagat	5579
ALDH1A2	25	intron 1 + 14586	actcatttattgggtcaaac C/G cttcttcaaccttaggatag	5580
ALDH1A2	26	intron 1 + 14595	ttggttcaaaagccttcttca A/G ccttaggatatgcattgagg	5581
ALDH1A2	27	intron 1 + 14711	gtttgagacattaacttcta A/G tccaactgaagatgctagtt	5582
ALDH1A2	28	intron 1 + (15327-15337)	gaagagcacagtagaagac (T)9-11 aaccttagcaataactattga	5583
ALDH1A2	29	intron 1 + 17258	atcagtcacatgtgtgggc A/G tacaacacttaatttaaaat	5584

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCB2	1	5'flanking - 673	agctaaagatcaaaagcacc G/C cttttccaccagcctcgcg	1
ABCB2	2	5'flanking - 646	ccaccagcctcgcctgctg T/G tcccttcacggacactctag	2
ABCB2	3	5'flanking - 563	ttgcaagcgtggtgctac A/C ggcgaacctccctgcctccc	3
ABCB2	4	5'flanking - 236	gctttgcgcgcgcgctaac G/T tggtagggcgatctgccc	4
ABCB2	5	Intron3 + 408	aaggaaactgaggccaagac C/T ctaaatgctgaactgcaca	5
ABCB2	6	Exon4 + 153	cctccaccatggtcacccctg A/G tcaccctgcctctgcttttc	6
ABCB2	7	Intron4 + 289	gtattcttttagcatcaag G/T ggcataagctgtctcttttc	7
ABCB2	8	Intron4 + 291	attcttttagcatcaagg G/C catagctgtgtctcttttc	8
ABCB2	9	Intron5 - 63	ttcttcaggttaactgctg C/T ggttctttgttccctcca	9
ABCB2	10	Intron7 - 185	gtctctgccttctcttgc G/T gcttcttctatctctactoc	10
ABCB2	11	3'flanking + 71	agcgcacttttcagctgcgg G/A tgcctctctttttatcatcc	11
ABCB2	12	3'flanking + 129	aaatgcataccttttccct T/C aagcttttattctctatga	12
ABCB2	13	3'flanking + 459	cattcagggagggccagg G/A tggagctgcagactgtctg	13
ABCB4	1	exon3 + 3	aacacccttattttatagat C/T caatgactgagtcagaatt	14
ABCB4	2	intron3 + 45	cagcatctctactatacca T/C gctctgcttttaaggttctot	15
ABCB4	3	intron3 + 498	actcaalaggtgttaggag C/T agagacaattcaatcacagac	16
ABCB4	4	intron3 + 515	gagcagagacaattcaaac A/G gacagaagcttttagatgaga	17
ABCB4	5	intron6 + 1030	tagttttgccatgtagaatt G/C aaaaagtgatagatggtgt	18
ABCB4	6	intron6 + 1437	gttaagcctgcttccatcaa G/A ttgatttattcttcttctta	19
ABCB4	7	intron6 + 2449	ttgacttgcagacactgta G/A catacttattcttctctgt	20
ABCB4	8	intron7 + 451	ccttgctgcacctgtgctgt A/C taagtttgcttattatagt	21
ABCB4	9	intron7 + 530	agtagagacagctgctgcat C/G acaccggagacagatcaactg	22
ABCB4	10	intron7 - 152	aacaggaatcatgaatttaag T/C tgttaatgattgaagccct	23
ABCB4	11	exon8 + 40	aggataaattgtttatgctg C/T ctgggtaccatcatggccat	24
ABCB4	12	intron8 + 130	ctgggtgactccagatata T/C agaagggttgtaaaattct	25
ABCB4	13	intron8 + 248	aatacacaggaagcttctaa A/G taagtaggaagtcactct	26
ABCB4	14	intron8 + 531	ctaaaggtgaatgattca A/G tacgtcccttggaactcacc	27
ABCB4	15	intron8 + 4240	ctgaggttccagcttattctc T/A tagagctgttacttagtct	28
ABCB4	16	intron8 + 4343	tgtagaagaaaaaagggtt C/T atattacagagggtctgac	29
ABCB4	17	intron8 + 4677	cccaagatattctcataact G/C tccatagtgcttgggtgcc	30
ABCB4	18	intron9 + 113	tttaccaggttcaactatt A/G ttatcatttttgcctccaaa	31
ABCB4	19	intron9 + 982	tgctctatacagttttgtt T/A taagtttagtaaatgatta	32
ABCB4	20	intron11 + 457	tcacgttgggtgacagagt A/G agacttcatctcaaaaaaaa	33
ABCB4	21	intron11 + 1337	tactcttggggagcctatca G/C cagggtgggtcagatagc	34
ABCB4	22	exon12 + 3	tgtttcttttctgcagat A/T ctctcggcatttagtgcac	35
ABCB4	23	intron12 + 1288	cagaccacactaacctctag T/C tggacctcagggtgtcagt	36
ABCB4	24	intron13 + 206	tgtaggaagaaaatagcat G/A tggtagaccattgtgaaa	37
ABCB4	25	intron13 + 988	cogtorgtttggagcttgc T/G acccttcttctactctcca	38
ABCB4	26	intron13 + (1413-1414)	ttatcttctacttattgttt (T) ctacgttaagttatgctaat	39
ABCB4	26	intron13 + (1413-1414)	ttatcttctacttattgttt ctacgttaagttatgctaat	40
ABCB4	27	intron13 + 1931	cttgcaaatgttgccttccc A/G caaaaaaaaagggaaggat	41
ABCB4	28	intron23 + 784	agtatctctaaactcttgc T/C atgcaggaataattttta	42
ABCB4	29	intron25 + 158	gaaatatattactgtattaa T/C gctcagaacttaataaag	43
ABCB4	30	intron25 + 2920	ctgagcttctctatcatct T/A ttccattctctggatgctgt	44
ABCB4	31	intron29 + 411	cttctctacattgaattot A/C ggtctctgaactttgacttt	45
ABCB4	32	intron32 + 458	agaaatgaattgccttac T/C gagctaaactcgaagcaca	46
EPHX1	1	intron1 + 110	tgcaaatgtctctactag C/T ttctagtgcataaatattg	47
EPHX1	2	intron1 + 143	aaatattgtgtgagctcttc G/A ctgtcgtggccagtcacca	48
EPHX1	3	intron1 + 1097	aatccagagaggagataga T/G tggaggttcaagggtggaca	49
EPHX1	4	intron1 + 1717	ttccaagcagagcagggg T/C gctcgtgggctgtgtttgc	50
EPHX1	5	intron1 + 1772	aaactcgtgctttctctccc G/T tctgggtcttaactcagtg	51
EPHX1	6	intron1 + 2054	gaaatgtaacaggcaact A/G tggacacagaagtagatta	52
EPHX1	7	intron2 + 1414	atttccaaaatctgtttggg G/T gtaactgaaacttgggaa	53
EPHX1	8	exon3 + 174	taccctcaactcaagactaa G/A attgaaggtatgtttgcaa	54
EPHX1	9	intron3 + 6583	ctgtcaatacatgaagggg G/C ggcggggcactaagggtgg	55
EPHX1	10	intron4 + 34	agaggttccataactgccc G/A tctctgccaaagggtggccc	56
EPHX1	11	intron4 + 63	aaaggttggccgggtgtccc C/T acaaggtctctctccggcg	57
EPHX1	12	intron5 + 154	gcagtgctgaggcacgttg G/A ctggatctctctgtctgta	58
EPHX1	13	intron5 + 276	tgctgaccaaagctctggga T/C agcctgagcagaactcccc	59
EPHX1	14	exon6 + 130	gctgtgagctgctgtcccc G/T gtcaggaggaaggtattcta	60

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
EPHX1	15	intron8 + 206	ggcgctgctccggggg C/A cctcagtcagctccccagt	61
EPHX1	16	intron8 + 353	tggccctccagaaagaga A/G gggcctcagtgagggag	62
EPHX1	17	3'flanking + 708	aggtgcagactcatgcactc A/G gccctgaagagtgagag	63
EPHX2	1	5'flanking - (523-522)	aaagtcactggatagcccc (C) tccccgcccccaacagg	64
EPHX2	1	5'flanking - (523-522)	aaagtcactggatagcccc tccccgcccccaacagg	65
EPHX2	2	5'flanking - 522	aaagtcactggatagcccc T/C cccccgcccccaacagg	66
EPHX2	3	5'flanking - 521	aagtcactggatagcccc G/T cccccgcccccaacagg	67
EPHX2	4	5'flanking - 516	actggatagcccccccc G/C ccccccaacaggcttatg	68
EPHX2	5	5'flanking - 515	ctggatagcccccccc G/C ccccccaacaggcttatg	69
EPHX2	6	Intron1 - 74	tggctgcttctcaatgaata T/C gaacagtgtctgttccatg	70
EPHX2	7	Intron3 + 72	ggcattaggtcagaaatcca T/C tgaagtgaagcttgagatca	71
EPHX2	8	Intron4 + 473	gtgtgtctctactttatct A/G caaaagtgattgagtgag	72
EPHX2	9	Intron5 + 276	caagaaggatgttcaagg C/T catctgaactcaactttga	73
EPHX2	10	Intron8 + 8	tctgctctccgggtggg T/C gctgtcttgagctgtctta	74
EPHX2	11	Intron9 + 1573	atgtctgaagactgatga C/T gatggagcgtgcactgctc	75
EPHX2	12	Intron10 + 207	gaacaggatggagatgact T/C gtttattgtcttttaaga	76
EPHX2	13	Intron12 + 911	tgaagagactgcactgtc G/T catccacatactacaggga	77
EPHX2	14	Intron12 + 2425	atcttctcagctgagcaaac G/T gaggctcagagggcttaacc	78
EPHX2	15	Intron12 + 2460	ttaaccccaactggcccaag G/A ccaggtacatgattgggtca	79
EPHX2	16	Intron12 - 281	aagtccttcaagaattat T/C ataagtgatccttctcaat	80
EPHX2	17	Intron12 - 268	agattattatagtagtacc T/G tctcattataggaataatga	81
EPHX2	18	Exon13 + 50	cctgagtcggactttcaaaa G/T cctcttcagagcaagcgatg	82
EPHX2	19	Intron13 + 1739	tgtctgaacagggtttica G/T atgacatatttctttgta	83
EPHX2	20	Exon14 + 33	atgcataaagtctgtgaagc G/A gtaagagacatgcttggga	84
EPHX2	21	Intron14 + 314	ggattgaggtctaacctca T/C ggggtgcacactgtgtatgc	85
EPHX2	22	Intron14 + 878	attcccttattccttcacac G/T gctgtgaactcattcattca	86
EPHX2	23	Intron14 + 948	gcacaggctgggtatgaagc T/C ggggtgcacactgtcagctac	87
EPHX2	24	Intron15 + 259	agagggttttcaactcttt C/T agtcaggtctctcagagaa	88
EPHX2	25	Intron16 + 459	tctcattgtcaagcagaa G/G atgatttccaactctctggg	89
EPHX2	26	Intron16 + 645	gtaagtgaacacactgtac G/A tgcagagcttctgcagagac	90
EPHX2	27	Intron16 + 985	gtcattatcatcatgacc G/A atgaaaatgacaaactgca	91
EPHX2	28	3'flanking + 12	aggtgcttaccacacatct T/C gcatggatggcagcttgtt	92
EPHX2	29	3'flanking + 374	tgttcacggagaatgcacgg C/T atgggagtaaccctttccc	93
EPHX2	30	3'flanking + 544	tagccacactgctttctccc G/A gcttccctagcagagtttgc	94
GAMT	1	intron1 + 429	ctcggaagctgagctcagg G/A agacagctgtccccgggtg	95
GAMT	2	3'flanking + 626	cactgacctcttgccttga G/A agaagggcggctcctgtgct	96
NNMT	1	5'flanking - 228	ataattttctgacagctc A/T agtgcctcctgtgtctaca	97
NNMT	2	Intron1 + 44	ccccactaatgtgagtcata T/C agatggagctcagggcacg	98
NNMT	3	intron1 + 149	ggataaaacgaattattgt A/G tagccttccacagtttaca	99
NNMT	4	Intron2 + 158	agataggcccatgtgtgtgc G/A ttttagtaaatgtgtatg	100
NNMT	5	intron2 + 433	gctgtagccatccaagccta T/G agaacttggctgtgagtgtg	101
NNMT	6	intron2 - 3064	atcatctgactgtgaagttc G/T agttctgttgtaactcaagt	102
NNMT	7	intron2 - 260	attcatggaggaagtcaca T/G gttagaagcaggtgtctagg	103
NNMT	8	3'flanking + 71	ggctcagtggttggggcca A/G tgggtcatctaggacggagc	104
NNMT	1	5'flanking - 390	aagaggtgaatggctcggg G/A gcttgagaagagagatggg	105
PEMT	1	exon2 - 4	agctcagagacctcctggc C/T gtgtgggtgagctcctttcc	106
PEMT	2	intron4 + 39	actgtccagacggggtatc C/T cactgctgtgtgagccccac	107
PEMT	3	intron4 + 1317	accgtccccagctggcccca G/A cctcctgacatgggectctg	108
PEMT	4	intron4 + 1355	ctggagccaggctgcagccg A/G agtgcctggcctcctctggcg	109
PEMT	5	intron4 + 5825	gtccaggcactgtggcccta C/T gtggagctccagctctcca	110
PEMT	6	intron4 + 6028	ggcagtggtccaaagaccag G/C atggactcctctctctacc	111
PEMT	7	intron4 + 6078	atctgtaccctgcggactc C/T aactgcttctggtccctcac	112
PEMT	8	intron4 + 6089	cgcggctctacatggcttc A/G tgcacacccccgcagat	113
PEMT	9	intron4 + 6379	tcagggttccccctccatc G/A cctcctcacccctgccctctc	114
PEMT	10	intron4 + 7339	tgaaggaaatcctgccaaga C/T ggcagatgcacacggggtca	115
PEMT	11	intron4 + 7619	ctctgcacatgtgtccag A/G gaggaaagcatttgacagg	116
PEMT	12	intron4 + 8858	ggcatgtgtgtgtgtgt T/G gtgtgtgagtggtgtcatgt	117
PEMT	13	intron4 + 9029	tttctggaccagaaagctgc G/A tctctgtccagggcctcttg	118
PEMT	14	intron4 + 9056	ggcagggcctctgtgacttg C/T gggaaagctgagctgagctg	119
PEMT	15	intron4 + 9512	ctgagctgggcagcagcatt A/G ctctgtgtgtgtgtgcaact	120

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
PEMT	16	intron4 + 9523	agcagccttactctgtg G/C gctggcactggcctgtggg	121
PEMT	17	intron4 + 9622	gacaaagtgtacaacaaggt G/A tctcgaactgggtcagctca	122
PEMT	18	intron4 + 10776	ccattctgtggtcttctttt G/A aggtcgaatgaaattccatg	123
PEMT	19	intron4 + 10912	tctgcccactttgtctcaga G/C gtgcaacaaggccttcagga	124
PEMT	20	intron4 + 11590	ggacactggcctgatgcaga G/C gtgtgtctctctcctgcag	125
PEMT	21	intron4 + 12090	ggccagggcacccctaccag G/C ctgagtcacacctgtccagc	126
PEMT	22	intron4 + 12263	tacccgccttccagatgga G/A cgggctgctcagggactta	127
PEMT	23	intron4 + 12448	tctgttccctctcctgctt G/A tagttcttgggctaaaatc	128
PEMT	24	intron4 + 12730	tgggaccagtgcgcaccca C/T ggcaccaaggacgtgtgtc	129
PEMT	25	intron4 + 13240	ggctccaggcacacacggg T/C cccagtacacctgtcgttt	130
PEMT	26	intron4 + 13494	tcogtggaaactagagatgg T/C aactccctgcaggtgggc	131
PEMT	27	intron4 + 13817	aactctccctgctgctgag A/G cagatcttggagcctcgcc	132
PEMT	28	intron4 + 14773	ccgcccgtgtcttcatgccc C/T ctatgcctctcactgctgg	133
PEMT	29	intron4 + 14951	gtcctgaggcccccctccac G/A gagcctgggtgcccctaca	134
PEMT	30	intron4 + 16896	gcctgactgtcttggagao T/C ggtcttggcggcctgtg	135
PEMT	31	intron4 + 19439	ccaggagcctctgaggcag G/A gggcttctcaaccaacacac	136
PEMT	32	intron4 + 19559	attttgcagcctgtcact C/T cctttcatatgaagcaagg	137
PEMT	33	intron4 + 20051	acagcactgcggggccacg A/G cctctgcagagcatttcat	138
PEMT	34	intron4 + 20816	tggcctctgtgctccatc C/T agccacttcagtgacgtg	139
PEMT	35	intron4 + 21196	ggctggcctggcctggat C/G atcgtgacaggtttatgg	140
PEMT	36	intron4 + 21628	acagggtggggccaggcto G/T ggaagtggccggcgtgagc	141
PEMT	37	intron4 + 21586	ccgcttcccgtgctctgccc C/T gtacagaaagtgtccact	142
PEMT	38	intron4 + 22672	agcctccactgctgtgg G/C tgaaggcggggccgggc	143
PEMT	39	intron4 + 22713	tctaagcgtgtcttcttgg A/T ctgaaaaccaaacacctct	144
PEMT	40	intron4 + 23010	tgcggggcagcggggggga G/A ggcgagtggttccccaggt	145
PEMT	41	intron4 + 23588	gtcaggcgcctgcatccc C/T gcagccaaagtcttggcgga	146
PEMT	42	intron4 + 23627	gcactgcctgagccagga C/T ggtgaggtgggagccttcc	147
PEMT	43	intron4 + 23941	tggagggttgggactctaca G/A agpagagtggactcacggg	148
PEMT	44	intron4 + 24091	gacaccttctacgtcagc G/T ctgagacacgcccctgccc	149
PEMT	45	intron4 + 25348	caggccagtggaaatctac G/A taggtgaaagcatctcagc	150
PEMT	46	intron4 + 25603	taagcagtlaacactgatgc G/A tgaatgaaattccaacagca	151
PEMT	47	intron4 + 31540	cctccaggtgaggaacac T/C gtgaggagcatgcaacgtgc	152
PEMT	48	intron4 + 31637	gtgggtgagagccaggag G/A gtgagggtctcaaggtgtg	153
PEMT	49	intron4 + 31642	ctggagacgcaggacggtga G/A gggcttcaagggtgtgtt	154
PEMT	50	intron4 + 35593	ggaggagctgaaagagctgg G/A gctcgggtcaggtgttca	155
PEMT	51	intron4 + 35647	actttgaggcaccaccgac C/A tgcctgtcgtgaggagac	156
PEMT	52	intron4 + 35862	tccagtggtggtctgttcc G/T cgtctcagcagcactcag	157
PEMT	53	intron4 + 35882	ccgtctcagccgagcactca T/G cggccaggtgtgctgactc	158
PEMT	54	intron4 + 37141	ccacagggccggatgcttga T/C acttctcagctcaggcgtg	159
PEMT	55	intron4 + 38862	tggagagaccacctcagaca C/G caaggacgggcatgcatgg	160
PEMT	56	intron4 + 38872	acctcagacagcaaggacgg G/T catgcatggttcccggcag	161
PEMT	57	intron4 + 39140	atgtctcaaatctcccctcc C/T gggaaatctaggcacagtc	162
PEMT	58	intron4 + 39635	caggccaggagcaggtgg G/T cctcctcagaggagcagggc	163
PEMT	59	intron4 + 39713	actctgagcatgtgcttcc C/T tcttcttccagggcagca	164
PEMT	60	intron4 + 40436	cctgttctgcttggacccc G/A gaggcagacagaggccct	165
PEMT	61	intron4 + 47485	acaatgactgttgagccct C/T gaggcagctgtgtcacgtg	166
PEMT	62	intron4 + 48131	actggggatcctgaatccc G/A cctcctgatgccagtggagc	167
PEMT	63	intron4 + 48558	cacagtgtaactgttaggc C/G acggccacatcttgcggag	168
PEMT	64	intron4 + 48702	gagatggggcggttcggga G/A gcaaaagcagggaaggcaga	169
PEMT	65	intron4 + 50302	gcattgtcatggcagggc T/G gttcccaactgagtgaggcc	170
PEMT	66	intron4 + 54102	ggccgctgctcctgcagcc A/T tgggtctcctgtggcagttct	171
PEMT	67	intron4 + 54220	cccaggagcagatcttctcc G/A ccagacgtcttcttctcct	172
PEMT	68	intron4 + 54371	gcagataatgtcagctgg G/A tgcattgtgttctgtccc	173
PEMT	69	exon5 + 79	tggcctgtactctctaagc G/C tcaccatcctgctcctgaac	174
PEMT	70	intron5 - 6796	ggagggaagtcagcttctac A/C gatgtggtctccagcttcc	175
PEMT	71	intron5 - 6636	ttttctctctacccctttt T/C gttcagaggcagaggtgtgc	176
PEMT	72	intron5 - 6448	gttgggcaggctctgacag G/A accctcgggaccagctcctg	177
PEMT	73	intron5 - 5218	ggagccctggtgaagaagc C/G ttacgcccagggcctggagg	178
PEMT	74	intron5 - 4824	ggacaggccgggggtttagc G/A gctcgtgaggggggggg	179
PEMT	75	intron5 - 4249	tcaccagagtgatttctcgc G/A ggcagggtcctgggtagcc	180

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
PEMT	76	intron5 - 4230	gaggcagtgccctgggtag C/T cactggcggggtccatgag	181
PEMT	77	intron5 - 4182	ggagaglaagggtggggg G/A cacttggacagggaggtcg	182
PEMT	78	intron5 - 3369	ccagggtgggcccgtgct G/O tggcctggtgtggcccag	183
PEMT	79	intron5 - 2625	cagggaagctgggcccgtga C/T gaggctgggttttggccac	184
PEMT	80	intron5 - 1200	attattgtgagcatgggaag A/T gcacatttggcacacatgt	185
PEMT	81	intron6 + 606	gcctggctlagacgcccacca A/G tgacccctgatgtggcagca	186
PEMT	82	intron6 + 1229	tttgtccaggaaggggac G/A gcagccaggagcgctggat	187
PEMT	83	intron7 + 716	atggagatgtgtcccccg G/G gggcagaggacctggctc	188
PEMT	84	intron7 + 1537	ctctggggacgctaagcc G/A cctccagaggacatcagcca	189
PEMT	85	intron7 + 1718	gggttccaggtgtctgagc T/C ccccgccatgtaggaccca	190
PEMT	86	intron7 + 2695	ggcttgggggacccctggac C/T catttctagaaaacagcctt	191
PEMT	87	intron8 + 140	ccagggtcccgaggtcagc C/T ggccatggtagcttacaatg	192
PEMT	88	3'flanking + 179	tacttggaggcgtcaggg G/T tcacctggccatggccatag	193
PEMT	89	3'flanking + 394	gatgacactgtcttccctaa A/G tgaatggcctgtgtcgacc	194
GSTM3	1	5'flanking - 144	ccaacgcggccttagtgcg G/T cctggcagcggccctgtga	195
ALDH5	1	5'flanking - 2808	cttgacactgtggactctc C/T ccacgtcccctaataccatc	196
ALDH5	2	5'flanking - 2575	gcagtcccgccggtagaga A/G ggtccggtcttcccgctgt	197
ALDH5	3	5'flanking - 2537	tttgggtgaactgtaaaan C/T tgcctgtattoaggagata	198
ALDH5	4	5'flanking - 940	cttcaactatctgggaaca C/T tccactctgttttaatttca	199
ALDH5	5	5'flanking - 785	tgggaagctgaaneggat G/T ctgagacctgtgttgggg	200
ALDH5	6	exon1 + 183	ccgacaggtcaacccctaac C/T gggagggtcattggcacgt	201
ALDH5	7	exon1 + 257	ctgaaagcagcccggaag C/T cttccgctgggtcccat	202
ALDH5	8	exon1 + 320	gcggggccggctgtgaacc G/T cctggcagacctagtggagc	203
ALDH5	9	exon1 + 605	acttgcgcccgactcgcga C/T aggcaacactgtgttatga	204
ALDH5	10	3'flanking + 1527	aaagtccaactgtgaacc G/A tagaasaaactctgttcc	205
TGM1	1	exon2 + 179	tccgaatgcggcagatga C/T gactggggacctgaaccctc	206
TGM1	2	Intron9 - 811	acttaccactctgtctctc C/T tgcaggcctcttctgtca	207
TGM1	3	Intron9 - 272	ccgacactctgtaccttgc C/G ccactccacagcagcagc	208
TGM1	4	Intron10 + 54	tcagtcatgggtctctgt C/T ccaacttcacgcgtgactga	209
TGM1	5	Intron10 - 51	aggaggccgggggtcaggcc A/G cccctcagaccctctgtca	210
TGM1	6	Intron12 - 47	ggaggtccctgggggaagcc T/G catgtagggaagcaggctc	211
TGM1	7	Intron13 + 72	ggtaaggacatcagggg G/A gcgctaagccagcagcaggc	212
TGM1	8	Intron14 + 1671	atcttlaaccacaccccga C/G catgtggggaggttctca	213
TGM1	9	Intron14 + 1691	ccatgttggggaggttctc G/A tcttaaggatccgcagagc	214
TGM1	10	Intron14 - 1634	tccttgccctccctctcag G/A gaggctagaacaaccttcaa	215
TGM1	11	Intron14 - 1459	ggaaacccctcagaaccag T/C tccaagcgaalacttggc	216
TGM1	12	Intron14 - 801	cagaatecaaaagtgagtg G/C gaggcaaggagtcggtag	217
TGM1	13	Exon15 + 233	ctcgggttggagcttagccc T/C gtccagaggcaatggact	218
TGM1	14	Exon15 + 369	ggagtcagcttccacttga C/A tgggggaacagatctaata	219
GGT1	1	intron1 + 85	ttatccagtgaagtggtctcc G/A tcaactcttttctgttgg	220
GGT1	2	exon3 + 68	gacggccaggtccggatgt G/T gtggagctgtctggggcac	221
NQO1	1	1 intron 1 80	aggaggtttaggggttgg G/A ctgaattttgttcttgaact	222
PIG3	1	5'flanking region -47	gggaaggagaaaggaaaga G/A gggagggtgtttctgtta	223
PIG3	2	intron 2 243	taacacgggagcggcagag A/G agtccagcttcttagactc	224
PIG3	3	3'flanking region 282	agcaggcccccagccctgcc G/A ctactccctgggccccacc	225
NQO2	1	5'flanking region -434	tttctgttcaccacgggcc C/G tcaattctgaaccggatag	226
NQO2	2	5'flanking region -406	gtacccgggtaccagccag A/G gttgggggcccggggcgca	227
NQO2	3	5'untranslated region -102	tcctgcggctcctactggg A/O gtgcgctgtcgaaggtga	228
NQO2	4	intron 1 1919	tcactcaaatagagctgagt T/O agtcaactcagcttggacc	229
NQO2	5	intron 1 2004	acaaactcacatgccaccag C/G catatgatgaacatgtaa	230
NQO2	6	intron 1 3391	aaagcagagggtgtgcagg C/T gcccctggccctaggctagg	231
NQO2	7	intron 1 3456	caaggccctcatcctcagg G/A ggccaactcttctgttttag	232
NQO2	8	intron 1 3595	actgccagctttagggtca T/C tcttgaagtgtgtctgtg	233
NQO2	9	intron 1 3596	ctgccagctttagggtcat T/C ctgtgaagtgtgtctgtgt	234
NQO2	10	intron 1 3598	gccagcttttaggttcttc T/C tgaagtgtgtgtgtgtca	235
NQO2	11	intron 1 3651	ccctgcactttgaaggatg A/G atgtgacctctcccacatc	236
NQO2	12	intron 1 6036	tgtgtgcggcttctcat C/T cccagccctctgtctcatc	237
NQO2	13	intron 2 14	atggcagtgatgattccat A/G ttgtgagtaagacttttt	238
NQO2	14	intron 2 192	gccacgtggaagtgtataa C/T tatctgaattatctgttt	239
NQO2	15	intron 2 635	ccctctgttagccactagc A/C ccactccctgctctgcccc	240

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
NQO2	16	intron 2 885	agtagcccccctccccacc G/A gctgtgacaaacccaaatgt	241
NQO2	17	exon 3 139	ctgatttgatgcatgaac T/C ttgagccgaggccacagac	242
NQO2	18	intron 3 36	aatgctctatttataaac T/C atctttatgtttttat	243
NQO2	19	intron 3 728	aacgtggcataaacaccac T/C ctatgccaacaaagcagg	244
NQO2	20	intron 4 1577	tgccctcgacaccccttcc C/T gacaccagccctttcttac	245
NQO2	21	intron 4 1832	tcggccggccacgtggagcc C/T gctttcctctcgacccac	246
NQO2	22	intron 4 2583	tgtgttaagcacagctct C/T gtcccctccctgctgcca	247
NQO2	23	exon 5 330	ctgactgttcagcgtgcc A/G gccatctgagggcgtgat	248
NQO2	24	exon 5 405	atccaggattctacgatt C/T gctttgctccaggtatgac	249
NQO2	25	intron 5 21	gtatgtctcttgataagg A/T tcactatggatgttggagg	250
NQO2	26	intron 5 253	atggcaaacaaaggagtg T/C cagggtgcaggtgacgggg	251
NQO2	27	intron 6 2435	cccccttaaatcatttaac T/C gaatggtatgaacaggtgt	252
SULT1A1	1	5'flanking region -1597	gcagagtaaggactact C/G aagaaggaggaactgtgggt	253
SULT1A1	2	5'flanking region -1481	gaggggtatcttcatgaaga G/T tccaggaaaggttaagatt	254
SULT1A1	3	5'flanking region -1376	cgtttcatatgttactgat C/T atacaatggatctcagggtg	255
SULT1A1	4	5'flanking region -1375	ggtttcatatgttactgat A/G taacaatggatctcagggtg	256
SULT1A1	5	5'flanking region -1370	catagttactgatcataca A/G tgaatctcagggtgaacct	257
SULT1A1	6	exon 1B -65	aacctgcattccccacaca G/A caaccacatcagccactgc	258
SULT1A1	7	intron 1B 442	gagccaccctgcttaggct G/A tcttttctgagtcacag	259
SULT1A1	8	exon 1A -197	gctgggtgcccagcaggaa A/G tggtagacaaagggcgtg	260
SULT1A1	9	exon 1A -159	ctgctggcaggagacagc A/C caggaggtcctagagcttc	261
SULT1A1	10	exon 1A -95	gagaccttcacacccctga T/C atctgggcttgcccagca	262
SULT1A1	11	intron 1A 60	ctggtttcagcccagccc C/T gccactgactggttttga	263
SULT1A1	12	intron 1A 69	agccccagccccgacctga C/G tggctttgtagtgcggca	264
SULT1A1	13	intron 1A 174	tgtgtgtgttaagggaac G/A ggcctggctctggcccctga	265
SULT1A1	14	intron 6 11	catgaaggaggtgagaccac C/G tgtgaagcttccctcatgt	266
SULT1A1	15	intron 6 17	ggaggtgagacacactgga A/T gcttccctcatgtgacacc	267
SULT1A1	16	intron 6 35	gaagcttccctcatgtgac A/T cctggggccggccactcac	268
SULT1A1	17	intron 6 71	ctcacaggagaccaccaggg T/C caccagccccctccttgg	269
SULT1A1	18	intron 6 108	tggcagccccccacagcagg C/A cgggttccccatctgct	270
SULT1A1	19	intron 6 111	gcagccccccacagcagccc G/A gattccccatctgctctt	271
SULT1A1	20	intron 6 270	ctccctgccaagggtgtgc C/T acccaggccacagtcagtg	272
SULT1A1	21	intron 6 488	ttttacttttctgaatcag C/T aatccgagcctccactggg	273
SULT1A1	22	intron 6 509	aatccagagctccactgagg A/G gccctctgctgctcagaacc	274
SULT1A1	23	exon 7 600	ccctctgctgctcagaacc C/G aaaaaggagattcaaaagat	275
SULT1A1	24	exon 7 645	gagtttggggcaactcct G/A ccagagagacagctggactt	276
SULT1A1	25	exon 8 902	gctgtgagggggtcctgg G/A gtcactgcagaggaggtgtg	277
SULT1A2	1	5'flanking region -547	tgtttcttttctgttatg G/C atccatgctctgtccaccc	278
SULT1A2	2	5'flanking region -425	tgtgggtgacgtgggcaag G/A aacctggcaccttcaagac	279
SULT1A2	3	5'flanking region -358	ctttccaggcctgctctat C/T cagtttctctcttctgct	280
SULT1A2	4	5'flanking region -355	tccaggcctgctctatcca G/T ctttctctcttctgctgg	281
SULT1A2	5	5'untranslated region -28	actcggcgaggagggcac A/G aggcaggttcccaagact	282
SULT1A2	6	intron 1A 85	ctgactggccttgtgagtg G/A ggcaagtcaactcagcttccc	283
SULT1A2	7	exon 2 24	gagctatccaggacatctc T/C gcccggccatggagtagct	284
SULT1A2	8	intron 2 34	gccacccacccctctccagg T/C ggcagtcaccaacttggcca	285
SULT1A2	9	intron 5 77	cagcaaacctgtgtcgacac T/C ccttgcctctctccagtg	286
SULT1A2	10	intron 6 684	actgggtcccgagggtcga G/C gagctggctctatgggtttt	287
SULT1A2	11	3'untranslated region 895	gctctgagctgagagggg T/C tctggagtcactgcagagg	288
SULT1A2	12	3'flanking region 98	cctcccgctccagctctc A/T acttgccctgttggggagg	289
SULT1A2	13	3'flanking region 817	ccactgactcggggttggc A/C aggtgcccagggtggcaaa	290
SULT1A2	14	3'flanking region 1006	ccttcctcggaggctgct T/C taccgcctgaggggcgcct	291
SULT1A2	15	3'flanking region 1464	tccgtagccaggaaggtt C/T ggtgaccagagcagccccc	292
SULTX3	1	intron 1 332	cctgcttctccttttacct G/T ctggtgtgtgacctggac	293
SULTX3	2	intron 1 1167	taggaatggtaagcgtgtc G/A ttgcttctgtggcactca	294
SULTX3	3	intron 1 2872	catcttcactgagcagac G/A aagcttctggcctgggctg	295
SULTX3	4	intron 1 6242	caccttggcttttaccagc A/G tggaaacattttacctgaat	296
SULTX3	5	intron 1 6601	gcgtggcttctggaggagg C/T gagaggagagtgaggggccc	297
SULTX3	6	intron 1 6768	agcttgaaalgagccagact C/T tcttgggacctgttgacccc	298
SULTX3	7	intron 1 6905	agtactttgttttacctcc C/T catctcacaactttgccat	299
SULTX3	8	intron 1 7464	gccaggatcccttgaggagc G/A acatgaacacagccaggagc	300

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
SULTX3	9	intron 1 7833	tgcttcgggctgggcttggc G/A ggggcagctgtgtccgggc	301
SULTX3	10	intron 1 8189	caaacctggggcccttaatgc C/T gcacaccagagccctccttc	302
SULTX3	11	intron 1 8316	ctctcacacagggcgggagc C/G tcttccccttgaggcagagc	303
SULTX3	12	intron 1 8617	agacagagggctggggccaaag C/T cagggttgcgggcttctct	304
SULTX3	13	intron 1 8631	gccaaagccagggttgcggc G/T ctctcctggactgtcaggcc	305
SULTX3	14	intron 1 9493	ttttcctcttagagcttccc G/A tctgtctctgtctcaggcc	306
SULTX3	15	intron 1 10306	caggcggggagcctgaatgc C/T ggcgtctgtgggttgcggc	307
SULTX3	16	intron 1 11987	tcataaaalagatatcag T/C acacttttggaaatttag	308
SULTX3	17	intron 1 13085	ctctgtcccggtttagaga C/A agcccatgcccagagctct	309
SULTX3	18	intron 1 13108	ggcatgcccagagctcctgg G/A gatttccaccccagaaacgc	310
SULTX3	19	intron 2 700	gaaccatctggagctgttc C/T gtaactgctgcccaggagcc	311
SULTX3	20	intron 2 818	agccatagtagctacggc G/A atcagcgtcgggagggggc	312
SULTX3	21	intron 2 1677	actccacttcccctgaaccc C/T accccttcttctctctctg	313
SULTX3	22	intron 4 4954	cgctccgaagggcggggg C/T tggaggtctcaagacgtga	314
SULTX3	23	intron 5 3632	ccagctgactcccacaccag C/T ggtcagagaacattgtctt	315
SULTX3	24	intron 5 3662	acattgtctttaagggttc C/T gaagtgtcgaataaagaa	316
SULTX3	25	intron 6 1874	ctgtatctcagagagctgac A/G atggaagaaattctaaagca	317
SULTX3	26	intron 6 2133	agaccgttgcctcagttta T/G cccacagctcagccctcct	318
SULTX3	27	intron 6 2524	ggagggccagggctgcctg T/C gatgccagagcagctgact	319
SULTX3	28	intron 6 2573	agctcatactgctcctggg A/G tgtttatataaacactgcca	320
SULTX3	29	3'flanking region 12	gttcccgccgtgctgcag C/G gtttctgcttgggggtag	321
SULTX3	30	3'flanking region 445	ttcaagcctgttcttctga T/G ttctgttggagagagctcc	322
TPST1	1	5'flanking region -288	accgcgcccatgcccagct A/C atttttttgttttttt	323
TPST1	2	intron 1 3520	agaaagcagatgaatgaa C/G agtgacgcttgacaaacag	324
TPST1	3	intron 1 3610	ggcagaagagaaatagca A/G ctataaacaacaataaatt	325
TPST1	4	intron 1 20828	tattgtcttccacctgttca A/G tgtgtctgtcgtataagtc	326
TPST1	5	intron 1 -6761	aatccactacttcttctga T/C aattctagaggccacagaga	327
TPST1	6	intron 1 -544	tagaacaagtgaaatttta C/T gttcttagtggtttatggt	328
TPST1	7	intron 1 -526	tacgttcttagtggtttatg G/T ttggcagtttcccccaaca	329
TPST1	8	intron 1 -234	tcaagacatttaataatgca C/T atgttctcagctaacctttt	330
TPST1	9	intron 1 -48	ttatgtgggttttaagcatg A/G ttctaaasaaatttaataa	331
TPST1	10	intron 2 -18944	aaaacattagaactgggaag G/A ttataaatcttttagcttt	332
TPST1	11	intron 2 -18687	tatgtcacccataataacat A/G ttctcttaaaactagtacta	333
TPST1	12	intron 2 -18501	ttggaagtgaaacttaagta A/G gtgcctgaaanaacagggta	334
TPST1	13	intron 2 -159	gaatggggtatttccctcagt G/G ctgcccaactgctgctcttg	335
TPST1	14	intron 2 -19	acctgttgcttaaaactcac G/A cctgctttgttttccaggt	336
TPST1	15	intron 3 158	tgctggggaagaaagatgc C/G gtctggagctgttgaattt	337
TPST1	16	intron 3 3779	agcagggcacgtaccctccc C/T ggcacaccatgtgttacc	338
TPST1	17	intron 4 292	ttgtattttcattatgaac C/T atgaatatctcagctgaaa	339
TPST1	18	3'untranslated region 1518	gttctgtacatgttctaa T/G gttttgtagaacscgtgtgc	340
TPST1	19	3'flanking region 264	acggctcttggcctgcatc C/T ctttttgagtgaatttct	341
TPST2	1	intron 2 578	tcacctatcatctcactgc G/A aggatgccagatacctccc	342
TPST2	2	intron 2 789	cttaagccatcgtgcaggtc A/G ttctgtcttctgtctcaatt	343
TPST2	3	intron 3 2009	cccaggctggagtgatgag T/G gtgatctcggctcactgcaa	344
TPST2	4	intron 3 2017	ggagtgtagtgatct C/T ggcctcactgcaactccgcc	345
TPST2	5	intron 3 2035	ctcggctcactgcaacctcc G/A cctccgggttcaagcagtt	346
TPST2	6	intron 4 104	aatgttcagttctcaattc C/T tggctatctgatttcttct	347
TPST2	7	intron 4 379	taataaatcaacttttgt C/T cttttctgtcttataaggt	348
TPST2	8	intron 4 588	tactgcagcctgatactct G/T gcttaagccatcctctcac	349
TPST2	9	intron 4 626	cacccaggtcctctgtag C/T taggactgcaggtgcacgcc	350
TPST2	10	intron 4 718	cccaggctgtctagaactc C/G tggcctgaaggatgcccct	351
TPST2	11	intron 4 873	gttgatggccttattatac G/A ttctcattacagcttctagt	352
TPST2	12	intron 4 949	caaatattgaaatgggac C/G caggcctgagggaagacttt	353
TPST2	13	intron 4 1033	taagctcagcatttctgagc G/A tgtgtgtatttaggaata	354
TPST2	14	intron 4 1051	gcgtgtgctgattttaggaa A/G taacagttatcgtattgaa	355
TPST2	15	intron 4 1356	gattcagctacataccagc C/T gacattgacaggtgaatggc	356
TPST2	16	intron 4 1707	gtctccttaaaagggtgtc G/T ctgcccctggcttgcgccag	357
TPST2	17	intron 5 215	aagaccgcctgacccaaac G/A gtgaaccccgtctctacta	358
TPST2	18	intron 5 341	tgggagcagaggtcagct G/A agctgagatccagccgttgc	359
TPST2	19	intron 6 31	ggacttcaactggggttccc G/A ctgcttctgggtggccccc	360

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
TPST2	20	intron 6 273	gtitgtcgcactggggac A/G gggcaggagccaccatg	361
TPST2	21	intron 6 693	aaaggggtttttgaactt G/C gtaattcaagatttaagat	362
TPST2	22	intron 6 1635	tctcgggtacagaggtggcc T/G tgaacaaacatgagctctc	363
TPST2	23	3'untranslated region 1147	cttcccactttcagatctc C/T gcaaatgacttcatggcaa	364
SULT1A3	1	exon 8 843	cgcttcgatcgccactatgc G/A gagaagatggcaggctcag	365
CST	1	intron 1b 6302	agagctccccagagaggact A/G tgaggctgatgatcatga	366
CST	2	intron 2a 1004	gagtgagccccatctcta C/T aaaaattttttttaaagta	367
CST	3	intron 2a 1395	atgcctaagtttaccagtagc T/C aggcaggaaaggcacaacca	368
CST	4	intron 1d 473	ccagagccctgaggttggtgc T/A ggggccccctcatgagctgcc	369
GST	5	intron 2b 726	ctatctctccagtgccctctc T/C gtcctgtctggaccctgct	370
CST	6	intron 2b 745	ctgtccctgtctgacccctg C/A tggggggccacagagccggc	371
CST	7	exon 3 85	tcactagtgttctgtctgtc G/A tgaactctatgcccgtgcc	372
CST	8	intron 3 308	tgtctgaggtcaggagttc G/A agaccagcctggccaacatg	373
CST	9	intron 3 853	ttttgtctataaaatggca G/A ttctatgtggcccaagctga	374
CST	10	exon 4 198	gagcagtgatccgggcaa C/T ggtcggcggggagtgcca	375
SULT1C1	1	intron 3 2280	gcaaatitttgatlttta G/T taccgtcagggttttaccat	376
SULT1C1	2	intron 3 3742	gcagatctcactttctggca G/A attccctgaattgtctccc	377
SULT1C1	3	intron 3 4453	ttcataggccttttccctca C/T ttgttttgtaattgtata	378
SULT1C1	4	intron 3 5234	gaaaagagactagaggcagg A/G gagctttgcagttctttaa	379
SULT1C1	5	intron 3 6175	tggctggcaggaggtgagg G/C agtctctctctctctgctcc	380
SULT1C1	6	intron 4 205	acatgaggcaggatccaga T/C tgaatgtttggagggaacta	381
SULT1C1	7	intron 4 408	ggctcagcctgttaatacca G/C caatttggaggccagggcg	382
SULT1C1	8	intron 4 429	caatttggaggccagggcg G/C gtggtacacaaagtccaggag	383
SULT1C2	1	5'flanking region -110	tcctgttaactcacagagaa C/T ggaagggtggaacgggacc	384
SULT1C2	2	exon 1 15	gcactaatggccttaccaga C/G atggagggttttaccattga	385
SULT1C2	3	intron 1 297	gtgactgtgtttttttttc A/C ttcccaatctaggcccttat	386
SULT1C2	4	intron 1 363	gagtggtgagctgagagg T/G gttcctgtggtctgatttggg	387
SULT1C2	5	intron 1 2300	gggtctactatcagcagccac C/T acctcaggaggtgacttc	388
SULT1C2	6	intron 2 455	agagcttggagcaaataga T/G aaaaaaaacatctagaact	389
SULT1C2	7	intron 4 55	caaaatctccaaacacccta G/A agggaaagatcttttcttt	390
SULT1C2	8	intron 4 111	ctgctctttaaagtgacaa T/C tctcactctcttcaggact	391
SULT1C2	9	intron 5 1857	ctttgtgttactttgttt T/G acttggtaaaaaagtgtgt	392
SULT1C2	10	intron 5 2082	tctctcctagagatggagg C/A gtcccacagccacagtgatg	393
SULT1C2	11	intron 6 933	agctactgaacctctccac A/G taactgtatttcaggggcag	394
ST1B2	1	intron 1 80	acttgccataaaatcatta G/T catcttaataaagttaata	395
ST1B2	2	intron 2 -352	aacatttaaatgacttlla T/C agcaatgcacaggtataata	396
ST1B2	3	intron 2 -85	attacataatgctcaaaat G/A tcttgaaaaactggttgca	397
ST1B2	4	intron 4 460	gtactgacattaaaaata T/C ctgatgttataatccata	398
ST1B2	5	intron 4 470	ttaaaaaatatctgatgttt A/G tatatccataaagactaat	399
ST1B2	6	intron 4 518	tttaagattgtctcatatt C/G ttacttctttgtttactaa	400
ST1B2	7	intron 4 616	aattgtttatgaaatagact T/C ttatctgttttttagtgccct	401
ST1B2	8	intron 5 58	ctgcctcatgctgtaaaagg G/A ttgatatttgccttccact	402
ST1B2	9	exon 6 612	taatagaatcaaaagaggga A/C atcaagaagatcattagatt	403
ST1B2	10	intron 6 582	aatacattacttccatttaa G/A tagtctgtttttgtggctt	404
ST1B2	11	intron 6 3130	agatgaaaaatttttcaa A/T ttttaaaagccttgaaaatt	405
ST1B2	12	3'untranslated region 907	tttaaatgtctcaatcaca C/A atctgaagaataagagatt	406
ST1B2	13	3'flanking region 50	tcagatccagttttgttcc T/G ttgattctgatttccaaat	407
ST1B2	14	3'flanking region 328	tttgaccaggacactgtgt T/G ccactgtctgtaccagggtt	408
ST1B2	15	3'flanking region 446	gtatgtcagattttgaaat C/A tttttctatctatcccta	409
CHST2	1	5'flanking region -260	agccggacagtcggcgggc G/A gtgacccggggccgctccc	410
CHST2	2	5'flanking region -56	gcgctggggaccagccggc C/T gccgcctcggagtcgggc	411
CHST2	3	3'flanking region 218	agggatgaacacatctttg T/A attctaaggcagaaccaa	412
CHST2	4	3'flanking region 383	gcagagaccaatgttttgt G/C ctgagctgtgttcagaaaaa	413
CHST2	5	3'flanking region 952	tactgaacattctgcagaa T/C gttatactctggaagaaat	414
SULT2A1	1	intron 2 478	ggctgggctctgtacacac T/C tcttctactgtgtgaatt	415
SULT2A1	2	intron 3 382	caaaaccccttaaatctt G/A ttctatctgtctcagaact	416
SULT2A1	3	intron 3 409	tcgtctcagaactgtgtgc A/G tgactctaggatcgclalat	417
SULT2A1	4	intron 5 249	agctgaaattacaggcaca C/T gccaccacaccagctaatt	418
SULT2A1	5	intron 5 395	aggaatgagccacggcggc G/A gccaatatcagctttaat	419
SULT2A1	6	3'flanking region 33	ttctctgttaaaagttaaca G/C ggttggcaggccaggtgt	420

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
SULT2A1	7	3'flanking region 46	gttaccagggtggccaggc A/G cgggtgttcacgtctgaat	421
SULT2A1	8	3'flanking region 199	ttagccaggcgcattggctc A/G tctctgaatccagcactt	422
SULT2B1	1	intron 2 4162	ttctccctctcctcccat C/T cgcacacaggtgtctcat	423
SULT2B1	2	intron 3 879	gaggccatccagctctggg G/A ctggacctgggggtttgg	424
SULT2B1	3	intron 4 3882	ttccagctccttctctggc C/T ggtgacctcctcctgga	425
SULT2B1	4	intron 5 1780	cctgcagaagggtccctt C/T catgtccagcagtaatggc	426
SULT2B1	5	intron 5 1814	taatggctgcagcatggagc G/A ttgtggggcattgagacag	427
SULT2B1	6	exon 6 789	ccctcttctccagggtctg C/T ggcgactggaagaaccactt	428
CHST4	1	5'flanking region -1092	atgaagccttggtccatctc G/A ctgtgtctgcccagcacctg	429
CHST4	2	5'flanking region -941	ctgcagagagaaacaggaa G/A ggaagagagccacacaatt	430
CHST4	3	intron 1 -150	caggaaatgattggagaag G/T actgtgacctgttggcac	431
CHST5	1	intron 1 -144	ggcctcttgggttcagcca A/C gacagggtactcttagcacc	432
CHST5	2	intron 2 17	caacgttaagagcgtttctca T/A tctcagctccttgtttct	433
CHST5	3	intron 2 139	aatccagcactttggagg C/A ggaagtgtcggatggatca	434
CHST5	4	intron 3 1829	gactgtgtgtctctattca T/C ataggaaataattcatg	435
CHST5	5	intron 3 2037	aactgaacacacacacaa C/G tgcagagaagcaaacaaaag	436
CHST5	6	intron 3 2134	aagcagctaaattgtgttc G/A tacaggtgcaattggcagg	437
CHST5	7	intron 3 2528	atgtaagtttcgcctggg G/A cagtgtcagcactcctgt	438
CHST5	8	intron 3 2674	gcacttatctagaaaggcc A/G ttctgaagactcagcagg	439
CHST5	9	intron 3 7039	ctgctcccgccggccccc T/C gggaccgcagccacgtctga	440
CHST5	10	intron 3 7211	gtagcccccagagaccccca T/G cttcaacatccattctagg	441
CHST5	11	intron 3 7294	ggagcttcagtggttggg T/C acccccagctcttctccat	442
CHST5	12	intron 4 108	gcagggtcctgcactctgca G/A ggggcaatccaggtggag	443
CHST5	13	intron 4 402	agcactggaaaaagctacgt T/C gcaactgtagcggagtgag	444
CHST5	14	intron 4 547	ctcctgtcccccattggagg C/G gaaggagcagaggtgagtc	445
CHST5	15	intron 4 1142	gccccaggtctcatagctcc C/G catggcagtgctgggattt	446
CHST5	16	intron 5 1187	ccctggcagtaattggggc A/G tgggatgggcatggggccc	447
HNK-1st	1	intron 1 139	gtgtttgggactgaaga C/T ctccctagttcggggacta	448
HNK-1st	2	intron 1 1020	acctgagcagaaattctct T/C ctctgtgaatgaaattg	449
HNK-1st	3	intron 1 1091	aagaatttgaacatcaca G/A gcaacttgacgttatctcg	450
HNK-1st	4	intron 1 1971	ctataactatttcaacata C/T gaaacagccataattggatt	451
HNK-1st	5	intron 1 2096	attagaattatttacc A/C agaaatccaataaaccctg	452
HNK-1st	6	5'untranslated region -91	ctatccagtgacaagaggaa C/A caagaacctcagttcaggg	453
HNK-1st	7	intron 2 -530	agtggcagaggcagagaagc G/A tcagtgttcttcttct	454
HNK-1st	8	intron 2 -466	gctacatcttgcagccagt C/T agaattttaaacacagccag	455
HNK-1st	9	intron 2 -92	acggaalatattgtctgat A/T cttaactgactgaatcact	456
HNK-1st	10	intron 3 152	catggcctccgttctctcat G/A ttacagaggtgtgagggag	457
HNK-1st	11	intron 3 312	cacagtgcccttatgccttg C/T agcagggcgcccttcaggct	458
HNK-1st	12	intron 3 1948	tcctttgatgtacagttt T/C gtgtgaatttttcagtt	459
HNK-1st	13	intron 3 2140	ttacacctggagaggagcac C/T gcagcgttcttaactctgo	460
HNK-1st	14	exon 4 187	agaagccatttctgaggaa C/T tgaaggtgggcccagccagg	461
HNK-1st	15	intron 4 581	cctgtcttccctagctgg G/A atgaggggtgcaacttggaa	462
HNK-1st	16	intron 4 615	tcgtgaaggccctctcacttc G/C taacccccctcttgatcta	463
HNK-1st	17	intron 5 7	gattgttclaaatgggtgt G/A tgggtctactgaatgtccac	464
HNK-1st	18	intron 5 123	acctgaaggagctggggcc G/T tccagacagccctgttttg	465
HNK-1st	19	intron 5 721	ataattatgggtctgtctta T/C gaaatttagcttcagacagg	466
HNK-1st	20	intron 5 867	tgctgccacagagtcggg G/A tcaactcctggcactgtttg	467
HNK-1st	21	exon 6 444	ccaggagcattttcttccat T/C gaggagtcgccgaaacgt	468
HNK-1st	22	intron 6 94	ctgggttctgacttggcag A/G ttgatogggggccacagag	469
HNK-1st	23	intron 6 247	catgaagtgacatctttt G/A ttaatagaanttagcaggca	470
HNK-1st	24	exon 7 696	aggaggaccggacagagac C/G cggggatccagtttgaaga	471
HNK-1st	25	exon 7 870	gagaccctggaggacgatgc C/T ccatacatctaaagaggc	472
HNK-1st	26	3'untranslated region 1110	tcaaatattttattagacc T/C ggggctaaccaggtgagat	473
HNK-1st	27	3'untranslated region 1178	ccacacccctcctttgagga C/T gcccggggtctccacagggc	474
HNK-1st	28	3'untranslated region 1393	ggaagcatcacacagctta G/A gagcgttttcttcagggt	475
HNK-1st	29	3'untranslated region 1452	tgggttctctggtctgtc A/G ggggtgcttaccatcaact	476
HNK-1st	30	3'untranslated region 1540	gcaaggggctgctgaatc G/C cagagacttttgagcatca	477
HNK-1st	31	3'untranslated region 1696	gggtgtgtgtgttccagg G/A tccatctttccagaatccat	478
HNK-1st	32	3'untranslated region 1829	aggggagcgttttctacct G/A agaaggggagtgctttgag	479
HNK-1st	33	3'untranslated region 2211	tcacagcgtgcggcttctg G/T caacaaggtaggccctggtg	480

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
HNK-1st	34	3'untranslated region 2212	ccagcagtcggtcttcctgg C/T aacaaggtaggccctggtgc	481
HNK-1st	35	3'flanking region 1016	cacacgaagggtgacactca G/T ggcctgcaggcccccaggt	482
HNK-1st	36	3'flanking region 1152	gcctgcttgcctcatctgga A/C tctccgaagcagggaacag	483
HNK-1st	37	3'flanking region 1291	gccgagaccctcagcaggat A/G gtgcagttccgggctgggc	484
STE	1	5'flanking region -605	caggttctaaataataat C/T gaagggtgagtggtttac	485
STE	2	5'flanking region -536	taaaattttcaggtctgctt A/G agagttaaaggcaagggtt	486
STE	3	5'flanking region -231	cctttttcccaaccctga C/T ggcagacttgggaatttga	487
STE	4	5'untranslated region -64	tgcagcttaagctctgctt G/A gtatttgaagatataaac	488
STE	5	intron 1 69	aaatataagatgaatttat G/A tattacaagctcttaaaaa	489
STE	6	intron 1 311	caatgagaaataaagcaag C/G agggtagaggaggtgaat	490
STE	7	intron 1 655	tctaagaagtagggactat G/A agaaccctatgtatctata	491
STE	8	intron 1 671	ctatgagaccctatglat C/T tatatcacccataglatct	492
STE	9	intron 1 772	aaaaggcaggttgaagatg C/A agggggggagtatgcagaaa	493
STE	10	intron 1 1715	taaccatttgccttaacctt A/G tcatttttagccaagtcatt	494
STE	11	intron 1 1928	aaatgatcatattcaggaa A/G tcaaaatctctgacttaga	495
STE	12	intron 1 1953	aaatctctgacttagatacc C/T ggcataataatcaaatga	496
STE	13	intron 1 2087	aatttgaaagaaattgaag T/G tctgtgtttttattttatca	497
STE	14	intron 1 2323	taggtatgtaggggtgcc G/C ttatatacatagttgttaat	498
STE	15	intron 2 165	tctattccatgaccacaatt T/G ttacctgtacttgaatagt	499
STE	16	intron 2 1707	cctaggaccaacatgagac A/G taatataccatcagtaaat	500
STE	17	intron 3 850	ggtgtccattccctcaagaa T/G ttatcttltgtttacacac	501
STE	18	intron 4 1653	agtaacaggctagtagata T/C ataataactgagcccaacg	502
STE	19	intron 4 1899	tacatgaacttagagaatca A/G gtatgacacacacacacaca	503
STE	20	intron 4 1930	cacaccaacaataaattac A/G cagaatgataaaagatttg	504
STE	21	intron 5 666	ttctgatcatgtagtaacaa T/C tataaagaaataataatgt	505
STE	22	intron 5 982	aggcaagcagaaccttttg A/C ctacacacaacattattat	506
STE	23	intron 7 369	agattttatcctctctctt T/C ttgagttgaagaataagt	507
STE	24	intron 7 447	caaccttcaaggtaagtgg C/A aaaaaatagaattcaata	508
STE	25	intron 7 672	aatctgtcttttgaccat A/T ctgtcagtgaggtcagga	509
STE	26	intron 7 858	gttaccagaggactaaac A/G gtgtcttctgttgcacacgg	510
STE	27	3'flanking region 218	cagccctcccaagtagctagg A/G ctacagacatgtcaacct	511
ADH1	1	5'flanking region -55	atcatgtgtgaactggaat C/T ggtgtttattcaagcaaaa	512
ADH1	2	intron 1 268	acatttgcgttaaacgata A/G ttatttccaagctaatcatg	513
ADH1	3	intron 3 442	aaatggaggctacatggcta C/A ggcagatgagctgacctt	514
ADH1	4	intron 6 56	tacaacttgaggatgcatt T/G aggtctcagaatatatgttt	515
ADH1	5	intron 8 74	gtctagcagaatggaagg G/A tgaagagatgagaatatta	516
ADH2	1	intron 2 340	ctatttttaagcgtgcat T/C cttaacataagacttaatat	517
ADH2	2	intron 3 91	aaggcaatggagagcgaag T/G gcttgacaaagtcaccgag	518
ADH2	3	intron 3 205	atgtattgtaccttcaacc A/G ttatgtaccgagtatctact	519
ADH2	4	intron 7 108	acaattgacaaggcaagatt T/C tgaacaacaatcaaaataa	520
ADH3	1	5'flanking region -254	tgagagaagagaagcaggaa C/G ttgagagaggaggaagagag	521
ADH3	2	intron 2 355	tatgcattctctatattat A/G caagacaaaattttgagat	522
ADH3	3	intron 3 32	acactcagggaacatgcctt G/A gttcaccatcacaagattag	523
ADH3	4	intron 4 6	ctgcttgaataatgagtaag C/T ttctgtatgctttcttgcac	524
ADH3	5	exon 5 453	agcacccttctccagtacac A/G gtgttgatgagaatgcagt	525
ADH3	6	exon 6 815	ttcgtttgaagtcacgggc A/G gcttgacacacatggtatgat	526
ADH6	1	intron 3 249	tgaactggacttgaagta C/A aatgagacaaaatttttg	527
ADH6	2	intron 6 1072	taaccctatactgtattgc A/G tcactttcaacaggcagct	528
ADH6	3	exon 7 885	gtctgtgtgtttgttgggt G/A ttgocctgccagtttcaact	529
ADH6	4	intron 7 1292	gttgagaacactgcctagt C/A ccgtctgtgttcttagaatt	530
ADH6	5	intron 7 1616	ctatcacagaataatccgca T/C ggaacacaaagcagattacg	531
ADH7	1	5'flanking region -528	tgtgcagccacagaaagttt T/C acttaactttctacacctaa	532
ADH7	2	intron 1 361	tcagtgcagtgtgctgcaat C/T gctgcagtggttcaatggga	533
ADH7	3	intron 3 183	aacctcaacctttgaagga A/G aaccttccgtgtttataaa	534
ADH7	4	intron 4 76	tgaattgaaatattatcat G/A tttattttgtgtatcaaca	535
ADH7	5	intron 6 615	tggcctgcgtaagagagact T/A ggaataatggaataagcca	536
ADH7	6	intron 8 532	aagttaaacatctaccacaa T/C ttatgtatgccattgtactat	537
ADH7	7	intron 8 651	gtgtctattttttcaagta G/A ggcacaaaatttcttattt	538
ADH7	8	intron 8 760	catttttagatgaagaccaa T/G gtgtgaagcaastaata	539
ADH7	9	intron 8 1207	tctccacatttggctagccc T/C acaggaatcatatttatga	540

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
MGST1	27	intron3+4429	attggaggtgacgatctc T/C gtgatgctggggagaaatc	661
MGST1	28	intron3+4817	attgctatagaagagagtaa G/T gtaagcagaaatagttttc	662
MGST1	29	intron3+6077	tttgaaaitagtgcttttaa T/C agtlatctttttccacagag	663
MGST1	30	exon4+304(3'UTR)	aagaattctgtacttccaat T/G tataatgaatactttcttag	664
MGST1	31	3'flanking+1581	ttgtgtgcatgaacatgca C/T ggtgcaagcgcaacacacac	665
MGST1	32	3'flanking+1729	tatgtggagcaatttgaaaa A/T agtatatttaagccattaa	666
MGST1	33	3'flanking+3407	ggatcactgtaaaagatccc G/A gagtactccatgtcccagt	667
MGST1	34	intron1B+36	ggagaaagggagccgcatgca G/A aggtggcagccagggagg	668
MGST1	35	3'flanking+25	gggtaaacccattttgaata T/C tagcattgccaatattcgt	669
MGST1	36	exon4+266(3'UTR)	aaagaaatcatacaactca G/A catccagttggcttttaag	670
SULT1A2	1	intron 4 1728	tcagcttcctcctttgccaa A/Δ ccaagagatgagctggcctg	671
SULTX3	1	intron 1 6415	tgacctctccctgttagtgt G/Δ ggggcagctctttccagtgt	672
SULTX3	2	intron 5 2457	ggccttaaaagggagttcat C/Δ ctctctgcttccagggctc	673
PIG3	1	5'untranslated region-93	tcgcgagggatcacagcgccc (CCTGY)n cagacaatatttagccgtg	674
ADH2	4	intron 7 + 108	ccattgcaagggcaagatt T/C tgaacacaaatcaaaataa	675
ADH2	5	intron 3 +(1721-1723)	actgcatagaatttaagaa GAA/ Δ ctgtttattctctccag	676
ADH2	6	3' untranslated + (2305-2306)	gttaatgctttccactctc AG/Δ gggaggaatttgatttga	677
ADH5	1	5' flanking - 115	taactgctgtaaaagttaac G/A gggagccctttcccgacaa	678
ADH5	2	5' flanking - 114	aactgctgtaaaagttaac G/A ggaagccctttcccgacaa	679
ADH7	16	intron 8 + 727	ttcagatccctgtaagccag G/A tatatttttaccatttta	680
GSTM1	1	5' flanking - 694	tacgaattggctaaattaca C/T agtacttagccagatgaccg	681
GSTM1	2	5' flanking - 661	gatgaccgaaggactcagta C/T ccgagggcccttaacagaa	682
GSTM1	3	5' flanking - 658	gaccgaaggactcagtaacc G/A agggcccttaacagaaaca	683
GSTM1	4	5' flanking - 656	ccgaaggactcagtaaccga G/A gggcccttaacagaaacaca	684
GSTM1	5	5' flanking - 537	tagggggagactaaagccct G/C ggaatagctttcgaatcaga	685
GSTM1	6	5' flanking - 525	taagccctggagtagcttt C/G ggaatcagaggaagctcgt	686
GSTM1	7	5' flanking - 465	aattaaattccaggttggg G/A ccaccacttttagctgtac	687
GSTM1	8	5' flanking - 383	ccgagagaagggctgagga C/T acccgggcagggcagagaa	688
GSTM1	9	5' flanking - 382	ccgagagaagggctgagga A/T ccgagggcagggcagagaa	688
GSTM1	10	5' flanking - 378	gggaagactgagggacccg C/T gggcagggagggagagggag	690
GSTM1	11	5' flanking - 343	agggagaagagctttgctcc G/A taggagctgctgtgtgt	691
GSTM1	12	intron 2 + 118	tactgagctgcaggtctc T/C ctccctgggcccggtag	692
GSTM1	13	intron 3 + 233	agtgaagtcggctgtctc T/C ctgtctgtgttatggag	693
GSTM1	14	intron 4 + 26	tggtggtgctcaatgtgt G/A gggggaaggtgcttctctcc	694
GSTM1	15	intron 5 + 140	actatcagcaattatttcca C/T gactcaatgcatgtcaac	695
GSTM1	16	intron 5 + 577	ctgccaccccttagaagga A/G ctcttacttttccctgct	696
GSTM1	17	intron 5 + 645	gctgctggtatccagagga T/A gccaggtgcttggcgctcc	697
GSTM1	18	exon 7 + 519	caccgtatatttgagcccaa G/C tgcctggagccttcccaaa	698
GSTM1	19	exon 7 + 528	tttgagcccaagtgcttga C/T gcttcccaatctgaagga	699
GSTM1	20	intron 7 + 2421	cagcaccgtgagaatctc A/G taagtgtagctgttactgt	700
GSTM1	21	3' flanking + 42	atttctcctggccatctac C/T cagactgtctgtctgtgt	701
GSTM2	1	intron 1 + 7	ggaacatccgggggtgag C/G aggtccgctgggggtggg	702
GSTM2	2	intron 1 + 45	gggacgggggtgctgggg C/T ggggaagtgtgggagcgtg	703
GSTM2	3	intron 3 + 70	gactcatctcctctccca G/C cttagaggtgttaagatcag	704
GSTM2	4	intron 3 + 224	agcaggccctggctcctct T/C tgccttgcatatgggaagg	705
GSTM2	5	intron 5 + 100	ttgattcctctgttgagtt C/A ttgtcttctgactctaa	706
GSTM2	6	intron 5 + 341	tcctcttggtggttcagg T/C ctgctggttcagggtga	707
GSTM2	7	intron 5 + 696	occttgctagacacagag C/T gctgatttgcatttcaa	708
GSTM2	8	intron 5 + 723	ttgtgatttcaatcttt A/G gctaggcagaaagtctcc	709
GSTM2	9	3' untranslated + 1006	ctcagcccgagctgtcccc G/A tgttgcataagggagcagca	710
GSTM2	10	3' flanking + 139	ttctgctggcctagtaagg C/T gcttgagaatttctgtccc	711
GSTM3	2	5' flanking - 144	ccaacgcccggattagtcg C/T cctgcacagccctgtgga	712
GSTM3	3	intron 7 + 165	agcctaactctataccctg A/G aggcactgtctacaaaaaa	713
GSTM3	4	intron 7 + 257	ctgttgactgggtgggtc T/G ttataagattgtgtatttt	714
GSTM3	5	exon 8 + 91	cccagtggggcaaacagcct A/G tatgctgagcaggagcaga	715
GSTM4	1	intron 4 + 67	ttgctgagttgggtgcta T/C gctcaggtgagctgtgtt	716
GSTM4	2	intron 7 + 77	gtgtgtttccagctcctga T/G ctgcataagaataacttgc	717
GSTM4	3	intron 7 + 80	gotttcccagtcctgact G/A cataagaataacttgcatt	718
GSTZ1	1	5' flanking - 546	agcaggcccccagccgac C/A gctcgaagccctgagcc	719
GSTZ1	2	5' flanking - 321	tgctgaccagccggccgc T/C aaggagtcacaagaggcag	720

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
GSTZ1	3	intron 1 + 2890	aaatactgcatcaaaacca G/A gccacgtctgttggggga	721
GSTZ1	4	intron 1 + 2896	ctgcatcaaaacccggccac G/A ctctgttgggggacccaa	722
GSTZ1	5	intron 2 + 255	tttcccaacactgctctcca A/G agcccttggcaaccatgtt	723
GSTZ1	6	intron 2 + 1560	caaccactgttaaggccctg G/C gggggcaggttaaacaaa	724
GSTZ1	7	exon 3 + 94	ccttgaaaggcatcgactac G/A agacggggcccatcaatctc	725
GSTZ1	8	intron 4 + 297	agaaggaggagtttgcctgg C/T ctgtccctctgtccagg	726
GSTZ1	9	intron 6 + 94	tatctgaaccagcctccag G/A ctgttggggcctgacagt	727
GSTP1	1	intron 1 + 269	ctccccggggctccagaaa C/G ttctttgttgcctgcagt	728
GSTP1	2	intron 2 + 134	ccccggggcctcttctgtt C/T cccgctctccggccatgcc	729
GSTP1	3	intron 5 + 438	gtgtgtgcgctgcgtgtgc G/A tgtgtgtgcgtgtgtgtg	730
GSTP1	4	intron 6 + 162	cccgtgtgtggttccctag C/T cccctgcccgtgcagctctc	731
GSTT1	1	5' flanking - 103	taaagagtgtcccaggcgtc C/T gtccgcccgaaggggcaca	732
MGST1L1	1	5' flanking - 105	tgctccgctgcctgtgggc G/A gggcgtggggcgtgtcgt	733
MGST1L1	2	intron 1 + 277	agtgctgtgagagagcag G/A ttctgggggggagatgtg	734
MGST1L1	3	intron 2 + 8030	gggttatccagagccccc C/G gcccccaccacacatatga	735
MGST1L1	4	intron 2 + 8499	gtatggcaggagtggtgtcc C/T ggcagccatagaggtatg	736
MGST1L1	5	3' untranslated + 468	cgccacctgtgaccagcagc T/G gatgcctctgtggccaccag	737
MGST2	1	5' flanking - 46	gtcagcattcaagtcag A/T agcgcatttatcttccgt	738
MGST2	2	intron 1 + 176	gttcaccctgcgcctgtct A/C cctctctccaggggcaag	739
MGST2	3	intron 1 + 204	ttccaggggcagcagagac T/C gagaacattccagagattag	740
MGST2	4	intron 1 + 373	ttacaagtgtccaaaggaa A/T cgtgcctgtcttaaacctg	741
MGST2	5	intron 2 - 3245	cctctgtgttggccacctc G/A gctcccaagtgctggat	742
MGST2	6	intron 2 - 1998	agccgagggtggcggtatc T/C gaggcaggagatcgagacc	743
MGST2	7	intron 2 - 1640	tgttattccttgcatagcc A/G taataaagtatgaatttt	744
MGST2	8	intron 3 + 41	actgtgtctaatgtgact A/G tgaigtcttaaacgttaagg	745
MGST2	9	intron 3 + 453	atcagagtgtctatgttcag A/G tatatgaacttggcttcat	746
MGST3	1	5' flanking - 520	acaaaaaggccctaaccagc A/C taatccattcacttccgga	747
MGST3	2	5' flanking - 356	cgcttaaaacccgtacggcg G/A ctctgtgtggggcaaatat	748
MGST3	3	5' flanking - 234	clgggggagtgatgtatgt T/A ttgagaatgagaggagtaa	749
MGST3	4	intron 1 + 74	agcctttggcaggcactcc C/T atattacagctatcgagc	750
MGST3	5	intron 1 + 682	agaaaaagccoccttctttt G/C tgggtggcggccgggco	751
MGST3	6	intron 1 + 832	cggtttacaagctacataa T/C agcgtcggggcaggtaagt	752
MGST3	7	intron 1 + 1919	aataaaaattcctgagtttct G/C tcaactgctcttaccagacc	753
MGST3	8	intron 1 + 1991	tgtaatggcgaacaggaas A/G ttgtactctcttcaatgc	754
MGST3	9	intron 1 + 4458	tcttcacatcctcctaacata T/C agttagcttccactctccaa	755
MGST3	10	intron 1 + 4676	tgaatgtcaatgcaattgt C/G gggggatgttactttcat	756
MGST3	11	intron 3 + 278	cgcctgaccctctaaacc G/G atgttgcactctccaggcct	757
MGST3	12	intron 4 + 423	cttgcccttttgggtggg T/G gtgggtgtgtcacagagag	758
MGST3	13	intron 4 + 506	gtcagagagagaaacaaag T/C ggggaaggtggaaagggat	759
MGST3	14	intron 4 - 162	tcacagatattttattttcc C/T gactgaactaacttaattc	760
MGST3	15	intron 4 - 130	acttaattctacctaatttg G/G gtggggagtagtggccaaa	761
MGST3	16	intron 4 - 105	gggtggttggccaaatcat C/G aaattgttaacttttgcata	762
MGST3	17	intron 4 - 85	aaatattgtgtaatcaacc C/T taggtgttaaaaaggttg	763
MGST3	18	intron 5 + 105	atccccgacacttgggggco G/C aaggcaggcagattgctga	764
MGST3	19	intron 5 + 197	aaaaaatacaaaattagcc G/A ggtgtgtgtgtcacacctg	765
MGST3	20	intron 5 + 222	tggtgtgtcacacctgtagt C/T ccagctacttgggggctga	766
MGST3	21	intron 5 + 374	ttttatgtactatatttt T/C ttcttgggaatttgagaaa	767
MGST3	22	3' untranslated + 517	atgaattacctttatttcca G/T ttacatttttttcaata	768
MGST3	23	3' flanking + 168	agtctgattgtgtgatga G/T gtatgtcatgccacagtga	769
GSTA1	1	5' flanking - 266	ttgcaaaaagagcaaatct C/A ggtgaatgtattgtatga	770
GSTA1	2	intron 2 + 1220	gagacacaggctttcctaag A/G tatgacaacaccataactag	771
GSTA1	3	intron 4 + 1813	aaaggcaccacactggggg A/C attattttgccatcacctga	772
GSTA1	4	intron 5 + 732	gaaggtgtgtcatgaagg T/C ggaagtactcccaaggag	773
GSTA1	5	intron 6 + 333	ttatcccatatgtgccaca A/G tgaacgggtctgagcagagc	774
GSTA1	6	3' flanking + 412	ctttcttgcctttgcacaa A/C caatgattctgtctgtgtg	775
GSTA4	1	intron 1 + 280	gcattgtggaaggtgggct C/T ggaatcgtcccgccgtggc	776
GSTA4	2	intron 3 + 176	ggaatcacttcttttcaa T/G agttccataaagctggccg	777
GSTA4	3	intron 4 + 94	acaccacatttactttagt C/G ttacatagttagtagatca	778
GSTA4	4	intron 5 + 1062	cacacttgtgcacatgcaga C/T acccatgggcatcaagagt	779
GSTA4	5	exon 6 + 487	cagatgtgattttactccaa A/G ccatttttagcttagaagag	780

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
GSTA4	6	intron 6 + 595	tgagctctgagagcaaatga G/A agatgttagcaccctaaaca	781
GSTA4	7	intron 6 + 630	taaacatcccccaaggat T/A cctaccattctccttctgag	782
GSTA4	8	intron 6 + 3943	tcttcgtatctataatccc T/C tttttagtccttaaatgt	783
GSTA4	9	3' untranslated + 1099	taatacaaacgaatgtctc G/A taastgactctcctctgagc	784
GSTA4	10	intron 5 + (370-371)	gttgcgaacagctgtctca (TA) gctgacatcctccctgataa	785
GSTA4	10	intron 5 + (370-371)	gttgcgaacagctgtctca gctgacatcctccctgataa	786
NDUFA1	1	5' flanking - 1437	agggtcaaaaatcctgatta T/A acctacattgaagcttttaa	787
NDUFA1	2	intron 2 + 3071	aataaaagtacatggcatai C/A ttgtatgggaacagacttgt	788
NDUFA1	3	3' flanking + 1218	aactccatgtgtataaagca A/G caccacagatgacacttcca	789
NDUFA1	4	3' flanking + 1411	ggattgtgccatcccttgat C/T/G ggcaatgaccttttactttt	790
NDUFA1	5	3' flanking + 1411	ggattgtgccatcccttgat C/T/G ggcaatgaccttttactttt	791
NDUFA2	1	intron 2 + 1087	aacatacaaaaattagccgg A/G tatgtggcgggacactgta	792
NDUFA2	2	intron 2 + 1089	catatacaaaaattagccggat A/G tggggcgggacactgta	793
NDUFA2	3	intron 2 + 1356	ttccctgaacaccccttg T/C ggccatccagaatccagccaa	794
NDUFA2	4	3' flanking + 467	cacagcctcatgggtcagcc C/T actccagagggtgacttccc	795
NDUFA2	5	3' flanking + 744	ggagcagggccctggcca C/T agccgtgagcagtaagcagg	796
NDUFA2	6	3' flanking + (844-845)	tatagtctacaaagaatgaa (ACAC) aaagatcataacaatagcta	797
NDUFA2	6	3' flanking + (844-845)	tatagtctacaaagaatgaa aaagatcataacaatagcta	798
NDUFA3	1	intron 2 + 2656	tcctctgtccctccctgc G/A caatttatcttcccttggcc	799
NDUFA3	2	exon 4 + 241	aggcccccagccggagtg G/G tgaagaaactgtgagcacct	800
NDUFA3	3	3' flanking + 1019	tccttaccctgactggcacc A/G gctctggagccccagtcct	801
NDUFA5	1	intron 3 + 2155	agactctagcctgttacct G/G aacataaggttccctgaaa	802
NDUFA5	2	intron 3 + 2493	ggcatattgttagtttctc G/T gtctcaatttcatcatctat	803
NDUFA5	3	intron 3 + 2712	acaattttgaactgttcc C/T taacacaggcttttctgaa	804
NDUFA5	4	3' flanking + 1296	aggctctaaaaggatfgc A/C atttgctattgtgtcttc	805
NDUFA5	5	intron 3 + (30-31)	aagtcagttttgtgtctg (GATTTGTGGTATCCAG) tgtaa	806
			catttaacaaaaaa	
NDUFA5	5	intron 3 + (30-31)	aagtcagttttgtgtctg tgtaa	807
			catttaacaaaaaa	808
NDUFA5	6	intron 3 + (427-428)	attaagtagcagttataaa AG/Δ tctagactgctgattcatat	809
NDUFA5	7	intron 3 + (4733-4734)	tatagggaattttataatata TA/Δ ggatattgaacattcagtt	810
NDUFA6	1	5' flanking - 1148	tttataatttatatgtta C/T gtgctttctttgtatagct	811
NDUFA6	2	5' flanking - 363	actaccagagagcggcg G/A cagccggatagcaggacgct	812
NDUFA6	3	exon 1 + 26	ggggagcggcgtccgcaag C/T tacttctaccgccagcacct	813
NDUFA6	4	intron 1 + 1318	attcagcagtttgaascat A/G atgtttgcctggcagaatcc	814
NDUFA6	5	intron 2 + 562	agttaaagaatctgaaaagt G/C tcagaatgattaccctga	815
NDUFA6	6	5' flanking - (861-862)	ctgtaaaatgggatgtga (T) ggtacctactgacctatga	816
NDUFA6	6	5' flanking - (861-862)	ctgtaaaatgggatgtga ggtacctactgacctatga	817
NDUFA7	1	5' flanking - 731	accaaccaaaaggtctatcaa A/G ggggtgtcctctttgacccc	818
NDUFA7	2	5' flanking - 434	aaaggggaaccatcagaaccc C/T gtgatgaaatgagaatcggc	819
NDUFA7	3	5' flanking - 395	gctccggatccggctgc A/G ggggttagggcaggttagag	820
NDUFA7	4	5' flanking - 100	agaggagtcacgtgcttcgg G/A gagagcctttataggacgtt	821
NDUFA7	5	intron 1 + 92	tcacctccctctaaagccgg G/A acccttgcctctcccgat	822
NDUFA7	6	intron 1 + 133	ctccctgggaacccccagct A/C gtcaccccttcagccggga	823
NDUFA7	7	intron 1 + 136	cctgggaacccccagctagt C/G accccttcagccgggaccc	824
NDUFA7	8	intron 2 + 89	tcctttagacccctgaancc G/C agggctgacatcctgcaacc	825
NDUFA7	9	exon 3 + 196	ggcggcgggaatctgtccc C/G? ctccatcatcatgtgtctg	826
NDUFA7	10	intron 3 + 4203	gcctccacccctggggcgcc T/G cctccatcaccacccctcc	827
NDUFA7	11	intron 3 + 4604	gggccttgtgtacgtggag A/G ccaaaagtgggaaggagg	828
NDUFA7	12	5' flanking - (1360-1353)	agggtccagggtccctgct (CAGAGGCT) aacactggccg	829
			aagagaaag	
NDUFA7	12	5' flanking - (1360-1353)	agggtccagggtccctgct aacacigggcgaagagaaag	830
NDUFA7	13	5' flanking - (1240-1239)	tgatagagccctgatccacc CA/Δ ctctctgaaacttttgtct	831
NDUFA7	14	intron 2 + (4142-4143)	catttttgactgaggtgac AG/Δ gggcccaacagcgggcatg	832
NDUFA8	1	intron 1 - 75	tttgtttctctattctgac C/T cgcagtgaggtaaagctgaga	833
NDUFA8	2	intron 2 + 790	caaacctagacaaagtgtgc C/T ctttatccagaagtgcag	834
NDUFA8	3	intron 2 + 900	ttcaggagataaaaagctct G/A attgctcagggcctgagatgg	835
NDUFA8	4	intron 2 + 3837	gaagttgtcttgtaagtgag A/G taagaatgtgactacata	836
NDUFA8	5	intron 2 + 3942	tcattgttttcaagagat G/T cccctaaccacgctttctt	837
NDUFA8	6	intron 3 - 66	gaggagacaccagagggcg A/G ttgatgttacagatttctc	

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
NDUFA8	7	3' untranslated + 520	ttattttctggaccaagtaa A/G gatgggtccgtgcccacac	838
NDUFA8	8	3' flanking + 367	gtcatcaaggaggccctcc A/G ggtatagaagtgcagaaactt	839
NDUFA8	9	3' flanking + 777	attcttttttactactagg C/T ttttctccacatctgact	840
NDUFA8	10	3' flanking + 1053	aaagaasagccctgtgta T/A ctgccatggccgttttga	841
NDUFA8	11	3' flanking + 1190	gattctctaatgaaasatga G/T acttttttttgcatttttt	842
NDUFA8	12	intron 2 + (449-453)	ggtcattgtgcagtactctaa (GTAA) aaaaaactaagctgtgta	843
NDUFA8	12	intron 2 + (449-453)	ggtcattgtgcagtactctaa aaaaaactaagctgtgta	844
NDUFA8	13	intron 2 + (707-708)	ctcattttgaaagactctc (A) acctgtctgtaccaaaatg	845
NDUFA8	13	intron 2 + (707-708)	ctcattttgaaagactctc acctgtctgtaccaaaatg	846
NDUFAB1	1	intron 1 + 8451	cagcaccctgtaggccctc G/A ggtgtgtgagctgccatga	847
NDUFAB1	2	intron 1 + 8495	gacacaggcattctgcagac G/A ctgacaaattttatggcag	848
NDUFA9	1	5' flanking - 807	gatggctctttgtagaaca T/G gccatctctcaaggcgacc	849
NDUFA9	2	5' flanking - 769	accacagtttaagaaasat T/C acaagccattgccttagaga	850
NDUFA9	3	5' flanking - 353	cacacccctattttgtttct C/G ttctccacttttccctcgt	851
NDUFA9	4	5' flanking - 322	ttccctctgttttctcc C/T cttttctctctctggccc	852
NDUFA9	5	intron 1 + 447	ttcatatgagcacaatgga A/G atgataattatcaatacca	853
NDUFA9	6	intron 1 + 1039	ggcttgatgttcagcctgag G/A caagaattaggaggtttag	854
NDUFA9	7	intron 1 + 4010	aetgtatccaaagagatc T/G cattctgcccattgagaa	855
NDUFA9	8	intron 3 + 49	gccaaataaattctaaag G/A tcaatttttagggatagg	856
NDUFA9	9	intron 3 + 107	aatcttctccagantggc C/T aagggctctctgttccca	857
NDUFA9	10	intron 3 + 1183	ctctctggaatattcatac A/G gattattgtatccctta	858
NDUFA9	11	intron 3 + 1395	cttctagttcttttgcct C/T aagttttgtatccctgt	859
NDUFA9	12	intron 3 + 2363	agaaatagtcagaaatg C/T ccaataacactagcttta	860
NDUFA9	13	intron 3 + 2608	gtctttgttttccctgata A/C agtctctgttaccctttg	861
NDUFA9	14	intron 4 + 561	attttataaattctttgat A/C ctgggggtcttattcaact	862
NDUFA9	15	intron 4 + 860	atttctgagtgatgacag C/T agagctgtcaacttttaa	863
NDUFA9	16	intron 4 + 879	gcagagctgtcaacttttt A/T aaaaaataatttagcttaa	864
NDUFA9	17	intron 4 + 893	tttttaasaaataattt A/G gcttaasaaataaasatt	865
NDUFA9	18	intron 4 + 1090	atcattgtcttttaaaagt T/C aagtagtgtaatttcagta	866
NDUFA9	19	intron 4 + 1188	aaccaatcctttttttt A/T tcttccagaacattgtatt	867
NDUFA9	20	intron 5 + 161	gggtgtgtgagtttga C/T gtttgaugtgctctct	868
NDUFA9	21	intron 5 + 373	cttttccacccttgcac C/T agtggttttgccaactct	869
NDUFA9	22	intron 5 + 457	gocaggagagtgactatc A/C caagtgcttatgctccttt	870
NDUFA9	23	intron 5 + 3113	galtttctcttctcaat G/A taagcttctcttaasataa	871
NDUFA9	24	intron 5 + 3339	tctaaactcaaacaggttt G/A ttgttttattgtttggtg	872
NDUFA9	25	intron 6 + 414	tatagttttgcttttccag G/C atattacatatatggtaga	873
NDUFA9	26	intron 6 + 518	ctttcatttctttatagc T/G tgaagctcatttcttata	874
NDUFA9	27	intron 7 + 974	ggattatgcgtacttgaaa A/G tacttgatagcgggtat	875
NDUFA9	28	intron 8 + 368	acatttaattttgatgagta T/G cacaatgctccagaggctg	876
NDUFA9	29	intron 8 + 954	gcattgcaatcagttatag T/C ctatagaagaattacattc	877
NDUFA9	30	intron 8 + 1253	tcctcttgaaattgtagata G/T gtaactacacatttctatc	878
NDUFA9	31	intron 8 + 11608	gaaagatgctgtatgaat G/A accaaaaattcgtgaagaaa	879
NDUFA9	32	intron 8 + 11930	ctacaaatataattcaaat C/T gtaactatggaatgacaa	880
NDUFA9	33	intron 9 + 1998	tgtttttcaagcctttaac G/A gctgtggaacctgtctca	881
NDUFA9	34	intron 9 + 2238	ccagctacttggaggctga A/G gttggaggatcacttgagcc	882
NDUFA9	35	intron 9 + 2885	acagcgtctgtcttctgc A/G gttctataggctagcttac	883
NDUFA9	36	intron 10 + 801	tacaaatagttctcttac G/A ttatacttgagaaagtgt	884
NDUFA9	37	intron 10 + 910	tgcagactttcagtggtga G/C gatgaggatgctgtct	885
NDUFA9	38	intron 10 + 1180	aaactgagtcagacgccc G/A tctcagaaacaggggct	886
NDUFA9	39	3' flanking + 554	gtgcagcacttaggaatta T/G gaacttctaagagttctt	887
NDUFA9	40	5' flanking - (1129-1128)	taaacagtagggcagata (TC) gatggaacagccaagatt	888
NDUFA9	40	5' flanking - (1129-1128)	taaacagtagggcagata gatggaacagccaagatt	889
NDUFA9	41	5' flanking - 341	tgtttctctctccacttt T/A cccctgttttcttccccc	890
NDUFS1	1	5' flanking - 3	tcttaggggtgtctgtgt G/G cagacagtttagcagaacag	891
NDUFS1	2	intron 1 + 445	gtgttagcaatggctacago T/C tctgtttgtgtctgttt	892
NDUFS1	3	intron 1 + 470	tttgttctctgtttgtt G/T gtccattgaccaggtggc	893
NDUFS1	4	intron 1 + 502	acgttgacagcctttttt A/G ttctttaactaacgggaaa	894
NDUFS1	5	intron 1 + 557	ttttgaaaagttagccagg A/G ttgcattgacaaatacaaa	895
NDUFS1	6	intron 1 + 5218	tatctcagaatctcagga A/G catltagtagcagctatgc	896
NDUFS1	7	intron 3 + 1371	agccctcaaatagatag T/G caatgggaatgaacacaga	897

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
NDUFS1	8	intron 5 + 414	tttgaacagaggtctcact A/G tttgtccaggctggcctg	898
NDUFS1	9	intron 10 + 812	ggtgcggtggcgcatctc G/A atctcggtcactgcagcct	899
NDUFS1	10	intron 11 + 233	ggaggccasggcaggcagat C/T gcctaagtgcaggattga	900
NDUFS1	11	intron 11 + 283	ggccasctggcgcaacccc G/A tctctactaaaaatacaaaa	901
NDUFS1	12	intron 11 + 585	ctgtatgtcttaattttaa G/T taatttgcaattttat	902
NDUFS1	13	exon 12 + 1251	gcaccactgtttaatgctag A/G attcgaagagggttgaat	903
NDUFS1	14	intron 13 + 5159	attacttttagaaaacgtgt T/G ttactgtatctcaggcata	904
NDUFS1	15	intron 14 + 250	aaaaaltgttatattagta G/T acctgtgttcasaaattgca	905
NDUFS1	16	intron 14 + 550	gataaagtctcactatgtt G/T ccaggttgatctcaactcc	906
NDUFS1	17	intron 14 + 2429	ctgaataacaaaaatagc C/T ggggtgggtggcatgtgcct	907
NDUFS1	18	intron 14 + 2530	ttacagttagccagatcac G/T ccactgcctccagcctggg	908
NDUFS1	19	intron 14 + 2659	acacatttaatttttcat T/C gaaaactactgcagttatgt	909
NDUFS1	20	intron 16 + 150	agaaacatgtattcagaaa C/T aggaattcaagttacagt	910
NDUFS1	21	intron 18 + 279	cactgttagcaattatgg T/C gaattttccaaagtgcaaa	911
NDUFS1	22	3' flanking + 182	tctaggataattataataa T/A aataatcatagtaacaatgg	912
NDUFS1	23	intron 11 + 3226	aaatgtatgtctgtcttt T/A aacatttggtaatagtaaat	913
NDUFS3	1	5' flanking - 194	tctgcacaaaggagctagga C/T cagctcacctcacgatttc	914
NDUFS3	2	intron 1 + 46	cagggtcaggcgagcgagc G/T gccagtgagagagctcct	915
NDUFS3	3	intron 6 - 439	aaagctgtgcaaatgtact G/A ctttagatctggactgtgaa	916
NDUFS3	4	intron 6 - 280	ggtaggtgagcagctagtt G/A gagctcctgatgtggagt	917
NDUFS4	1	5' flanking - 439	aactgaatcacgccgtgac T/A gagggcttgcgaagtgaatc	918
NDUFS4	2	intron 1 + 1829	gaaaaaaatcttaataagca G/T ggaagcgttttttaatac	919
NDUFS4	3	intron 1 + 2057	ettaetgggaatctacat C/G taaaattcaattttatgta	920
NDUFS4	4	intron 1 - 521	ttcattttaactaattttat T/G tctccccttttgtaagg	921
NDUFS4	5	intron 3 - 1259	ataaattatgtatttatta G/A tctaatatagccagccata	922
NDUFS4	6	intron 3 - 1174	aatatataattatagaaa T/C ctccagtgagcaaccatgt	923
NDUFS4	7	intron 4 + 10682	cacaatataggcacaacit A/C ctacccaaagcactaaceagt	924
NDUFS4	8	intron 4 + 12299	tttactatagatatagg A/T atagactatagagttatct	925
NDUFS4	9	intron 4 + 12560	accaaatagggtattatga G/A gctcatcttttatataag	926
NDUFS4	10	intron 4 + 18801	ggaaagacttgccttgcag T/C gtaaccgaacacctgttat	927
NDUFS4	11	intron 4 + 19888	tcgcacagctgagagagca A/G gggcgtgttttcagtaccc	928
NDUFS4	12	intron 4 + 20178	agaaagatgagttatact G/A tctaacttaaccattctaa	929
NDUFS4	13	intron 4 + 23016	ctctctgtgaaagtaaggt T/A atgttgaaacagttatata	930
NDUFS4	14	intron 4 + 23124	actttcttggagatggagt T/A ccagcagttgggaatgta	931
NDUFS4	15	intron 1 + 766	tgtgatgatttttttttt T/A ggtgttataaccttccatt	932
NDUFS4	16	intron 1 + 1261	ttctttctcttttttttt T/A gagatcattctcacttga	933
NDUFS5	1	intron 1 + 388	ccaaacatagccagccttc C/T ggtgttaactccggctgtt	934
NDUFS5	2	intron 1 - 13082	agtagccgagattgcacca G/A tgcattccagcctggcacc	935
NDUFS5	3	intron 1 - 12905	gtttcaacaaaggactaca G/T agtagtaggaatttctgt	936
NDUFS5	4	intron 1 - 12564	attttcatcacacctcaact T/G aaggtatcacagccttaaga	937
NDUFS5	5	intron 1 - 12561	ttcatcacacctcaactaa G/A gtataacagccttaagaatg	938
NDUFS5	6	intron 1 - 10561	acaaatgtgtatgtggg C/G ggtgtgtgagcaggtgtcat	939
NDUFS5	7	intron 1 - 9065	ccgtgtctctcggctcag G/A gtacaccttttccctttaga	940
NDUFS5	8	intron 1 - 8871	tcacacaggtgtctgtagata T/G aggaacgcagaccttgcctt	941
NDUFS5	9	intron 1 - 7312	aaatccttggcttctagaat G/T ggtcactgatgtatataat	942
NDUFS5	10	intron 1 - 6827	aaactctgctccccgattc A/G cggcattctctgcctcagc	943
NDUFS5	11	intron 1 - 6725	agtagagcggggtttcacc G/A tgttagccagcatgtgtcag	944
NDUFS5	12	intron 1 - 6631	aggcgtgagccactgcgcgc G/A gccatgaccttcttctata	945
NDUFS5	13	intron 1 - 6531	cccaacagctcccaatgtaa A/G acagatctattatattctg	946
NDUFS5	14	intron 1 - 6346	gcaacagactctgacctata T/C cccatagggtacagctgag	947
NDUFS5	15	intron 1 - 6327	atcccatagggtacagctga G/C gactttaatcagaaggag	948
NDUFS5	16	intron 1 - 6122	tagccttcttttactctac T/C gttctcccaatcacaccc	949
NDUFS5	17	intron 1 - 2512	acaaactcttaagtgcgaatt T/C tgcagtcgaagtgagctta	950
NDUFS5	18	intron 1 - 1945	tttaatctcctttaaatlta G/A caatttcaaacctagggtta	951
NDUFS5	19	intron 2 + 75	tttttttttttttttttt G/A aagtctcaactttgtccct	952
NDUFS5	20	intron 2 + 148	ctgtagcctctgcctccag G/A ttacggcagttcgttaact	953
NDUFS5	21	3' flanking + 150	cagattcaagtggtttctct G/G cctcagcctcccaagtgct	954
NDUFS5	22	intron 1 - (10682-10681)	attataaacactaaacaaac AT/Δ gtgtgtctcttttagaggg	955
NDUFS5	23	intron 1 - 10272	aggaacaagtactaccctt G/A aaaaagaagatgaacaa	956
NDUFS5	24	intron 1 - 2069	accagacagagttccctta C/Δ ttgttttctgtggcaaga	957

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
NDUFS6	1	intron 1 + 26	ggccgctgggtacagatgc A/C ccttctccagccgcacctc	958
NDUFS6	2	intron 2 + 1076	ggatcatggtggtggagagg G/A gcttgtctgtggtgttg	959
NDUFS6	3	intron 2 + 1260	cagttgtcagtaagtggg T/G atagggtaaagtctctttc	960
NDUFS6	4	intron 2 + 1413	caaaaggagcicatggcattg C/T gaatggacatttctccgt	961
NDUFS6	5	intron 2 + 1568	tggagaaggagggtttctc T/G tagtggatcggtatggt	962
NDUFS6	6	intron 2 + 1692	gaccgtggtgacggaggttt C/T ctggcatcgatgggtgtt	963
NDUFS6	7	intron 2 + 6488	tagcttaataattattggc A/G ttcatgttcgaatgactga	964
NDUFS6	8	intron 2 + 6563	tttaacttttattttaa G/A tccatgaatgggtcggat	965
NDUFS6	9	intron 2 + 6740	aaagatttaaacctacat C/T ttatgcccaatcattgat	966
NDUFS6	10	intron 2 + 6832	gcgagggactcatttacag A/T ggttgacacttcaactgtt	967
NDUFS6	11	intron 2 + 7054	ttcactgcggagcttggc G/A tggaaacccggagccggct	968
NDUFS6	12	intron 2 + 7186	ggtcagggtcaccccttggc T/C ggcacactaaatgacggg	969
NDUFS6	13	intron 2 + 7225	ggggcatcccggtcagtc G/A ccagtgtcggagcgtcagca	970
NDUFS6	14	intron 2 + 7810	cttcacacttggggcggga C/T gctgtagaaggacacaaag	971
NDUFS6	15	intron 2 + 11080	gtaactgttcagtgottt C/T ctttggatttcagttaaac	972
NDUFS6	16	intron 2 + 11657	gggacagaacgatgtgtg G/A gagaagagggtggcagag	973
NDUFS6	17	intron 3 + 208	cgaaaaccccttcaactg T/C gaagtgtggggcctggt	974
NDUFS6	18	intron 3 + 1031	ctagagtggactgggcacc C/T ggcagtccctcctggtgt	975
NDUFS6	19	3' flanking + 270	gcttcagagagccaagtgg G/C tcttgaggtcagatgag	976
NDUFS8	1	5' untranslated - 45	agtgtagcctccgctccg A/C ttgactggcctgttgga	977
NDUFS8	2	intron 1 + 163	aggtagcggggagccggc T/C ctcaggccctcggccgc	978
NDUFS8	3	intron 3 + 123	ttctgagcctgttccact T/C ttaaatgattatggtatg	979
NDUFS8	4	intron 6 - 505	aggcaaggcggccgggac G/A gtgctaacgttgttaacc	980
NDUFS8	5	3' flanking + 491	ggccttgagctggcctgct C/A cagccacactccttctctg	981
NDUFS8	6	3' flanking + 693	ttcatttcatttgcagtg G/A aaaccagctccgagagtg	982
NDUFS8	7	3' flanking + 1267	tttcccaagtaaccggc G/A tcaggctgtggcattggagcc	983
NDUFS8	8	3' flanking + 1362	cgctgggttcttcccttac C/T gtggtctccaggcacttac	984
NDUFS8	9	3' flanking + 1449	tgtagaacaggcctatggc G/A cccacccacagtcgccca	985
NDUFS8	10	3' flanking + 1572	cagcccccagagcctgtgt C/A gctgtgtgggcttaggat	986
NDUFS8	11	3' flanking +(783-784)	cagagaccttgaccccccc (C) atctaccatcettlccaaa	987
NDUFS8	11	3' flanking +(783-784)	cagagaccttgaccccccc atctaccatcattlccaaa	988
NDUFB3	1	5' flanking - 1439	ttaaaagttagctttttt G/A cgggacaggtgctcagc	989
NDUFB3	2	5' flanking - 1436	aaagttagcttttttgc G/A ggcaggttgctcagcctg	990
NDUFB5	1	5' flanking - 213	ggcagatgaactctctacc A/C aagaaggccaaacggcgc	991
NDUFB5	2	intron 1 + 6288	gggagtttattacctagg T/C cagttaagttaagaaggct	992
NDUFB5	3	intron 1 - 1581	cttcgggacactgtatct A/G ttcttccctgttlacct	993
NDUFB5	4	intron 1 - 1487	ccctcttagaccgtatag T/G tctagcatagatctgcaca	994
NDUFB5	5	intron 2 + 556	ttgttggacatctgccac G/A gtatataagctctgaatca	995
NDUFB5	6	intron 3 + 467	ggcgcacatgcactccagcc C/T gggcaacagatggactct	996
NDUFB5	7	intron 3 + 497	agttagactctgtccccc C/G caaaaaaacataatcct	997
NDUFB5	8	exon 5 + 397	atgtagtctctgaagata T/C atgaagacaaatggcctgc	998
NDUFB5	9	intron 1 +(231-215)	attagcatttctaaacgtt GTT/Δ attcaccatccaaattaag	999
NDUFB7	1	intron 1 + 68	cctgaacacctggaccccca G/A ggttgacccccaggctgg	1000
NDUFB7	2	intron 2 + 266	ggcctctctaggccctgtt T/C gatgggacagggcagtg	1001
ABCA1	1	5' flanking - 278	ggcccgccggggagagg G/C acgagaccgggacccata	1002
ABCA1	2	5' flanking - 99	acataaacagagggcggga G/C gggcgggggggggagag	1003
ABCA1	3	intron 1 + 159	gcggttttaaatgggagao G/T atgtctatgacagctctg	1004
ABCA1	4	intron 1 + 506	gaattggctatatgtcccc G/C ggaactggagcggcacagtc	1005
ABCA1	5	intron 1 + 5897	gtacaaaccccttagcttt T/G gcaaacctcctttagagcc	1006
ABCA1	6	intron 1 + 5929	ttagacccgatttaaatgc C/T tccctctcatgagctctt	1007
ABCA1	7	intron 1 + 5962	aagctcttctggtccact C/T ttccatcactaaagtga	1008
ABCA1	8	intron 1 + 5985	cccatcctaggtgagagt A/G agatccctctcttactt	1009
ABCA1	9	intron 1 + 11416	ttacagtgccctttatagg G/A agaaagaaagattgtct	1010
ABCA1	10	intron 1 + 11935	ttctgtggagcaaatagag G/A gctgtcagacacttggtcc	1011
ABCA1	11	intron 1 + 12281	gaotgttattttgaaaa T/A cttaataacagtagttttt	1012
ABCA1	12	intron 1 + 12924	gtgtgacatcttactc T/C aggtgaacctcggggaag	1013
ABCA1	13	intron 1 + 13002	gagccatcatcacagattct C/G tctagctcacatgaattga	1014
ABCA1	14	intron 1 + 17715	ggagctgacttttggaag C/T ctctcctttccaccagag	1015
ABCA1	15	intron 1 + 17848	gagggctgactgtccctt T/C gataggagccagcactaaa	1016
ABCA1	16	intron 1 + 21384	gtgggtggaggaattggag G/C agaaagcttgccaaagtgc	1017

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCA1	17	intron 1 + 22145	gtgcttctaaatcaacgaa C/G tgattcctggagagcagctt	1018
ABCA1	18	intron 1 + 23063	ggaggcaccctgacaccca G/A cggagtagggggcggtgtg	1019
ABCA1	19	intron 1 + 23131	agtgtcatatgtgctgacc G/A tggagcttgttgcggtt	1020
ABCA1	20	intron 2 + 156	ggacacaggactgtgtgtc T/C ggtatggcatgtgcttat	1021
ABCA1	21	intron 2 + 384	gctgtgggtgaagtgaatta A/G tggccacctcttagagatc	1022
ABCA1	22	intron 2 + 1081	agtgcagccaaaattgcasa G/A tcataccattcaaatata	1023
ABCA1	23	intron 2 + 2801	aagaaaagtatttatttca A/G gtgtgatgcttagattgt	1024
ABCA1	24	intron 2 + 2830	tgcttagattgttagattg C/G aaagatctggcttgcattt	1025
ABCA1	25	intron 2 + 2856	tcgtgcttgcattctgtaca A/G ctgcagaaactgggctcag	1026
ABCA1	26	intron 2 + 3187	tgatagcttggctgcagc A/G taccgacgttcattgcagc	1027
ABCA1	27	intron 2 + 3190	tagctgttgcctgcagcata C/T ggacgttcattgcagctc	1028
ABCA1	28	intron 2 + 3194	tgttgcctgcagcatacga C/T gtctattgcagcttctgt	1029
ABCA1	29	intron 2 + 3204	ggcatagggagcttcaatgc G/A cagtctgtctctcagat	1030
ABCA1	30	intron 2 + 3401	acataagcctgtgtgtgc T/C gccaggaagactagaacgc	1031
ABCA1	31	intron 2 + 13927	gtccacacatctggcact A/G tgcataaggctgggaatcag	1032
ABCA1	32	intron 3 + 4163	ccagcccacttcatottacc G/A tagttacctcttagatgt	1033
ABCA1	33	intron 3 + 4262	tgtaaaaggaggaactaagg T/C gccaggaactttctgcttag	1034
ABCA1	34	intron 3 + 4306	ccctctctcacttctccaa C/T gctgtatcatgaacccat	1035
ABCA1	35	intron 5 + 240	gacagagaagaaagctccag G/A gaagaatactacagattgg	1036
ABCA1	36	intron 5 + 490	gatggcatttgaactgtt G/A tctttaaaagtgaaactt	1037
ABCA1	37	intron 5 + 563	tatctgggagtggtggttt T/G ctgactgagcattggctgc	1038
ABCA1	38	intron 5 + 1051	ggctacacaaactgtcttcc C/T tgggcaagtaaaagagccaa	1039
ABCA1	39	intron 5 + 3051	tagagaaacagictaattct G/A ttcttcgtaaatagtcga	1040
ABCA1	40	intron 5 + 3127	aagtcctatgatttttaggc A/G aatgtgctctcttctctct	1041
ABCA1	41	intron 5 + 5924	ctttcttccacaaattgcc C/T cccagagctttctggaagg	1042
ABCA1	42	intron 5 + 6831	ccagtcctcagccttccca T/C tgcctatgctgtctgaaa	1043
ABCA1	43	intron 5 + 12678	gtccacgcctctgtctaccc G/C accctctggccatctctct	1044
ABCA1	44	intron 5 + 14214	cagcttggctccagagccct G/A gacctggctccagaggtcc	1045
ABCA1	45	intron 5 + 14257	gctgttcccccgtgtgtgc C/T cagaggcctggatgtgtgc	1046
ABCA1	46	intron 5 + 18078	ctcacacacacatgcacgt G/T acagccaaggtgtgtgact	1047
ABCA1	47	intron 5 + 18795	ctggctcttctctggacgt G/A ccagctaaaggaatctcc	1048
ABCA1	48	intron 5 + 18948	gcattgggtgactaagaac G/A catattccctatctctatgg	1049
ABCA1	49	intron 5 + 19053	ctcccccacattaaaagt T/C aaggatgctttatcaaatg	1050
ABCA1	50	intron 5 + 19148	ggcccaagaacatgcatth C/A gcaigtccctaaalgaagc	1051
ABCA1	51	intron 5 + 19229	atgtcacagctgtgagctca C/T atgtgtgggaagatcagg	1052
ABCA1	52	intron 5 + 19405	cttgcctcaattattctgtc T/C atataactcaattactga	1053
ABCA1	53	intron 5 + 19534	catgtgacctcttagctcc G/A cggatgaactctgtctcca	1054
ABCA1	54	exon 6 + 474	gaacacctctctgggttct G/A tatcacacacctctctctcc	1055
ABCA1	55	intron 6 + 210	gcaacctggcgtcatggcc A/C gctgtttaaataaaattga	1056
ABCA1	56	intron 6 + 334	acagttctggggcaataacc G/A tggtaagggttatgatct	1057
ABCA1	57	intron 6 + 2288	cttcttcaaaagcttgggt C/T cactggaccagatgaagt	1058
ABCA1	58	intron 6 + 2322	atgaagtgaatagtttgg T/C ccagaaaggaaattaaatga	1059
ABCA1	59	intron 6 + 2820	gtgtttgatacattctgag T/G ttcagtaaaagacctgatg	1060
ABCA1	60	exon 7 + 656	tgagctttgtgacctccaa G/A ggagaaactggctgcagcag	1061
ABCA1	61	intron 7 + 416	catcataaagatgacattg G/A ggcgtcacagttgaagagc	1062
ABCA1	62	intron 7 + 471	agaccacactatttagctta C/T ttagtataacattgcaag	1063
ABCA1	63	intron 7 + 504	ttgcaaaagaaaattccgac G/A aagtttttcagcctaggaa	1064
ABCA1	64	intron 7 + 679	gctctgttggaattctctc G/C ctaccccaaacatcatctt	1065
ABCA1	65	intron 7 + 1740	acaaatgctcacccttccg C/T tgaatgattgaattttgg	1066
ABCA1	66	intron 7 + 2122	tgattaaagtggtactacc A/G ggtgctttctgcatactcg	1067
ABCA1	67	intron 7 + 7753	taggaattccaaagctgaa T/C ttctactgaagctctttgg	1068
ABCA1	68	intron 7 + 8973	atggaaattgtttattgtt A/T ctacagattgccaattat	1069
ABCA1	69	intron 7 + 8976	gaattgtttattgtgact A/G cagattgccaattattatg	1070
ABCA1	70	intron 7 + 11327	ctaacaactctatttccatt G/G agtcttatataaagaatgg	1071
ABCA1	71	intron 7 + 11738	ctgacgtttaaggagaccg C/T gtatgtcctttgaggactg	1072
ABCA1	72	intron 7 + 12295	agtctgtaatattgttct T/A tttttcttagcttatgct	1073
ABCA1	73	intron 8 + 387	tagcaagccaaatcttita C/G caacacacatgcttgcatac	1074
ABCA1	74	intron 8 + 697	ggaaactgtgtgtgtctccc A/T gcataggaagctgagccagg	1075
ABCA1	75	intron 8 + 1312	attgctctgcagatccctc G/A cagccctctgtccttcttc	1076
ABCA1	76	intron 8 + 3036	ctttatgtgggaagaattt T/G ttttttattggggagtg	1077

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCA1	137	intron 40 + 252	gaaggtaaggaaatagtt T/C atttgcttgatccactggc	1138
ABCA1	138	intron40 + 319	agcactgaaagtcacacc A/G taacttgagaattaggtga	1139
ABCA1	139	intron 40 + 957	cttgtaactcttttttctt G/C tcatgggtgatagccatttg	1140
ABCA1	140	intron 41 + 146	tgaatgggcatcccgagc C/T cctccctgcccactcctgga	1141
ABCA1	141	intron 42 + 239	cattggtttatatgcttac A/G ttatgtgttagttattaaa	1142
ABCA1	142	intron 42 + 321	aataaatggttgatttgag T/A ttgagttcatagtcacaaa	1143
ABCA1	143	intron 42 + 322	ataaatggttgatttgag T/C tgaatttcatagtccaaaa	1144
ABCA1	144	intron 42 + 533	agtgaaaaattatgtatg G/A ataagtatgatacaggttct	1145
ABCA1	145	intron 42 + 546	tgtatgtatgaatgaatg A/G cgttctcaaaaagccaggtt	1146
ABCA1	146	intron 43 + 739	tacagccacacttaaatgg T/A cccattatgaatcatatt	1147
ABCA1	147	intron 44 + 18	taggtggaabegaaagtcg T/C tgaattttgctcaaaagact	1148
ABCA1	148	intron 44 + 264	acaeataattgctgttt T/G ttaagatataatttagta	1149
ABCA1	149	intron 44 + 279	tgttttttaagatataatt T/C agtgatttttgtaaatga	1150
ABCA1	150	intron 44 + 508	ttacatgtctacataaat C/T cccatgtacatgtaccta	1151
ABCA1	151	intron 44 + 1477	gatctccctcctgtctctt A/T cattttgcagtagcaatgt	1152
ABCA1	152	intron 44 + 1665	tgggttaagaactgatttg G/A ttggtatagctgtgagggcc	1153
ABCA1	153	intron 44 + 1956	gttgctcacactcaaat T/G ictgggctttctcatttgg	1154
ABCA1	154	intron 45 + 68	aatatctacttatgtgttt T/C ccacacgcatgacttcagg	1155
ABCA1	155	intron 46 + 808	ttatactgacttcaatagag G/C ttccagacaaaagtgttt	1156
ABCA1	156	intron 47 + 336	ttcacaattgaacacacac T/C aactgaacacatcatccc	1157
ABCA1	157	intron 49 + 55	aggggtggatcctgcgcc G/C acactcccgcccataggicc	1158
ABCA1	158	3' UTR(exon 50)+7949	aacaaaaatgggtgtctc C/T aggcacggaaacttggttc	1159
ABCA1	159	3' UTR(exon 50)+8226	aggagccacagttaacaata C/T tgggcagccttttttttt	1160
ABCA1	160	3' UTR(exon 50)+8682	aactttctccactttttcca G/A aatttgatattaaactaa	1161
ABCA1	161	3' UTR(exon 50)+8897	ttccagaatttgaatttaa C/T gctaaaggtgaagacttca	1162
ABCA1	162	3' UTR(exon 50)+9097	aactattttgaagaaacac A/G acattttaacacagttgaa	1163
ABCA1	163	5' flanking - (1033-1032)	tgaactaaattattagacat (AT) ggtgtgagcctgcattcc	1164
ABCA1	163	5' flanking - (1033-1032)	tgaactaaattattagacat ggtgtgagcctgcattcc	1165
ABCA1	164	intron 5 + 6368	ttctgatgggtgtgtgctg C/Δ tgaagatcatgactgggtg	1166
ABCA1	165	intron 5 + 9709	cattttctgtgaacccc T/Δ caccattcaggcagctgct	1167
ABCA1	166	intron 5 + 13816	tcctacttctcctttttt T/Δ catttgctctctacacccac	1168
ABCA1	167	intron 10 + (270-271)	cttttcaggaggagccaaa (G) cgtcattgtctgtgtctt	1169
ABCA1	167	intron 10 + (270-271)	cttttcaggaggagccaaa cgtcattgtctgtgtctt	1170
ABCA1	168	intron 20 + (611-612)	tttagccatcctctccccc (C) gccaccctccttattgagc	1171
ABCA1	168	intron 20 + (611-612)	tttagccatcctctccccc gccaccctccttattgagc	1172
ABCA1	169	intron 32 + (391-392)	gagtgccttgggtactctct (T) gatgggggactccatgata	1173
ABCA1	169	intron 32 + (391-392)	gagtgccttgggtactctct gatgggggactccatgata	1174
ABCA1	170	intron 37 + 847	gctgtatattggaatgccc C/Δ gtttcaaaagcaaaagccaa	1175
COMT	1	5'flanking - 1287	cgtatgatattcccaattct G/A agtccagatcaactgaaat	1176
COMT	2	5'flanking - 1217	tgtgattatgggaaggagaa G/A cttttctgtgtgtgtccccc	1177
COMT	3	5'flanking - 503	cagggtctccaggaggagga G/A tgtgtatctctccattgctc	1178
COMT	4	5'flanking - 425	gagaagtgggaagtctgccc C/T agtggggccggtgctgtgtg	1179
COMT	5	5'flanking - 277	cccagcccgagtttcccac C/T tgggaaggggctacttgtg	1180
COMT	6	intron1 + 12058	ctggcccatgggaaggagg G/A agggggcccgacggggcca	1181
COMT	7	intron1 + 12070	agggggggggggggggggc A/G cggggccacagtaaggagt	1182
COMT	8	intron1 + 18831	tgtgtgttcttggtaaac C/T agcccttggcttacacatc	1183
COMT	9	intron2 + 832	cctctctcttggccacccgt G/G actacccccaactccggccc	1184
COMT	10	intron3 + 90	ggagaagctgttatccccc A/G ttccagggggctgggaacc	1185
COMT	11	intron3 + 425	ccccaaggtgggcgtttcgg T/G gattcagagaggcagctct	1186
COMT	12	intron3 + 671	ggctcctgctcttttggaga G/A gggggggccgtgctgggg	1187
COMT	13	intron3 + 676	ctgctcttggggaggtgg G/T gggccgtgctggggatcca	1188
COMT	14	intron5 + 75	tcagcctcagcctctccaa G/C agccaggcattccagttag	1189
COMT	15	intron5 + 310	accagacaccaggggagaaa C/T ggcaaggagccaaaggagt	1190
COMT	16	intron5 + 346	agatgggggggggaaggccc G/A ctctggggccagcctgctct	1191
COMT	17	intron5 + 3023	aaggcagccgcccctgctaa G/A gcttagggcattgtctcct	1192
HNMT	1	5'flanking - 211	cagagggcagatgacagctt C/T cgttaagatttcaactgctg	1193
HNMT	2	intron1 + 5409	aetataactgataattgg A/G acatttcattgtggcctagt	1194
HNMT	3	intron2 + 2561	cacttggcttggacaagaa A/G agaaggcctacaagaaaag	1195
HNMT	4	intron2 + 2895	caatcagaaatgaagaaa A/G ctccaagaaaatttaagt	1196
HNMT	5	intron2 + 3977	accaaacttggaggtgaaa G/A ttatgatgtatgttcagt	1197

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
HNMT	6	intron2 + 5296	ttacatagtgagttggag T/C cccaggattttatttcc	1198
HNMT	7	intron2 + 13317	caaccctcatgaattcttag C/T tgggatgggtccctataca	1199
HNMT	8	intron2 + 14682	gtatgtgagcaaatgagttc A/Δ ggagagatttaaatcccta	1200
HNMT	9	intron2 + 15406	gtctatgcattcatgcctcc G/A tctaaccagctgtctaccta	1201
HNMT	10	intron2 + 28943	atgtgacttaacttcaggt A/G tatcaatctccctgaatgt	1202
HNMT	11	intron4 + 49	cagaagaagagcttttcaga A/G tatatataatgaatctct	1203
HNMT	12	intron4 + (1942-1943)	tttgagaaaatttaaggta (A) tcttctatggcccacttcca	1204
HNMT	12	intron4 + (1942-1943)	tttgagaaaatttaaggta tcttctatggcccacttcca	1205
HNMT	13	intron4 + 2405	ccctgtgacaaagcagataa C/A ctatgctttatitgltcca	1206
HNMT	14	intron5 + (80-81)	cctgtgtttgaaagaagctt (TT) atatattttgtcttattat	1207
HNMT	14	intron5 + (80-81)	cctgtgtttgaaagaagctt atatattttgtcttattat	1208
HNMT	15	intron5 + 235	ctttcttttgggaaatag T/C ctittgtctctatatatga	1209
HNMT	16	intron5 + (702-703)	tacttacaggttgattttag (AT) acacagcagactctgtcttc	1210
HNMT	16	intron5 + (702-703)	tacttacaggttgattttag acacagcagactctgtcttc	1211
HNMT	17	intron5 + 749	ttcacacagaccccatctt T/G aacaccatagtccacaaat	1212
HNMT	18	intron5 + 1101	gtggcagcctattctgtat T/G atattcatcaatcatcaga	1213
HNMT	19	intron5 + 1137	acagaaaaagtattgtagac G/A gaataacaattcattgaga	1214
HNMT	20	intron5 + 1348	aaggagacatgaatgtcca C/G aagtaacigagaactgatta	1215
HNMT	21	intron5 + 1673	caaaagaaaggagtaaga C/G tcaacatcagtttagctttt	1216
HNMT	22	intron5 + 2022	attttatttgggctttcta C/T gtctctctctctaaagcta	1217
HNMT	23	intron5 + 2285	tgtcatacttaactttaa G/C atccagagtaaatgaggag	1218
HNMT	24	intron5+4159	taccagtggcccgcaacc C/T tcttatagtagtttaaal	1219
HNMT	25	intron5 + 4501	aatgatccacaaatctacta C/G tctttgtttcttcaatga	1220
HNMT	26	intron5 + 5251	cacacacacacacacaca C/G caaatggagccgcagaca	1221
HNMT	27	intron5 + 5802	gaaaaagaaacttgctta C/T atcatgttgaacaaagat	1222
HNMT	28	intron5 + 6189	tccaatccacctctccta G/C agcatatccctcagttacct	1223
HNMT	29	intron5 + 6297	gtcttgatctctcttgag T/A taattgactctggaactt	1224
HNMT	30	3'flanking + 458	tatgtcactctcaagaact C/T tataagaccagaagctctct	1225
HNMT	31	3'flanking + 993	ctgaaatgaacactgaacc G/A ttaatcatactgatgtac	1226
HNMT	32	3'flanking + 1793	gtggagcagacgttttgg G/A ctgatatttgcattata	1227
GAMT	3	intron5 + 1411	ggtagactgggtccatccc G/A ocaaggagaccaggtgcc	1228
PNMT	2	intron1 + 35	ctgaggacaggggacaaga G/T gtctgctgggagtgaaagca	1229
CYP1A1	1	intron1+1590	ccactcttcaaaaggagta C/T atgtgacagcagctggaaat	1230
CYP1A1	2	exon2+160	gaatccaccagggccatgg G/A ctggcctctgattggcaca	1231
CYP1A2	1	5'flanking-731	gcttgggctaggttaggg T/G cctgagttccggctttgct	1232
CYP1A2	2	intron1+371	cttccctgtttcacactaa C/T ctttctctcttggaaatg	1233
CYP1A2	3	intron3+44	ataggcaggagaagcctga G/A acccaggttattgttcagt	1234
CYP1A2	4	intron5+81	tccctgtcaggaaactgtta T/C ataagaaagagggagcct	1235
CYP1A2	5	exon6+181	ctggccatcctgtacagca A/T ctggattcagcgtgccgc	1236
CYP1A2	6	exon6+295	cagctgcgcttccatcaa C/T tgaagaagacaccaccatc	1237
CYP1B1	1	5'flanking-3669	tgtatcctgtgaagcatcac G/A gttatccttctctgcacatg	1238
CYP1B1	2	5'flanking-3149	tacagcacttcccaacta G/C ttctctgtattttgagtca	1239
CYP1B1	3	5'flanking-1222	gggggaagcccccgcgc G/A agcgcctccggttccctta	1240
CYP1B1	4	5'flanking-376	ttccggagagcaagctcaag T/C cgcggagagggagggagt	1241
CYP1B1	5	5'flanking-265	ctgggacacagctgcggcct C/T gattggaggtgctgtgat	1242
CYP1B1	6	intron1+129	tgcgcgcagctgtgtccca G/A atgcaggaaaccgttacgcg	1243
CYP1B1	7	intron1+379	tgaagtcaagccttctct C/T tctgtcccagatgggac	1244
CYP1B1	8	exon3+(799-800)	agcttctgggagatttttt (T) gagtcaagacttaagggc	1245
CYP1B1	8	exon3+(799-800)	agcttctgggagatttttt gagtcaagacttaagggc	1246
CYP1B1	9	exon3+1284	agtatagtggttccatga G/T ttatcatgaatttaagta	1247
CYP1B1	10	3'flanking+2226	ttctttttttttttttt T/Δ aaaaatttttctatttct	1248
CYP1B1	11	3'flanking+(2226-2227)	ttctttttttttttttt (T) aaaaatttttctatttct	1249
CYP1B1	11	3'flanking+(2226-2227)	ttctttttttttttttt aaaaatttttctatttct	1250
CYP1B1	12	3'flanking+2230	tttttttttttttttaa A/Δ ttttctctatttcttaca	1251
PEMT	90	intron1 + (297-299)	attgtgagactcagaggt TGT/Δ ccgtgtagtcttgggatt	1252
PEMT	91	intron1 + 817	tcatgaagcctgttaaggcac A/G tcttgcctcccaagcgttc	1253
PEMT	92	intron1 + 830	aaggacatcttgcctccaa G/A cagcttcaatccagttctt	1254
PEMT	93	intron1 + 1035	gatttctctgaaggagctaa T/C accagttagttttgaaga	1255
PEMT	94	intron1 + 1573	agtgaggcaggagagactaac C/T ggtgtgtgaggggtggct	1256
PEMT	95	intron1 + 1759	gatttttttaagaagaa A/G gaaagaacatcacatcac	1257

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
PENT	96	intron1 + 2768	gcattctgctgccacagc C/A gggcacctccaggattcag	1258
PENT	97	intron1 + 2785	ggccggggcacctccaggt T/C cagaagtgactccagtagg	1259
PENT	98	intron2 + 4598	ccgtgggtttttttttt T/A ctctattctttgtgtgtg	1260
NAT2	21	exon2 + 288	atgttaggagggtatttta G/T atccctccagttacaaata	1261
NAT2	22	5'flank - 2053	ctggtttgcacacttttast T/C ccaggtgtcaggtttccac	1262
NAT2	23	5'flank - 1299	gaatcaccagtgccggaggt A/G taacagtgaacccagacac	1263
NAT2	24	5'flank - 1145	ctgtagaacacaaggataat C/T ggaggcagttgtacatgcc	1264
NAT2	25	5'flank - 1036	ccttccacacagtgcccgag T/A tcatgtggcagcagtcgaga	1265
NAT2	26	5'flank - 94	aaagatttgctaagagattc G/A cagaggcaaccigaggcct	1266
NAT2	27	5'flank - 643	atgtttatatttatattaa T/C attaatglaataaaattt	1267
AADA	1	5'UTR + 29	attaaagtacactattcagg C/T atcatgttaggtttactt	1268
AADA	2	intron1+138	gcgtggcctttgcacatgt G/A ttacttagaagtgtgttg	1269
AADA	3	intron1+142	tggccttgcacatgtttta C/T ttgaaatgtgtgttttt	1270
AADA	4	intron1+1033	ttccagcagagacaccaca A/G gtaaacaccccccgtaca	1271
AADA	5	intron1 + 1253	ttttttccctcatatttgc T/C gtctgtgtcacatgtga	1272
AADA	6	intron1+1366	ctctgtgagccttttaatt A/G ttaattcattcattactta	1273
AADA	7	intron1+1369	tgttagcccttttaattt A/C attcattcatttactcat	1274
AADA	8	intron1+2501	ggttacagaagaatgtgtg C/A ttggccaaatgatgtg	1275
AADA	9	intron2+1971	aaatgaggttaagtaggag A/C attttttttttttgtgc	1276
AADA	10	intron2+1988	gagaattttctttttttt A/G tgcaggagaatataacaa	1277
AADA	11	intron2+2341	aggtgacctttttttgtcc C/T atgcagacttaggtatct	1278
AADA	12	intron2+2546	gtctgacacagaagatcaa T/A ggcacaaigtgcaagacaa	1279
AADA	13	intron2+2609	taggaggtttcactggaaao T/C tgaattccactgagtcgga	1280
AADA	14	intron2+2663	tataaatacagtgtaaat T/C gttctgtgttttttaagta	1281
AADA	15	intron4 + 605	tgtgtcagtaaatattata T/C taagttaggtgaatgagaca	1282
AADA	16	intron4 + 821	tatatagtaggtgaatga G/T atcatglaattgtgagacta	1283
AADA	17	intron4 + 679	ttagagettcagcgaattc A/G tatactcttcagatgttat	1284
AADA	18	intron4+1680	gttaaatgtggataaatat C/T acaatttgcaaatatttgg	1285
AADA	19	intron4+1748	atttagaagttctatcacatc T/C ttlatagtatattcacact	1286
AADA	20	intron4+1771	tatatgtattacacacttc G/A aaacacaaaattttttt	1287
AADA	21	exon5 + 238	caagtcactcttcaaat A/G ttaattggagttccctgctc	1288
AADA	22	3'UTR + 121	ttagaasttggcttttcta A/G aatgtgtcagtttaagttca	1289
NTE	1	5'flanking - 535	ccagatctgtctccgattc C/T ttttaacttagactttctg	1290
NTE	2	5'flanking - 15	gttaatccccggcaaaace A/G gcaagcgccttgcagccccc	1291
NTE	3	5'flanking - 748	agcatggcgcggggaggag G/T gtggagggtcggaggagac	1292
NTE	4	5'flanking - 690	tgaataatttaaagggccg T/C gcttcggagccggccgaa	1293
NTE	5	intron6 + 605	tcttgccatatacttagtg A/G ggggtctacatcaggggtt	1294
NTE	6	intron6 + 748	agctccagcctctctctc C/T ggggtttatctcagcatct	1295
NTE	7	intron6 + 987	gggtcgtgctctgggtccc C/T gtgcgtcatgtagtctacct	1296
NTE	8	intron6 + 1882	tggcctcaagcaatcctccc G/A cctcggcctcccaagtgt	1297
NTE	9	intron6 + 2222	gaatgtttatgtgacacga G/A agactgtctcgtggtttc	1298
NTE	10	intron12 + 166	tatctgtgacccgggaagct C/G tggcctcgtcccaaggcc	1299
NTE	11	intron13 + 69	atccaggtccacccgctgcc C/T gtcttgatttttaacttg	1300
NTE	12	intron14 + 8	agcccccgtcgggttaggc C/T tgggaacctgcccgtgttg	1301
NTE	13	intron16 - 113	gccaccggccctgcgcctt T/C atatttttctaacccttc	1302
NTE	14	intron21 + 34	agggccggccggccagagc A/G tgcaggagatgtatccgg	1303
NTE	15	intron21 + 128	gaagaatcgtgcccctgag G/A gttcaaaccttaagtagga	1304
NTE	16	intron21 + 151	ttcaaaccttaagtaggacc C/G aggtcagagcatctgggg	1305
NTE	17	intron21 + 651	ccactgtctccagccggga C/T gacagagctagaacctgtt	1306
NTE	18	intron21 + 737	tggaaastgtctgtggatt G/T ttgttaggactctgggac	1307
NTE	19	intron21 + 1752	acagctggctcaggttga G/C tgggaactgggaagcaac	1308
NTE	20	intron21 + 1788	gaagcaacagctgggtcaaa A/Δ gtgacttttttttttggc	1309
NTE	21	intron21 + 1907	cactgcaacctctgcctccc A/G ggttcaagtgattctcctgc	1310
NTE	22	intron21 + 2065	ctgctcgttttatgttcag G/T tccccattagacagggaa	1311
NTE	23	intron21 + 2336	agtcggggcagcagagca G/A gaatttcagataaggaggaa	1312
NTE	24	intron23 + 41	tggggagagtggtggggg G/C ctggagcctcaattcttcc	1313
NTE	25	intron23 + 71	caaatcttttcagacctgag T/C tcaagtctcggcttccac	1314
NTE	26	intron23 + 81	cagacctgattcaagttct C/T ggcttccaaacacggagcct	1315
NTE	27	intron24 + 150	gtggggcggctgtgacctc A/G gccgtccgtattccgagct	1316
NTE	28	intron29 + 37	gccttcagcaacctgagc T/C cactgggttgggggatg	1317

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
NTE	29	intron29 + 370	cgctccaggtcagcgagccc G/A tggggccggctggccctccg	1318
NTE	30	intron30 + 56	ecctcccgacccacacacac G/A cacacgcgtgggcacacaca	1319
NTE	31	intron30 + 358	aaaaatcaaaaaaettaacc A/G ggcctgggtgggtgicctgt	1320
NTE	32	intron30 + 372	taaacagcgtggtgggtg T/C gctgtatccagctactc	1321
NTE	33	intron30 + 430	aaatcacttgaacctggag G/T tggaggttcagtgagctga	1322
NTE	34	intron30 + 655	gtgtcacaccagctatata T/C gcaatgctttctctcagg	1323
NTE	35	intron30 + 659	gcacaccagctatata T/C atgctttctctcagggcag	1324
NTE	36	intron30 + 760	tgaataggcatttgcac C/T gcatgccagctgtcccggt	1325
NTE	37	intron30 + 835	gcacacacgtagatggatg T/C ggcacctctgaccgagttaa	1326
NTE	38	intron31 + 40	tggtccctgcattgggtg T/C ggcacgctttgctacttaa	1327
NTE	39	intron31 + 41	ggcgctgcattgggtgt G/A gctagctttgctacttaa	1328
NTE	40	intron31 + 1329	gtctgtcaagggcaggacag G/A ggaatgtaggcggatgtg	1329
NTE	41	intron35 + 31	aatggcttctgtgtgtt G/A gactgggacccacgttctg	1330
DDOST	8	intron2 + 1299	atcttctgactgctggctt C/T ggcagtaactggtgttg	1331
DDOST	9	intron2 + 1581	gatacttctggtgggaaa T/C gacagagagtgtaaacagt	1332
DDOST	10	intron2 + 2822	gtttctcaacaggtgcttc T/G tgacgtttcagactggata	1333
DDOST	11	intron2 + 3392	cagaagcgtggggcctgc C/T ggcctccctgtgtgtgc	1334
DDOST	12	intron5 + 495	attgctgaaccaggaggg G/A gagggttcagtgcccaagg	1335
DDOST	13	intron6 + 226	ggactgcttgggtcacagc C/T tctgttttcccagatcc	1336
DDOST	14	intron8 + 303	aagagaataggctattag A/T tgaatttgttagcagaga	1337
DDOST	15	3'flanking + 40	cacgcgtggagacgggca G/A ggaaggggttattaggatt	1338
MRP2	1	exon 1 + 77	catattatagaaggtctt C/T gtccagacgcagtcaggga	1339
MRP2	2	intron2+192	atcaaatggctttagattt T/G gcataagaatggtagctctt	1340
MRP2	3	intron 1 + 413	gataagttctagaactgca A/G ctaatgatagtagtagaag	1341
MRP2	4	intron2+3639	gtcatatccaccccccaat C/A gacccaataggtagaatgaa	1342
MRP2	5	intron2+3989	agttatgaaccgattttt C/T gggactggtgttctagtct	1343
MRP2	6	intron2+4078	agtttccagatgtgtccc T/C aggcattcctgtgttagga	1344
MRP2	7	intron2+4171	cttattcttggtagtgg C/T ttctaccaccttagctt	1345
MRP2	8	intron 2 + 5373	gttaaggatagtgaactca A/G aattttatcacagtgcaa	1346
MRP2	9	intron2+4436	ggactagtggaagaattga C/G ctctcctgaataaagatc	1347
MRP2	10	intron 2 + 3930	aaaactggcaggagaatttc A/G ctggagctgcagtcaggact	1348
MRP2	11	intron 2 + 4257	gggtatgaaagttcttgc G/A gctgtggaggtcggtgt	1349
MRP2	12	intron 3 + 772	ggtataaggcaagattttt A/T aaaaaatttaattgctaatc	1350
MRP2	13	intron 7 + 1658	ggactctaccagcttagt G/T cctgttttctaatctaaaa	1351
MRP2	14	exon 10 + 40	tggccagggaaggtagacac G/A ttggagaacagtgaaactg	1352
MRP2	15	intron 11 + 1672	aacttttaagtcttaagac T/A ggaaggcctgtgtcttaggc	1353
MRP2	16	intron 12 + 148	ccctctacccgcccatgcc A/G ctttccctctttagaccat	1354
MRP2	17	intron 2 + 1020	agtgctgcgattacaagct G/C agccacctgcacagcctctg	1355
MRP2	18	intron 2 + 5227	taaccataattatgttct A/G tatgacatgaatttcattg	1356
MRP2	19	intron 2 + 5373	gttaaggatagtgaactca A/G aattttatcacagtgcaa	1357
MRP2	20	intron 2 + 5538	ttatgaggttaagcacatg G/T tcatgttttaaaagccttt	1358
MRP2	21	intron 13 + 180	catgagtttctgagccca G/C tttatctaatctataaatga	1359
MRP2	22	intron 13 + 1497	gtcaggggtcccccgtatgc T/C atagccagtttctctttaga	1360
MRP2	23	intron 15 + 169	atgagctgaagcaaggtt T/C tcagcccttcccctgata	1361
MRP2	24	intron 15 + 949	ttccaggtgacacatttct A/G cctaatttgggaatttaa	1362
MRP2	25	intron 15 + 984	tgttaatctagttcaatccc A/C ttatgaagaaggagggctc	1363
MRP2	26	intron 16 + 4059	caactgtatgcacagttat C/T aatttaagctccatttctt	1364
MRP2	27	intron 19 + 10899	atgtatgggtatttatgga G/A taagatattccatgctgat	1365
MRP2	28	exon 22 + 51	caagcaataggattgtttc G/A atattctcatcatccttgc	1366
MRP2	29	intron23+56	tactctgggtatctttctga C/T agggaggaaattattgtcc	1367
MRP2	30	intron 23 + 734	tggcccaactactgtactg G/A cactggggcactcaatgaat	1368
MRP2	31	intron 23 + 801	atggccagaccacactcac T/G gatttttagtgtatctgag	1369
MRP2	32	intron 27 + 124	gggtccctaaagtttcttt C/G ctctaactcaaggacctaa	1370
MRP2	33	exon 28 + 52	cagatggccagcaaggc A/C agatccagtttaacaactac	1371
MRP2	34	exon 28 + 84	aacaactaccaagtgcgga C/T cgacctgagctggatctgt	1372
MRP2	35	exon 28 + 129	agaggatcactgtgacat C/T ggtgcatggagaaggtagg	1373
MRP2	36	intron 29 + 154	ttcctagatggacagctc A/G ttccagaaactttgaaatgt	1374
MRP2	37	intron 30 + 91	gtgttaggtgtgctggca T/C agaattttctccaggtctg	1375
MRP2	38	intron 31 + 170	gccaaattttacatcacgc A/G aatgaacacgaacaggtta	1376
MRP2	39	intron 26 + 154	ctggctccatcttttaccac T/C ggaactattcttactcttc	1377

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
MRP2	40	3'-flanking + 739	gigaatttttataagct C/T gttcctttaaactttatc	1378
MRP2	41	intron 3 + 1145	acatccitcctccctcagtc C/T tcggttagtgccagtattct	1379
MRP2	42	intron23+432	tggcagtagagcagggtag G/A aggtattattctgcagaggaa	1380
ABCB1	1	5'flanking-196	gcttggagccatagtcag G/C actcaaatattttttatct	1381
ABCB1	2	5'flanking-18	tactcttaccctgtgaag G/C agaactgaagaaatctact	1382
ABCB1	3	intron1+71660	cttgcctggaggaaagggct A/C gaaatataccaatccaag	1383
ABCB1	4	intron1+80091	gaaataattcaagttctg A/C aataatcatgacctatag	1384
ABCB1	5	intron1+103126	gataatcatgaattcatc T/C gtgtctcaagaaaggctat	1385
ABCB1	6	intron1+103148	tgctcaagaaaggctatg C/T gataattgaattctgctag	1386
ABCB1	7	intron1+108428	aattatattcatcatctg A/G tcaccatttcacacaactca	1387
ABCB1	8	intron1+112042	cataagttgaatgtccca A/G tgattcagctgatgcgctt	1388
ABCB1	9	intron2+491	gcctctctgcttcgacggg G/Δ actagaggttagctcacct	1389
ABCB1	10	intron4+36	attaaattcacaataact C/T ggaatttgacatctcctta	1390
ABCB1	11	intron5+1596	ttagctctctactgcttca T/C agtgaagaatcaataactt	1391
ABCB1	12	intron8+1789	aaacactctgaatattaac C/T gctcctggaaacacagctca	1392
ABCB1	13	intron14+24	agttgtccttgcctttgcc T/C tctagagggtgcaaaata	1393
ABCB1	14	intron14+81	tgcaggaggttaggaacta C/T tataatcgggaaggga	1394
ABCB1	15	intron15+38	caaaccaacctgatttata A/G cataagaacattctactact	1395
ABCB1	16	intron17+73	gtttgttggctagggtctac A/G gtggaggtggaaacagaga	1396
ABCB1	17	intron18+564	caacagtaaatgtcaact G/A aaaggatgtctctgttta	1397
ABCB1	18	intron18+2062	tttccttgaggatgttat C/T ctctgttcttgagttcca	1398
ABCB1	19	intron18+2293	ccacatcaggttttccocag A/G ccccttggacagtttgaa	1399
ABCB1	20	intron20+557	aaacccttaacattgacac G/A tggatgttttctgggga	1400
ABCB1	21	intron21+24	cgtgcctctcttactggt G/A ttgtcttaattggccattt	1401
ABCB1	22	intron21+2725	ctgacctgttttggctgac A/G ggttttggcttccctcca	1402
ABCB1	23	intron21+4725	tcttggattataaagatcca A/G agagtaggaatgttaatt	1403
ABCB1	24	intron22+8507	tgcacttggaaanaacaa T/C atggaattgttaaatata	1404
ABCB1	25	intron22+8537	tgtaaatatacttttttt T/A aaaaaaaggacacatttat	1405
ABCB1	26	intron22+8565	aggaacattttatcagcat T/C atgacagactattacattt	1406
ABCB1	27	intron22+8952	caccttggttcatgtttt G/A caaagtactggcgttacca	1407
ABCB1	28	intron22+9520	caccacaataatctttttt A/G caatttgggtggcctctgt	1408
ABCB1	29	intron22+9836	agactctgacttagcatga C/T ggcagggaagagagactt	1409
ABCB1	30	intron24+377	taaaatcagatgttttga C/A taagtctgcaagcctttg	1410
ABCB1	31	intron24+1493	gggggggttccacacga A/Δ catggagctggacttgat	1411
ABCB1	32	intron24+1495	gggggttccaggcacgaac A/T tggagagctggacttgat	1412
ABCB1	33	intron25+342	tgcagctgtatcttctgg C/T tcaagcagctctctgctc	1413
ABCB1	34	intron26+134	cttggataaagtgtgagac G/G taataaggtctccaagtg	1414
ABCB1	35	intron26+1272	gtccttcaattttgttga A/G cttaaaacaggactctaa	1415
ABCB1	36	intron26+1384	tatttaagtgtgtttaaag A/G ttgtctataatgaattga	1416
ABCB1	37	intron26+(1987-1988)	aaggcttgaagagtgaag (AAG) gaggctattgtctccagac	1417
ABCB1	37	intron26+(1987-1988)	aaggcttgaagagtgaag gaggctattgtctccagac	1418
ABCB1	38	intron27+59	gcagccctctctggcctatag G/T ttgattataagggctgt	1419
ABCB1	39	intron27+80	ttgattataagggctgt T/C tccagaagtgaagaaat	1420
ABCB3	1	intron3+8	tctcctttggcaggtagg G/A tggcagctgggtccattg	1421
ABCB3	2	intron4+104	cttcaacctgtatgccaggac C/T tgggatgcttttctctgt	1422
ABCB3	3	intron10+219	gcagcagtggtgtcctccc A/G tggcagccccctcaggtcc	1423
ABCB3	4	intron11+(317-319)	atggtgccaggtgagtg GTG/Δ tccatctatctctgtttt	1424
ABCB3	5	exon12+19	agctgcaggactggaattcc T/C gtgggatgcacagtgctg	1425
ABCB3	6	exon12+(356-357)	aggtgggtgggtgggt GG/TGGTGGGTGGA ggtg	1426
ABCB7	1	intron1+220	acggggcaggaggttctgg C/A agaggacacctggagcgtg	1427
ABCB7	2	intron1+480	agtttaactccttctgaca G/A gctgtcttcttgatagcca	1428
ABCB7	3	intron1+(512-513)	gataggccaaaaccgtaact AT/Δ ctttccaaacatagaccgc	1429
ABCB7	4	intron1+1690	agttctccaataaggcagat G/A aagttagataaatttga	1430
ABCB7	5	intron1+5309	aattaatattcatttattgct G/A tatttgttcagtttatct	1431
ABCB7	6	intron1-11274	tgcttctttcaagccggc A/G gctttaaaaaaagttagct	1432
ABCB7	7	intron1-11085	caggttttcagggtcatgt A/G gacctgaagaaatgagag	1433
ABCB7	8	intron1-10037	attctcttttcaacttct T/C ttattacatttctcatcat	1434
ABCB7	9	intron1-21	ccactctgaactcctccc G/A ctttttcttctgacag	1435
ABCB7	10	intron3+(135-136)	ttctctaagaaaaaaa (A) catatttaattgaccatagtt	1436

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCB7	10	intron3+(135-136)	ttctctaagaaaaa catattaattgacctagtt	1437
ABCB7	11	intron3+333	aaaacaatttggtgtg G/A tttgttcaagtttattgt	1438
ABCB7	12	intron12+524	taaccactctgcccagta G/T gaaacacagtgccgaacca	1439
ABCB7	13	intron13+1543	alcctgtgagtgaggagc G/A tatggctagcataaatataa	1440
ABCB7	14	intron13+2400	tgttacccttactgctcatt C/G tcattcttccaccctgctat	1441
ABCB7	15	intron15+2201	ctccttctaaccttagcaa G/C agtctggagatttactatc	1442
ABCB8	1	5'flanking-2272	ggcttaggcctaaaggctga T/C gttggggcagtaacctga	1443
ABCB8	2	5'flanking-2070	agctatgaaaaaagaccc G/A tcttctagaggtagcaaaa	1444
ABCB8	3	intron1+25	aaacggaaaaacctactcag A/C gctggccattgaccgccgg	1445
ABCB8	4	exon2+308	tgtgtgcttggggtagcc G/A tctgtgtgaggtttcccca	1446
ABCB8	5	intron2+334	ccccacttaaaacatttgt C/G cctctgtctcccatcca	1447
ABCB8	6	intron4+12	cctgtctcgttactgccagc G/T gcaggtgcagagtggagt	1448
ABCB8	7	intron5+547	agttcatagcattctcgtc G/A gccccctcaggcctgctgt	1449
ABCB8	8	exon7+57	ggcaatgtcggactgtgcg A/T gccttgccttggggcaacg	1450
ABCB8	9	intron9+1231	tttcgcagctcagtgaca C/T cctcgcgtgccccgtttc	1451
ABCB8	10	intron9+2164	cctcttgaggctccttctag C/T gctgctaigtggagattct	1452
ABCB8	11	intron9+2645	ttcctgcctgtgcttcccc C/A gctgctttagcaagtgt	1453
ABCB8	12	intron9+2646	tcctgctgtgtgcttcccc G/A gctgctttagcaagtgt	1454
ABCB8	13	intron9+3229	caggccagcagggagtc G/A tgggtcagctggctccctt	1455
ABCB8	14	intron12+(113-114)	tcctccactgccacaaggg (GG) ccttcttcttgggcaatc	1456
ABCB8	14	intron12+(113-114)	tcctccactgccacaaggg ccttcttcttgggcaatc	1457
ABCB8	15	intron13+128	tgtctctggggagacctggc C/T gtcttcacatgtcctcagct	1458
ABCB8	16	intron13+305	ctcaggtctcagagaagct A/G tagtggaggtgctgagctgc	1459
ABCB8	17	intron14+135	acagtgtgtcagggagac C/G agaaccacagccaaaggcca	1460
ABCB8	18	intron14+159	accacagccaaaggggagac A/T gtctgtgtgtggggagagg	1461
ABCB8	19	intron15+747	gttggagccttgggtctgt A/G aggggacagagggaatcat	1462
ABCB8	20	3'flanking+333	cctatccctggctcacc G/A ggaaccacagctcccattctt	1463
ABCB8	21	3'flanking+1168	cctctttcaggggtgtgt G/A cagtgcattgatggagcagc	1464
ABCB8	22	3'flanking+(1719-1721)	tagaccgaggggcccggcc GTC/A ttctaacctgcctcggcc	1465
ABCB9	1	intron1+ 69	aggtgcacggccagggcag G/C gtgggggctgtgggcac	1466
ABCB9	2	intron1+8873	tggccagcagctggggcc T/C ggaactacctcaaggcttc	1467
ABCB9	3	intron1+8940	accagctcagcctggccagc G/A tgcacacggcccaagctgg	1468
ABCB9	4	intron1+11410	agatccaagggtccagagg T/C tggatgtgacctcogtgc	1469
ABCB9	5	intron1+12863	gggaagccagtgccacaa G/A gctctgagcttcaactcca	1470
ABCB9	6	intron1+19731	gccaaagtgtcaagctcagc G/A agggagggcctgacaggg	1471
ABCB9	7	intron1+29649	cagaatccagatgccgtaa T/C gttgttaagaagcctgcaca	1472
ABCB9	8	intron1+31793	ggccagccgggggggtac C/T ggccagaccgtgggcaaaa	1473
ABCB9	9	intron1+37537	agagtcacaggttgggtg C/A cccggggaaggtggcatcta	1474
ABCB9	10	intron1+38293	taccagcctgtgctttcag G/A gaccatgtgacctgtcaact	1475
ABCB9	11	intron1+44661	cccaggtgctgtgcttca A/G gcaggttgccgtcctgcag	1476
ABCB9	12	intron1+49576	aaagtggccctgtgtgt C/T ccttgaagccctaaagcacc	1477
ABCB9	13	intron1+64669	ccacagacaagccggtagc G/A cactcgcagctcaacacac	1478
ABCB9	14	exon2+448	cctgttttggccctgttc G/A tgggagctacatttcacto	1479
ABCB9	15	intron7+3364	ggtaccagagtggtgtac A/G gttggacaggaacgctgtc	1480
ABCB9	16	intron11+113	ggcccccaggagcttccca G/T actatcagcctcctggctg	1481
ABCB9	17	exon12+370	cccagcctgcagcactgaa A/G gacgacctgcatgtccat	1482
ABCB10	1	5'flanking-424	tcggtctgcgcctccgcc C/T ggtctcggcgtgagaaag	1483
ABCB10	2	exon1+491	acaaagggcggttgccccc G/T cagcggccggaactccggag	1484
ABCB10	3	intron1+37	ccattccctccggccggcc T/G ctcttctccacacggggg	1485
ABCB10	4	intron1+217	actgtttgcagattttaca C/T ttgttttctgttgacacac	1486
ABCB10	5	intron1+405	gcgtttatactttttttt T/A aaccaaaccacattattg	1487
ABCB10	6	exon3+185	agggccggggccaggcttc C/T gtagcatcagatgatgt	1488
ABCB10	7	intron6+1269	caaatccaaactgtgcctt C/G cacagaatgggttgaaaaac	1489
ABCB10	8	intron9+632	cccaactcacttgggtgag G/A gcaagtgatgtgaggt	1490
ABCB10	9	intron10+2373	tacctcagggcactcagaca G/C cctcaccatcagaggctca	1491
ABCB10	10	intron11+108	tccttttctgtttttgt T/G ttttttttcttgaggtg	1492
ABCB10	11	intron11+2379	cattgtttttatgtattc T/A gtgtgtgcatccatcatca	1493
ABCB11	1	5'flanking-(2596-2595)	tgtgttttagagctttctct (TT) gagacatttttctaaaggt	1494
ABCB11	1	5'flanking-(2596-2595)	tgtgttttagagctttctct gagacatttttctaaaggt	1495
ABCB11	2	5'flanking-1746	agctgaagtgaattagcac G/A atcaactcagttactacact	1496

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCB11	3	5'flanking-(326-314)	aggggaaggtttaaagga (T)9-12 gctctgtatgttttaagt	1497
ABCB11	4	5'flanking-135	agagaggttcccaagcacac T/C ctgtgtttgggttatgtct	1498
ABCB11	5	intron1+511	aaatagatgcaaaaaaa A/Δ tgaagcttgggtgcatgttt	1499
ABCB11	6	intron1+581	aattcagtttttaggtcac C/T caagccagtgaggatcacat	1500
ABCB11	7	intron1+(1938-1951)	aaagacgttttaaggcctt (A)10-13 gaaagaaaagaaactgtag	1501
ABCB11	8	intron1+4517	ggttcccaacatctcatct G/A ataaaaaaataattgccca	1502
ABCB11	9	intron1+5651	aaagagaatagggttagtga T/C tagtattcctgtccttaag	1503
ABCB11	10	intron1+(12200-12201)	aagagtggtctctagcccc GT/Δ gtttgatttggggcacttac	1504
ABCB11	11	intron1+13023	glitggctactttgattaaa G/A aagaagaagagataataat	1505
ABCB11	12	intron2+739	cctgcctatcttgcaccta C/T actggggaacagatgtg	1506
ABCB11	13	intron2+(921-922)	tattttagttcaaaaagt (CAGATCTTCTTCAGCT AATTAGAAATGT) tgcctgctcatttgatattca	1507
ABCB11	13	intron2+(921-922)	tattttagttcaaaaagt tgcctg tccatttgatattca	1508
ABCB11	14	intron3+844	agccacacgttctctattgc G/A tgggaagtttaaaaatggg	1509
ABCB11	15	intron3+2231	agtgaacctgagattgagct A/G tactgaactctctagaagag	1510
ABCB11	16	intron3+2406	aaaggggtgtctttaaatcc T/C tatgtttttctcatcaggt	1511
ABCB11	17	exon4+10	tttctcatcagggttacaaga T/C gagaagaaggtgatgccgt	1512
ABCB11	18	intron4+434	ccattttatagtatttctca A/G tgcctccacacagtttatcta	1513
ABCB11	19	intron4+518	gtagatgagtagctaaaaac G/T aaagtacgtcctgaataa	1514
ABCB11	20	exon5+120	ggcacaaatgacagatgtttt T/C attgactacgactgtgatt	1515
ABCB11	21	intron5+320	ggaggtgacccatgaatt T/C acttgatlatcatctccaag	1516
ABCB11	22	intron5+16076	agaagaggttaacagtaagcc T/G cctgatttacgacacatc	1517
ABCB11	23	intron6+303	atttgcaggtgtgttttgc G/C ggcaggttgagtgcttga	1518
ABCB11	24	intron7+1141	aaaggattcagcaggcatga A/G gaaagaaagctttgcaaga	1519
ABCB11	25	intron8+2463	ccattggctaataagcaatga A/C ctatgacatgtgtctaetta	1520
ABCB11	26	intron8+2677	tcaatgatgttacagtga A/C tctaatattgtatttaaccc	1521
ABCB11	27	intron8+2699	ctaakattgtattaaacca T/A gccacatgttaaatgaatct	1522
ABCB11	28	exon9+24	gtgtcagaatttacgacta T/C gagctgaagccctatgccaa	1523
ABCB11	29	intron9+108	cacctggctgtgtggcctcc A/G gaggaggtactgtttcaaga	1524
ABCB11	30	intron10+2475	taatactccaaaccacgga G/A ttatttcattaaagacatg	1525
ABCB11	31	intron10+2478	tcattccaaaccacggaatt T/A atttcattaaagacatgata	1526
ABCB11	32	intron10+2711	tttacagattgaaagcca C/T tgaagtgttcaggtccaga	1527
ABCB11	33	intron10+3539	agtgcctgttaattgatca G/G ttgtgcacagagaaaaatg	1528
ABCB11	34	intron10+3623	tgcaagaaggtgttcttca T/C gaccttctgaggttcagaa	1529
ABCB11	35	intron10+3661	gaattcattataaaaaaa A/T caactaatggagcgtgcat	1530
ABCB11	36	intron10+5100	gggccactctttggcttggc A/G atagactgtggccaatgaaa	1531
ABCB11	37	intron10+5292	gctatttggtagaacatct G/A ggcagatcaggtgaccttc	1532
ABCB11	38	intron10+5912	gagtaattcagtaaaaa A/Δ taangtggatttttaataca	1533
ABCB11	39	intron12+116	tgttccagtaataaggaat G/A gagggtcttctctgaag	1534
ABCB11	40	intron12+326	gataaatgacaaggcaatta G/C aacaatcaggaagcacaggt	1535
ABCB11	41	intron12+335	caaggcaattacaacaatca A/G gaagcacaggttcttccaa	1536
ABCB11	42	intron12+2572	cctcatccttgccaatgtt C/T ctttactgtttttgatgg	1537
ABCB11	43	exon13+23	tctaaatgacctcaacatgg T/C cattaaccaggggaatga	1538
ABCB11	44	intron13+70	atggcagttatgtatcaaa C/T agaaaggtgtagcatcatt	1539
ABCB11	45	intron13+(1578-1579)	ttatggcctctatttttc (C) tgcacattgtcagatga	1540
ABCB11	45	intron13+(1578-1579)	ttatggcctctatttttc tgcacattgtcagatga	1541
ABCB11	46	intron14+32	catcattcctgggagaac C/T aagaggtcatagaaggaaaa	1542
ABCB11	47	intron14+80	cacaattatacatttctt C/T tctgtatgttcccaagtcac	1543
ABCB11	48	intron14+439	tattgtgtaaaaaaacttc A/G ttgtatctcattctaaag	1544
ABCB11	49	intron14+(1262-1263)	cagcctttgcattatattt (T) gctgtgtgtctaacaggag	1545
ABCB11	49	intron14+(1262-1263)	cagcctttgcattatattt gctgtgtgtctaacaggag	1546
ABCB11	50	intron14+1283	gctgtgtgtctaacaggag A/G aaagagacacggattgtctc	1547
ABCB11	51	intron14+1339	tgagatagattataggacc G/A tgaccaatttttttttgg	1548
ABCB11	52	intron14+1359	gtgaccaatttttttttgg T/C tgaataatttttttgaag	1549
ABCB11	53	intron14+1480	tattgattgacataaccc G/A tctgggaaggatattct	1550
ABCB11	54	intron15+370	ccttttcaatgtctgcaca G/A cctatttaagatatccca	1551
ABCB11	55	intron16+(550-559)	aaagtttagtttctatca (T)9-12 gctactctgatggactct	1552
ABCB11	56	intron17+188	ttctctcccaattcctgg T/G ttttggtagcttctcatc	1553
ABCB11	57	intron17+194	tcccaattcatgggtttt T/G gttagcttctatcttctg	1554

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCB11	58	Intron17+(197-198)	caattcatgggtttttggtt (T) agcttctcatcttcttggg	1555
ABCB11	58	intron17+(197-198)	caattcatgggtttttggtt agcttctcatcttcttggg	1556
ABCB11	59	intron17+(289-296)	ttagaaggggacttctttt (A)7G(A)4 tctgttttagtttctct	1557
ABCB11	59	intron17+(289-296)	ttagaaggggacttctttt (A)12 tctgttttagtttctct	1558
ABCB11	59	intron17+(289-296)	ttagaaggggacttctttt (A)10 tctgttttagtttctct	1559
ABCB11	60	intron17+1070	tcagacttgggttttctat C/T ttcttcttgagaacaagt	1560
ABCB11	61	intron17+1651	tgttaaatatctcattgta T/C atctgacggattttcttg	1561
ABCB11	62	intron17+2226	ccttaagctctctctatca T/A gcacctgttctcaccagt	1562
ABCB11	63	intron17+2979	ctctctcttcttctcagc T/A ctacttttcaactgttggct	1563
ABCB11	64	intron17+3288	aetcccatatctcactta T/G ccatctcatccatgaatctt	1564
ABCB11	65	intron17+3289	atcccatatctcacttag C/T catctcatccatgaatctt	1565
ABCB11	66	intron18+97	aatatgagttttctaggtat A/G tatctagcagttttcaagt	1566
ABCB11	67	intron18+98	atatgagttttctaggtata T/C atctagcagttttcaagt	1567
ABCB11	68	intron18+892	ctctgaaggttctgataca C/T ctattttgtttgtaatcaa	1568
ABCB11	69	intron18+2681	atgtatgagatcaagtcagg A/G tcaaatatagacacccata	1569
ABCB11	70	intron18+3780	ggaccatctgttgggcaat C/G gttccagaaaatctgtgat	1570
ABCB11	71	intron18+5741	ctcaccgggtataatacaac C/T gtacgaaggttttctttt	1571
ABCB11	72	intron18+(5882-5883)	tgcgtattccctcagttgag (C) ttttttcaagccacagca	1572
ABCB11	72	intron18+(5882-5883)	tgcgtattccctcagttgag ttttttcaagccacagca	1573
ABCB11	73	intron19+10022	tgcgttaagttaaaaaaaa A/A gagattcaactataattgct	1574
ABCB11	74	intron21+322	caagattcaactactgcccc C/A aggggttgggttaacagggc	1575
ABCB11	75	intron22+257	ctgttcaatttctctctgca T/C agtgattcattccacattcc	1576
ABCB11	76	intron22+552	taattatacttcttctgt G/C ggggttaagtgggttgta	1577
ABCB11	77	intron22+569	ttgggggttaagtgggtg G/A gtacataaacacttctcaa	1578
ABCB11	78	3'flanking+243	aaacacacagaaatgacata G/A aactaaggcggcagggaatc	1579
CYP4B1	1	5'flanking-333	gaacattctacagtgctgt A/T tgaagaagcagtgattata	1580
CYP4B1	2	5'flanking-18	gagcagctgaaggcaggta G/T atgaaggctagggtctgga	1581
CYP4B1	3	intron1+341	tcceaaacctctgagatgta C/T atagaagtgagcaatccatt	1582
CYP4B1	4	intron1+542	cctatgggtggtcaggagc C/T gtgacaccttccaggttca	1583
CYP4B1	5	intron1+2856	gaggactttgcacatagtag G/A tgcctagctatattgttgc	1584
CYP4B1	6	intron1+6086	tttggacttaagactggg G/T cccgtgctagttgtgtgac	1585
CYP4B1	7	intron1+6598	ttttgggttgggggggg G/A cccatagtagggagacagct	1586
CYP4B1	8	intron1+6660	acctaagggttgcctcctg A/G agggagcagctcctagggg	1587
CYP4B1	9	intron1+7242	ccctgtctcccttaactca T/C gctggactgttccctttggt	1588
CYP4B1	10	intron2+107	gctgtgtactaagctctgg C/G agctgaggttccaccctac	1589
CYP4B1	11	intron3+361	atggttgggtgtaggacca C/T ggctggtcaccagaggtgt	1590
CYP4B1	12	intron4-492	aaaggctttcacatctaaaa C/A gtgtctctcttcttctgtc	1591
CYP4B1	13	intron4-315	ggattactatcatataccc A/G tgcgggagctcaccacct	1592
CYP4B1	14	intron4-157	ctccccacctctctgata T/C tccagcaggatggaggcag	1593
CYP4B1	15	exon5+22	acaagttggagagaaagct C/T gggaggttaagtcctttgac	1594
CYP4B1	16	intron5+125	cccaggagccttagcttgc G/A gggagacaggacctgtcat	1595
CYP4B1	17	intron5+(287-289)	tgtctaagccaatccctcct CCT/A accctctgttagcaggagao	1596
CYP4B1	18	intron6+54	gcttgggttctctctctgg C/T cctctatgccccctccct	1597
CYP4B1	19	intron7+(99-100)	agctcttaagcatttcccc (TC) ttctctcagcaaatataacc	1598
CYP4B1	19	intron7+(99-100)	agctcttaagcatttcccc ttctctcagcaaatataacc	1599
CYP4B1	20	exon8+114	tcctggtttctctactgcat G/A gccctgtaccctgagcaca	1600
CYP4B1	21	exon8+139	tgtacctgtgagcaccagcat C/T gtttagagaggaggtccgc	1601
CYP4B1	22	intron8+247	agaaggttgtcaacagggg C/T tgatattttgtgtctaat	1602
CYP4B1	23	intron8+366	tgtgggttgacagagctg A/G gacagctgggagagccagtt	1603
CYP4B1	24	intron8+650	cctttgcttgggtcagaca C/A cctgcttctctctctgggt	1604
CYP4B1	25	intron8+844	tcatatgtgagaatcccc C/A ccaagggtatccagacaca	1605
CYP4B1	26	intron8+1767	tccattccaagaattgtct G/T gttgtgtctgtggcaggat	1606
CYP4B1	27	exon9+53	tgtcatcaaggagagcttc C/T gccctctccccctgtgcc	1607
CYP4B1	28	intron9+652	agtcgggtgtgtctgagc G/T ctctgtcactgtgcagtgct	1608
CYP4B1	29	intron9+774	cctgttcaccaacctctgt C/T tgcaccaaggagcctgagc	1609
CYP4B1	30	intron10+33	tgggtctggagatcagacag G/T gttggggactggagggtca	1610
CYP4B1	31	exon12+224	ccagatggctcagggtgtga C/A ctccctgggaccaccctcc	1611
CYP4B1	32	exon12+270	ctgggttggaggagttgg G/A cccctgctctcaggaggt	1612
CYP4B1	33	3'flanking+129	tctgtgtctcaggtcacgt G/A gtgctcaggcattcagggt	1613
CYP27A1	1	intron1+295	aggaggagctgtcttggga A/G gaggtggcagaggcaatg	1614

Table 1

GENE	NO	LOCATION	SEQ	SEQ ID NO.
CYP27A1	2	intron1+17503	cagtcataaagcctctgt C/T ctctttagagaaggaggac	1615
CYP4F2	1	intron1+(145-146)	ccaagccctggcaacctca CA/Δ gtgattcaggctggccttt	1616
CYP4F2	2	intron1+193	tttaatcagctctctctct C/T ttccccattcaagtgtta	1617
CYP4F2	3	intron1+324	ccctgtctacctccggcac T/C gcccgctcctgcctctccac	1618
CYP4F2	4	intron1+367	tccttggaggtccctggccc G/C ttcttggcctcaggatct	1619
CYP4F2	5	intron1+402	ggatctcaccgtccatcccg T/C ctgccctcaggatgtcca	1620
CYP4F2	6	exon2+35	gcctgtctggctggccctc T/G ggccagtgccagcatccct	1621
CYP4F2	7	exon2+166	cgggttttccacaaccccc A/G agacggcaactgttttggg	1622
CYP4F2	8	intron2+125	ggcagagaagcagaggaggc A/G tcttactcttctctgctt	1623
CYP4F2	9	intron2+440	gggcctgtctccacttccac T/C acaccogaaggcacctttct	1624
CYP4F2	10	exon3+48	gttcgactcagctgtggc C/T acctaccgccaggctttta	1625
CYP4F2	11	intron3+701	agactccacccacgttggg T/A ccttttcttgacctgtg	1626
CYP4F2	12	intron3+742	cttccactgttggacgggc G/A aggtgagcaggggaatfg	1627
CYP4F2	13	intron3+1020	gcttagctttctccatgtc G/A cttttctatcaagggtggc	1628
CYP4F2	14	intron3+1039	cgcttttctatcaagggtg G/A cttttctcatgatgtcaac	1629
CYP4F2	15	intron3+1040	gcttttctatcaagggtg C/G ttcttctcatgatgtcaacg	1630
CYP4F2	16	intron3+1920	ccacctgtatccctctgtt G/C ctgtttctcatgtctggg	1631
CYP4F2	17	intron3+1945	ttgtctcatgtctggcgct T/A ctctacactggctgttat	1632
CYP4F2	18	intron3+2621	agcattctgtagaatgtga G/A ctgtgtcctcagggttgogga	1633
CYP4F2	19	intron3+2665	tgttgatcgtgtaggagc A/G gtccaaggcatgtcggaacc	1634
CYP4F2	20	intron6+194	gggttgaaactgtgtgtgt G/T gtccagagctgtgtggggac	1635
CYP4F2	21	intron7+67	tgtgaagtgtcagatgaag G/A atttgaactgttgaaggag	1636
CYP4F2	22	intron7+2811	ttccaaggaaattgccatt T/G aattctcctgttaactcaggt	1637
CYP4F2	23	intron7+(3096-3097)	gggttgggggttggggggg (G) ttactgccttctctccagg	1638
CYP4F2	23	intron7+(3096-3097)	gggttgggggttggggggg ttactgccttctctccagg	1639
CYP4F2	24	intron8+145	gggtgtgtctacacctgggt G/A ctgaagcagcccgagacc	1640
CYP4F2	25	exon9+44	ctctcctgggtcctgtacca C/T ctgcaagcaccaccagaata	1641
CYP4F2	26	exon11+48	gaaccctcaccaaccgct G/A tggggccggaccctgagtg	1642
CYP4F2	27	intron12+108	tgttccaaagtccagctctc C/T ttccctacacctctctggag	1643
CYP4F2	28	intron12+285	gcattgggtatccaggcacgg A/T taccctctctctattctc	1644
CYP4F2	29	exon13+238	agtgaaagcctagaattacc C/A taagaacctgttccacagtc	1645
CYP4F2	30	exon13+342	tgtgtctgaattgtcagtc G/A gccctattccagtgccaa	1646
CYP4F2	31	exon13+563	tagtgaactgtcttttata T/C gaatttccagacaggcca	1647
CYP4F2	32	exon13+707	aaatgttccggaccatagata G/C tgacgaaggtgacccagcc	1648
CYP4F3	1	intron2+258	cattaatgcacctctgcggg G/T ctctggcaggggttggg	1649
CYP4F3	2	intron2+916	ttaggacatgtctcagtc C/T acactgtctccacaaact	1650
CYP4F3	3	intron2+3417	atccagggtctacacagtg C/T acttctctcttggcttag	1651
CYP4F3	4	intron2+4090	gagagcatgaattgggtct G/A tgttctctctccagattca	1652
CYP4F3	5	intron3+89	tgtgtcctccagcgggtc G/A cgtgccatgtgcagacagg	1653
CYP4F3	6	intron3+243	tcaagtctgtctcagtc G/T gtctgtcactgtatatt	1654
CYP4F3	7	intron3+502	gggtctggggccagggtcc G/C taagtgaactgtctgagaca	1655
CYP4F3	8	intron3+755	ttttgtggcctgtcaggac A/T tgtgaacacatgtcagttc	1656
CYP4F3	9	intron3+855	gggacagacaggtgtctca G/A gtcttgtgaaggcattctg	1657
CYP4F3	10	intron3+970	cctgacatagctctcagtg C/T catgttaggcagtgctatg	1658
CYP4F3	11	intron6+122	gggggtttattatacctgat C/T gttgaaggactgtatgaat	1659
CYP4F3	12	exon7+159	gggtcacagactcacagatg C/A cgtcatccaggagcgcgc	1660
CYP4F3	13	intron7+2107	caggttgccagtgattttt T/Δ ctcaagaagtgttcatcaag	1661
CYP4F3	14	intron7+2255	gaccaagaagggtctaggag T/A gcaaggtggcttgggttc	1662
CYP4F3	15	intron8+132	cctcaatgcaaggttgtgt A/C caccctcgggtgtgaagca	1663
CYP4F3	16	exon9+59	taccaccttcaagcaacc G/A gaataccaggagcgtgtcg	1664
CYP4F3	17	intron9+13	attgaatggtagtgcaagt G/A ctgttgcctgttctgagc	1665
CYP4F3	18	intron9+36	gggtgcctgttctgagcct G/C tctctgtgtctgttcccc	1666
CYP4F3	19	intron9+167	accatcctgactgtctggg C/G aaaggttataggcccttagg	1667
CYP4F3	20	intron9+369	tccttaattcctaccctcc G/A tccagtcagggtattataa	1668
CYP4F3	21	intron9+458	tcattatccatccagtcct T/C gtccagcaaatctctcata	1669
CYP4F3	22	intron10+46	ctctcgtgtggaagaggg A/C cctcaggcaggagcatig	1670
CYP4F3	23	intron10+63	gggcctcctcaggcaggagc G/A ttgtcctgactgcccccttc	1671
CYP4F3	24	intron11+14	ccctgaggtgcgggcccccc C/G tctctgttttttccattcc	1672
CYP4F3	25	intron11+84	gatcaggagaatccaacatc G/A cctccctccaagacacac	1673
CYP4F3	26	intron11+113	caagacacacaccactgtct T/C tccaaggctggcggactgg	1674

Table 1

GENE	NO	LOCATION	SEQ.	SEQ. ID NO.
CYP4F3	27	intron11+164	cgccaccctcttctgtctc T/G cctccaggctctatgacctt	1675
CYP4F3	28	intron11+165	ggcaaccctcttctgtctc T/C cctccaggctctatgacctt	1676
CYP4F3	29	intron12+156	gaaaagcccacagagtg G/A ttgggttggtcctgaagga	1677
CYP4F3	30	intron12+253	gagctcggttaggtctcag G/T atatgcaagcccacatggg	1678
CYP4F3	31	intron12+346	ttgggtgcccaggccaggtt A/C ccggttgatggggcaggga	1679
CYP4F8	1	5'flanking-61	accatgtttaccatcattg G/T tctggagctccccagcccc	1680
CYP4F8	2	exon1+67	gtggcagcatccccgtggct G/T ctcctgtgtgtgtcgggc	1681
CYP4F8	3	intron1+707	taocgacaggtattcaca T/G tatttccacettatccactg	1682
CYP4F8	4	intron1+857	acacccctacccctcacatc G/A tgacacagctgggcccagaag	1683
CYP4F8	5	intron1+907	tgccatctccacccctcccc G/A tgcagggtcattctttat	1684
CYP4F8	6	intron2+668	ttgtgcacttccaccatag T/C tcatgcccctctgtctcag	1685
CYP4F8	7	intron2+818	ggcacagagccattggctca G/A gcccacaaatgcigagtac	1686
CYP4F8	8	intron2+1079	tatgcttgggtgttcagaa C/T atgtggacatgtaggagc	1687
CYP4F8	9	intron2+1194	ccggcccccttatgcccc C/A accctccttctctctctgc	1688
CYP4F8	10	intron5+45	aacatgggatggagtgagg G/T gtgggttgaggagagcaaa	1689
CYP4F8	11	exon8+(19-20)	ggccatgacaccacggccag (GCCAG) tggcctctcctgggtctgt	1690
CYP4F8	11	exon8+(19-20)	ggccatgacaccacggccag tggcctctcctgggtctgt	1691
CYP4F8	12	intron8+222	tttatttccccactaaactg C/G tatgcaagcttagtaaatc	1692
CYP4F8	13	intron8+334	cttgagagattaacggcaaa A/T accgcaatgacttttgacc	1693
CYP4F8	14	intron8+1999	ttctaatgacattattctc T/C tgccttttagctatgatcag	1694
CYP4F8	15	intron8+4184	caggagggcggtgtatgctc C/T ctggataattgttggtgtt	1695
CYP4F8	16	exon9+119	acgtgtgtctccagacagc C/T gactatccccaaagtgcc	1696
CYP4F8	17	intron11+282	gggttggtgggttccgggct G/C gtctcgtgcgcagtgggcc	1697
CYP4F8	18	intron11+340	tgacgtcagacettccacct C/T ggccccaggaactgcacg	1698
CYP4F8	19	3'flanking+35	atcacctacotttgaccaa T/C taacttttcagatttcggt	1699
CYP4F8	20	3'flanking+83	ctgtgttgcccctgtgctt G/C agtcccgaggatgccagta	1700
CYP4F8	21	3'flanking+90	ggccccctgtgctcagtcac A/G cggatggccagtagggggcg	1701
ALDH1	1	intron1+564	cattattttctcagccaa T/C tgttgcattggagcagatg	1702
ALDH1	2	intron1+710	gttctgagagtaactctgaa C/T ttgctcttttcacactgct	1703
ALDH1	3	intron1-3868	ccctttttatattccagaaa C/G agcctaactctttctctg	1704
ALDH1	4	intron2+2933	taagtatgctatactatatt T/C gatagatactatactata	1705
ALDH1	5	intron2-1646	caatgtgattaaactgaatgc C/T gcaaatatgcaatgtatag	1706
ALDH1	6	exon3+54	caggcttttcagattggatc C/T ccgtggcgtactatggatgc	1707
ALDH1	7	intron3+157	taggcccccttaacattgaac T/G atttcaaatgaatctgc	1708
ALDH1	8	intron3+339	tgactgtctcagaaatgat G/A ttaggtttattcaagcatt	1709
ALDH1	9	intron3+655	agcagttagatgagtcagag C/A ataataagttggggaggg	1710
ALDH1	10	intron3+735	gaagccaatttaacataaac C/A aataccaagatcaggttca	1711
ALDH1	11	intron3+863	gcaagatggttaatacaag G/A accatttattatccaaatat	1712
ALDH1	12	intron3+1757	agatgacaaagatttctctc T/A ttcaaaaattccctagcaca	1713
ALDH1	13	intron5+90	ttctctaaaacagatggatg C/A ttatgtatttgaatgtg	1714
ALDH1	14	intron6+213	cagggaagccaaacacaaagg T/C ttgggtcgaacagttcaact	1715
ALDH1	15	intron6+1323	ttttgaaataattctata C/T ttttaacttttaactttta	1716
ALDH1	16	intron7+638	gcaaaaggaagtggtggag G/A atactgtaccatgcaaaaaa	1717
ALDH1	17	intron9+(1462-1463)	aatggaattctatgttttt (T) gttgtattattttctatc	1718
ALDH1	17	intron9+(1462-1463)	aatggaattctatgttttt gttgtattattttctatc	1719
ALDH1	18	intron9+1757	tgactagaatttgattct A/G taatgaatgaatccagt	1720
ALDH1	19	intron12-1383	aatccacttattactctcc T/G gagaacttcaagtccctata	1721
ALDH1	20	3'flanking+40	tttaagtacaagttttgt T/C acagtgatttctctgtca	1722
ALDH2	1	intron3+1768	aaatttggtgctcatctgc C/A tggcccccttccctccctc	1723
ALDH2	2	intron8+52	gaaggtagccctggccacct G/C tgttggtgclccagccgatc	1724
ALDH2	3	intron8+69	cctgtgtgtggtccagacc G/A atcctgtcgtcccccagtg	1725
ALDH2	4	intron9+5197	gctttcttatgaccttggtc C/A atttccagttgtctgttg	1726
ALDH2	5	intron11+114	gagctgggtcagtttctcc T/C gggcagggtgtgtgtcga	1727
ALDH2	6	3'flanking+411	ggatagattttctgcccctc T/G tctgtgtgtgtgaacagct	1728
ALDH2	7	3'flanking+(432-433)	tctgtgtgtgtgaacagct TC/A ttttcatgcatattctttt	1729
ALDH2	8	3'flanking+488	ccatgaagatgtgttgaa G/T gtttcatgcatattttgt	1730
ALDH7	1	5'flanking-1455	ctgcctgtccaccccacag C/T agottgcacatcatccccc	1731
ALDH7	2	intron1+464	catgaatgaacttgggaag A/G atcattcttgcaatggact	1732
ALDH7	3	intron1+2269	aaatggatccacacagaa G/C agacctccctcaccggtca	1733
ALDH7	4	intron2+1349	actgagcttctgccaccggc C/T gctgcggccttcattgaga	1734

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ALDH7	5	intron2+1820	tccgtgtggaaggcaaccttc C/G ctcagcctcagtggttaga	1735
ALDH7	6	intron2+2046	aacctcaggcgtgcctcag C/G caggagccagcctggcccc	1736
ALDH7	7	intron2+2939	aagcacgcactgaacatga G/A tgagtgaatgaacgaatga	1737
ALDH7	8	intron3+7	tgccnagaacctgtgagc C/T ggcgggctgagggcag	1738
ALDH7	9	intron4+36	gccccttcgggtacaccttc T/C ccgtcagggcctcaggccc	1739
ALDH7	10	intron6+(116-117)	attctctctctctctctct CT/Δ ggaaccagctggagcagto	1740
ALDH7	11	intron6+263	cagacctcactagtgacct T/C gctgccccagcctcttag	1741
ALDH7	12	intron6+1298	gtagacagagctggactcca T/G ccttggtgataaggatcc	1742
ALDH7	13	intron6+1411	ggcagggtcacagcagagg C/T gggaggagccaaagggttg	1743
ALDH7	14	exon7+185	acctgcgtggccccgacta C/T gtctatgcagccctgagat	1744
ALDH7	15	exon7+339	tgcggcattgctgggtgc G/A gctgtggccattggggccc	1745
ALDH7	16	intron7+249	ccagggtctcagggtcagc G/A tgcatagatgaactccato	1746
ALDH7	17	intron7+277	atgaactccatccaccac C/T ggctatcctgaaggctgta	1747
ALDH7	18	intron7+498	gaccaaggctcggggattct C/T tgtgtccacagccctgag	1748
ALDH7	19	intron8+14	caggcaggtgggggtcggc C/T gggctggcagggtcaggag	1749
ALDH7	20	intron8+49	caggagcccgccgtggcag C/T accagtggtggcagcaggg	1750
ALDH7	21	intron8+111	tcaggacttggagtgtag A/T cctctggctctgtctctgc	1751
ALDH7	22	intron8+3219	atcctgaggggtcacaagg G/A gctcacgacatcctgttc	1752
ALDH7	23	exon9+33	gtgtgacccagaccagag C/T gggggctctgtgggaaca	1753
ALDH7	24	intron9+948	tcacagcccccagagctgac C/A ctttgttggccgtggccc	1754
ALDH7	25	intron9+1067	aggctcccaagcctgggtc C/T ctctggccccaccactct	1755
ALDH7	26	exon10+137	ccgcaatgcgcgcgcgcct G/A aggtgctgctgtggccat	1756
ALDH7	27	exon10+397	cgtcccaaccctgagagcc G/A agtgggaagcatgggaac	1757
ALDH7	28	exon10+1198	ctcttccccatgctgctcat C/T ctctggccccaccactc	1758
ALDH7	29	exon10+1475	cagggtggacotgatttc G/A tctctgtctctctggctga	1759
ALDH7	30	3'flanking+15	cctggcaatacttaccttc A/G gtgattgtctttgtgcat	1760
ALDH7	31	3'flanking+60	caacaggactctggaccaag G/C ccctggcgttggtaacaat	1761
ALDH8	1	intron1+98	agggaaagggatgtgtccc G/A tggccctgtgttcaggggg	1762
ALDH8	2	intron1+157	atggctgcaggggccatggg T/C acgggcttgcctcaggagag	1763
ALDH8	3	intron1+354	tctgtggcagacaaggatt C/G ggtcggggcaccagggtc	1764
ALDH8	4	intron1+851	tatgacagggtccatcaggcc T/G caacttctgtgtgtctat	1765
ALDH8	5	intron1+894	ctcagcatctgccccacag T/G gcttttgacacgttgrttc	1766
ALDH8	6	intron1-463	aaagaacctctcagatccct C/G gtttagtccagaaggagg	1767
ALDH8	7	exon2+61	gccttcaactgaggcgac G/A cggccggccgagttccggc	1768
ALDH8	8	intron2+8	ggccttcataaggtggccc A/G tggaggtggggcccccgg	1769
ALDH8	9	intron2+23	ggccgtggagagtgggccc G/C ggcagggtgagcagcgt	1770
ALDH8	10	intron2+(180-181)	ttcactctgaacactaca (A) gccacctgtgtgcaggct	1771
ALDH8	10	intron2+(180-181)	ttcactctgaacactaca gccacctgtgtgcaggct	1772
ALDH8	11	exon3+72	gactacgtctcagaacct T/G caggcctggtgaaggatga	1773
ALDH8	12	intron8+375	ctgcagcatcctaactcac C/T gtccgactcaaggctgccg	1774
ALDH8	13	intron8+463	aatcaacccccatggcaccoc G/A accgtcactgagagggtct	1775
ALDH8	14	exon9+33	atgctggagcggaccagag C/A ggcagcttggaggcaatga	1776
ALDH8	15	exon10+428	aggtgtcctcaactcaccca C/T cctccccaattccagccctt	1777
ALDH9	1	exon1+121	actgtgtgggtatggcgg G/A tggtagggagatgtgtgt	1778
ALDH9	2	intron1+67	cgcgatttccagccagcc C/G ccgttctgtgttctgcag	1779
ALDH9	3	intron1+103	tgcagcttgacttgagcc A/G agacagtgacagtggaggt	1780
ALDH9	4	intron1+1818	gaatttttggaaaaaaa A/Δ tgttccctttaggttgctt	1781
ALDH9	5	intron2+5891	tcaggacagggaagtaaga G/A gtttaccttctaatcttct	1782
ALDH9	6	intron2+6398	atcaaaaacacttctctat T/G atcgtctctgaacctgct	1783
ALDH9	7	intron2+9677	atgacgtgagtlitgtgt G/A tctttgttttttctgtct	1784
ALDH9	8	intron2+9991	gggagagtgagggaacctac C/T ctggcttctaactcttcat	1785
ALDH9	9	intron2+10198	ttgtcagagacettgtgtat A/G atccttactgtactatcag	1786
ALDH9	10	intron2+10256	ttagttagataactttttt T/Δ ttagggatggagatctag	1787
ALDH9	11	intron2+11382	catattceattctttatgt T/C ctttagaocaaagaaaggca	1788
ALDH9	12	intron2+11455	taaaccttlaagctcatcat C/T ggaccatctatgaatttct	1789
ALDH9	13	intron2+12044	atttaagtgaaagctattt C/T tagtttaaaattgagcag	1790
ALDH9	14	intron3+334	ctatttagcaactttttt T/Δ gacagtataaagtttca	1791
ALDH9	15	intron3+368	gttttcaacattgatatt G/Δ aaggttgtagggccatga	1792
ALDH9	16	intron4+191	ccctcaaggagcttatagtt T/A aggttgtagccactctgtc	1793
ALDH9	17	intron4+557	tagaaaattgtatgtt G/A aagcattactgttaggca	1794

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ALDH9	18	intron5+830	agttcaagatgattttag G/C ttcaggccctagttagctta	1795
ALDH9	19	intron5+838	atgatttttaggttcagg C/T ctgattgacttagcatgcaa	1796
ALDH9	20	intron6+120	agaaaagtgtgcacaaatagt A/C caaagaattcccatgtacct	1797
ALDH9	21	intron6+2569	ettaaaatctgctttaata T/C ttttttggggagaggacac	1798
ALDH9	22	intron8+1414	ccgatcttcaaaaaatagc T/C ggggtgtgtgtgtgtgtgtgt	1799
ALDH9	23	intron9+664	aaagttcacatttttttt T/A ataacttcaggtcaagagc	1800
ALDH9	24	intron9+2170	taatgcacacatttttttt T/A ctctatagggacatccaaag	1801
ALDH9	25	exon11+587	aaaacaaaaacaaaaaaa A/Δ cctgttctcttataggttc	1802
ALDH10	1	intron1+39	gggtgtggggaacattggccc G/T cgcgcgcactgtgtgactg	1803
ALDH10	2	intron3+2491	tgccgcgaagaattggcac T/A gctgagttctcatgcaagt	1804
ALDH10	3	intron3+2595	ttctgtacatcaactgtga T/A ggttgagggccagttctgt	1805
ALDH10	4	intron3+2775	taccgctttgccctgacca G/A ggttaaattcttcaataact	1806
ALDH10	5	intron3+3424	eggcaattctgcacacacccc G/A cgtctcatgcattttccctg	1807
ALDH10	6	intron3+3676	atgttgagagattgtgtgt G/A tttagcgtttaggtttttt	1808
ALDH10	7	intron4+481	tagaaaataagaggtttcag G/T tctctctgtctaataccggt	1809
ALDH10	8	intron4+769	atcctgottttatcctgaac G/A tcttgacaggcagagccaaaa	1810
ALDH10	9	intron4+796	aggcagagccaaaagccaca A/G ccaggagagctgtaccgaa	1811
ALDH10	10	intron5+254	attgtgtgtgcatatactt T/G ttttaaaaaagttaataat	1812
ALDH10	11	intron6+137	aatcctgttttctgtgtac T/C gtacctgtagctttttgtat	1813
ALDH10	12	intron6+923	eggctaataatgtaagag G/A aagggcctatcctgattagc	1814
ALDH10	13	intron7+331	tgtttttctgtatgaatcc A/Δ caggcattgtgtgaataca	1815
ALDH10	14	intron8+643	tttagaacatgacctgctg C/T ctctcccatatgtgagatga	1816
ALDH10	15	intron8+666	ctcccatatgtgagatgact G/A actcagcttttttttctcc	1817
ALDH10	16	intron9+2129	tgttttcatitttaaaaaa G/T gttgacttttgaattcatg	1818
ALDH10	17	exon10+(1894-1895)	tgtgtgtgtctactaataca CA/Δ tctgttcaaatgaacata	1819
ALDH10	18	3'flanking+31	gttttttgcacattttttt T/Δ ctcattttaaaattcttagc	1820
ALDH10	19	3'flanking+106	gtgtgtgtgtgtgtgtgt G/A gtgctatagtaaataggtt	1821
ALDH10	20	3'flanking+1630	aaaagcacgtgggaacaca A/G ttaatcatgtcttaccgtat	1822
ABCC7	1	5'flanking-834	gctaaaacactccaaagcct T/G ccttaaaaatgcgcactggg	1823
ABCC7	2	5'flanking-729	cctccttgacagattttttt T/Δ ctcttcaagtctgttcta	1824
ABCC7	3	exon1+125	tagcaggagacccagcgccc G/C agagaccatgcagaggtogo	1825
ABCC7	4	intron1+6200	ctatgtgagacgttaagaag G/A tagagtgcccaagaaggaa	1826
ABCC7	5	intron1+7538	agttctcttcttagcatgg C/A ctacagaggtgcacttact	1827
ABCC7	6	intron1+13519	gaacttaaatctttagtca T/C acaattgtgtctacatactg	1828
ABCC7	7	intron1+14110	attcacagatattttttt T/Δ aatttgggggaagtgtgt	1829
ABCC7	8	intron1+14293	ggcaggcagatttctgctc C/Δ tataaccagagcttatcag	1830
ABCC7	9	intron1+14316	taaccagagcttctcagag C/G atttatgtcccaagagaa	1831
ABCC7	10	intron1+14433	cagaataacaatgatgctc G/A gaaaataatgggtatttctg	1832
ABCC7	11	intron1+14824	acgttttgacagtgtccaa G/C tttctttcttaagcttaa	1833
ABCC7	12	intron1+23401	aatattttgaaatcacta C/G ggtatcctgcatagtgatt	1834
ABCC7	13	intron3+879	gaaaaatttcagttctatca C/A ccccatgaaaatacettta	1835
ABCC7	14	intron3+922	acttatcttaacaaagatga G/C tacacttaggccagaatgt	1836
ABCC7	15	intron3+933	caagatgagtcacttagg C/T ccagaatgttcttaagtct	1837
ABCC7	16	intron3+13704	tttttccaaataaaaaaaa A/Δ tcaggtgatctgttaagt	1838
ABCC7	17	intron3+13758	tattaaagaacatgtgtctt A/G aaacagattagggaacta	1839
ABCC7	18	intron4+240	ctctgtgtgtgttttttt T/Δ ctctatgtcatgttatcatt	1840
ABCC7	19	intron4+376	ttatgttcagcaagaagagt A/G taatatatgattgttaatga	1841
ABCC7	20	intron4+586	tgtccagacaagagcccaa T/C tgccaggccctcattttaggt	1842
ABCC7	21	intron4+1089	tttcaatctgaacattttac G/A taagtgaagactttgttaga	1843
ABCC7	22	intron4+1615	aaagttaggtgtgtgtat C/T tcttcttcttctcaatgtt	1844
ABCC7	23	intron4+1946	aatacaaacacattgagct T/C tgcctatacttttcaagaat	1845
ABCC7	24	intron6+783	tatcaagtgtttgagtcac A/G tagcactttgttgaatccc	1846
ABCC7	25	intron6+(1128-1131)	gattgattgattgattgatt GATT/Δ tacagagatcagagagctgg	1847
ABCC7	26	intron7+(731-732)	gtagcaatgagaccattttt (T) cttaggttagctccatgtt	1848
ABCC7	26	intron7+(731-732)	gtagcaatgagaccattttt cttaggttagctccatgtt	1849
ABCC7	27	intron7+1434	gaatgtttgtttgaacctg T/C ataattgtgcatgaattgt	1850
ABCC7	28	intron8+752	cagctctcttctcagctcc A/G ttcttcttattatcaccta	1851
ABCC7	29	intron8+1109	tatggcaagacttcagat G/A cgtggacttaattcttctt	1852
ABCC7	30	intron8+1312	atgaagcattcatttttt T/Δ ctccgtccaatgttgatta	1853
ABCC7	31	intron9+(6521-6522)	gtgtgtgtgtgtgtgt (GT) ttttttaacgggttttggg	1854

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCC7	31	intron9+(6521-6522)	gtgtgtgtgtgtgtgtgtgt ttttttaacagggtattggg	1855
ABCC7	32	intron10+2119	gaacactttatagtttttt T/G ggcacaaagatctagctaaa	1856
ABCC7	33	intron11+3867	tttttctcaagaaattaga A/Δ ggggggagaattgtttaa	1857
ABCC7	34	intron11+11844	tgaatcaaatcatctaaaa A/Δ gctttcagaaccagacttt	1858
ABCC7	35	intron11+12144	atattcaacaggtttacata T/C acttacaacttcacacat	1859
ABCC7	36	intron11+20975	gtgtggatgtaaatgccag G/A gtaatcacatagcatctaa	1860
ABCC7	37	intron11+27057	atggaagagaaggttttagta G/A aggggaggaagggaggtg	1861
ABCC7	38	intron11+27131	gagagagacttttttttt T/Δ aaggcagaggtttactacct	1862
ABCC7	39	intron13+152	gtattactcaaatctgac T/A gccctactgggcccagggttc	1863
ABCC7	40	intron13+287	tttgcagttcatgtgcttg T/C gatatatattactttaatt	1864
ABCC7	41	intron15+(85-86)	atcatatatatgcacacac AT/Δ aaatgttatatatcacat	1865
ABCC7	42	intron15+106	taaatgttatatatcacac T/A gtatcatgtataagtatgc	1866
ABCC7	43	intron15+3341	ggaagtataaattgttaaat A/C actgagaccacaacttacaa	1867
ABCC7	44	intron15+5556	tgtattgactaataagtaat A/T attttgggagcagctttatga	1868
ABCC7	45	intron15+5919	tgttagttctatgtggaac C/A gtgggaaataattttatat	1869
ABCC7	46	intron17+2479	caaaaaggatggaagtcag A/C ggaagagagacccttatgt	1870
ABCC7	47	intron18-81	oogtatgcaaaaaaaaaaa A/Δ gaataaatcactgcacacac	1871
ABCC7	48	intron19+751	cattaataaataacaaatc A/G tatctcttcaagaagtggca	1872
ABCC7	49	intron19+820	tgacatttgatgtatgatta T/C tctaatttagtctttttcag	1873
ABCC7	50	intron21+1532	ttacctttaactttttttt T/Δ agtttgatcagctctcttta	1874
ABCC7	51	intron21+1607	atgcttttggagttgggtct C/T ataattgtatagaattgtt	1875
ABCC7	52	intron21+11260	atgtggacaatcatgacta T/C atgcttttacttctctat	1876
ABCC7	53	intron22+(130-131)	agaatcaatattaacacac AT/Δ gttttattatggagtcac	1877
ABCC7	54	intron23+1828	ctgtcctaagtttaaaaag A/Δ aaaaagaaaggaagaagaa	1878
ABCC7	55	intron24+(7100-7112)	cctttacaaactcttagaca (T)12-14 agtttaacatgttacaac	1879
ABCC7	56	intron25+237	actcttcccccttgcaaca C/T atgatgaagcttttaatac	1880
ABCC7	57	exon27+115	gggtgaagctcttccccac C/T ggaactcaagcaagtgcag	1881
ABCC7	58	exon27+334	ggatgaataagttttttt T/Δ aaaaagaaacatttggtaa	1882
ABCC8	1	5'flanking-1099	aaagggctgaaggggtctt T/C cttttgtgtccctgactg	1883
ABCC8	2	5'flanking-(424-422)	caccccaccacccaccac CAC/Δ aagllaacgttctgccccac	1884
ABCC8	3	intron1+1212	agcctgggcaacatagtgag A/G cccccccgcccctttotaca	1885
ABCC8	4	intron2+1003	aggaggactgtgaatcccag C/A ctgcattgtttggctgggt	1886
ABCC8	5	intron2+1253	caatcactaagggaagatc C/T agtaaccagcaagatgaga	1887
ABCC8	6	intron2+1382	cccagactgcactcctgcag T/C gctgctgtctcctgtgtt	1888
ABCC8	7	intron2+2371	tttcagagctgtctggaat T/A tagggggcaggtggggggg	1889
ABCC8	8	intron3+1957	cctacccttagccacggg C/T cccacatagatgaatgg	1890
ABCC8	9	intron3+(2088-2089)	agagaacccctcattaacca (CCA) gggcgtgctgaccagtctc	1891
ABCC8	9	intron3+(2088-2089)	agagaacccctcattaacca gggcgtgctgaccagtctc	1892
ABCC8	10	intron3+2204	taaagcacagttatcaacc G/A tggatggatttgccttttc	1893
ABCC8	11	intron3+2286	ttatctccccctgaaggac A/G ctcacagagccagaaatc	1894
ABCC8	12	intron3+2312	cagagccagaaatctagaa C/G agggaaagtgaggggagg	1895
ABCC8	13	intron3+2356	ctgtgaactgagggacaga A/G ggaatgggtattggagaa	1896
ABCC8	14	intron3+2359	tgaactcagggacagagg A/C aatgggtattggagaaatgg	1897
ABCC8	15	intron3+2370	gacagaaggaatgggtatt G/A ggagaatggcagccctcca	1898
ABCC8	16	intron3+2382	tgggtattggagaatggcc A/G gccctccaagggtctgtgt	1899
ABCC8	17	intron3+4910	ggggacagccttcagctgtg G/A aatctctccgctctataga	1900
ABCC8	18	intron3+4969	catttctccagctcctgaggc A/G ttagagcagaagggccatgc	1901
ABCC8	19	intron3+5003	ccgatgctctgcccctcat C/G ctatgtctcctctgcagga	1902
ABCC8	20	intron3+5019	ccatctaatgtcctcctgc A/C gggaccacaaggtggatggca	1903
ABCC8	21	intron4+14	ggtgggtaagcagggccac C/T tggccaggttgggtggga	1904
ABCC8	22	intron4+187	agacactgcactgtgcccac G/A tgtgtctacccaggggtcc	1905
ABCC8	23	intron4+204	cacgtgtgtctaccccagg G/C tccagagggaggggggt	1906
ABCC8	24	intron4+254	gttcgtgaggttggggat G/A actttcgttagaaagggag	1907
ABCC8	25	intron4+357	tgtatcatatcgtcacgct G/C gtaaatgaatgaatgaatgt	1908
ABCC8	26	intron5+92	ggcattaggtaaatcctg G/A tgggacaaaaggggaactg	1909
ABCC8	27	intron6+4205	tctgtagaagtacatgggg G/A catgaagatcattggctga	1910
ABCC8	28	intron6+5519	gattccccgggaatgttaa A/C aggaacgggtcttcttaaac	1911
ABCC8	29	intron6+5575	tctgaccagtagccagccag G/C ggggcaagtttccatccccc	1912
ABCC8	30	intron6+6587	gttgccatctgagatcttgc C/T ggaagtacacaagagacct	1913
ABCC8	31	intron6+6747	ttccactggccttttctgct C/T agtaattgtacattacagg	1914

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCC8	32	intron9+191	gaggagctgctcccggtg A/G gacaggaagcggcatggc	1915
ABCC8	33	intron10+1963	cccaggagtcacactccct T/G tgcagctagaccatggtg	1916
ABCC8	34	intron10+2724	cctgggcatgtttttctat A/G taacagcatcaaaagatg	1917
ABCC8	35	intron10+2938	gcccgcacaggaactccac G/C tgcacagtcacataggag	1918
ABCC8	36	intron10+3094	tccgaggatgtgtttttt T/Δ cctccgttagtcagcagt	1919
ABCC8	37	intron10+3368	tcctgctcatatgcggcacc A/G tcagacttctggcagcaa	1920
ABCC8	38	intron10+8897	ggtttgattaaagcctca C/T ggcagagaattcgccatc	1921
ABCC8	39	intron11+308	tgtgtattgagaagtatg G/A gaattccagacagaaagct	1922
ABCC8	40	intron11+1171	gccctctcatttccctcca G/A tgcagcgtttccagtg	1923
ABCC8	41	exon12+7	gcctctgtccacagacttcc G/A tggccacgcagcttctc	1924
ABCC8	42	intron12+356	accaagaaatgagggcacc G/T tccaccgtgctgcccct	1925
ABCC8	43	intron12+934	tgggttcaagatggaatgg G/T gcataactcagcaaaattat	1926
ABCC8	44	intron12+1370	ggagggaggtggcaggg G/G atgaaggcagagcctgttg	1927
ABCC8	45	intron15+412	ggaggtgggcccagagtg C/T gttcttgggaccacaagg	1928
ABCC8	46	intron15+688	actcccccggcccactcac A/G tctgccaccttccctccg	1929
ABCC8	47	intron16+4464	actcatctccagattatgc G/A agagagaggttggtactgg	1930
ABCC8	48	intron16+4574	ttgaagatcttaagtgttt T/C tggttcactcatttccaaa	1931
ABCC8	49	intron16+5011	agctaaagcacaacagcct G/T tgacctggcagcattccca	1932
ABCC8	50	intron16+7808	tgtcctactttttttgac C/G ctataacttccgtactcg	1933
ABCC8	51	intron16+7730	ccagctcctagtgggtgga G/A ggaaggacatcggttgggg	1934
ABCC8	52	intron16+8369	ttgcaactgagttaggccc T/C ggagagcttactgtgtgtg	1935
ABCC8	53	intron16+9708	tgcacttgcgcctacttat T/G ccagacccaatgattgggc	1936
ABCC8	54	intron17+651	tatagttaatgggctctg A/G gtccctcaaaccttccctc	1937
ABCC8	55	intron17+692	cccttacctctcaaaaaac A/G cttggatcccttagaggtg	1938
ABCC8	56	intron17+1541	ctcaggatcttcttgaggga C/T atggttcacttccatgagag	1939
ABCC8	57	intron18+580	actaagcagatttctacaa C/T tgcacttcccattccccttg	1940
ABCC8	58	intron18+658	gaacaagccctgagaatgc C/T ttccgaccccctactcccg	1941
ABCC8	59	intron18+660	acaagccctgagaatgct T/C ccgcaacccctactcccgcc	1942
ABCC8	60	intron19+93	gcccttccatgatcaccca T/C acccagccatctcactcccc	1943
ABCC8	61	intron19+123	tctcactccccagggtcta T/C ctgacttccagccctccct	1944
ABCC8	62	intron19+219	cataggggagagggcaggaa C/T ggaaggagggagagagccc	1945
ABCC8	63	intron19+845	tagtatttaacctgccaaa C/T gctgtgtgaagtgtgacct	1946
ABCC8	64	intron20+338	tccctccacaagcttagac A/G aacaggattctctgtgaet	1947
ABCC8	65	exon21+10	tttgtgacagggcatcaac C/T tgtctgtgtgtaacgccag	1948
ABCC8	66	intron21+192	caaggtatgcacaaatgccc C/Δ attgcaagcttcagatggg	1949
ABCC8	67	intron23+17	gaaggtgggtatctcaggg A/G tggccaagcagccaccctg	1950
ABCC8	68	intron23+67	gttctgtcgaacctgaact C/T ataaaggtcttctgtctt	1951
ABCC8	69	intron26+268	gtgagcgtctgcacatccaa G/C taagattgttttctctcc	1952
ABCC8	70	intron26+308	cgataagtggtgtaattg C/T ccatccccccatgagttc	1953
ABCC8	71	intron26+348	cagctccctgcccctccctc A/G ctctctctctctcagccagc	1954
ABCC8	72	intron26+807	gacagctgtgagtcaggcc G/A gcccgcagctgagaaggcc	1955
ABCC8	73	intron26+834	cagctgagaaggcggcagt G/C gtcagatgggttgagaaac	1956
ABCC8	74	intron28+(118-121)	cctccaaaaataaaaaaaa AAAA/Δ cagaatgaaggaaatagaa	1957
ABCC8	75	intron28+1348	tgggttaagcgaagcaggg G/A tgaacgctttgagtttgt	1958
ABCC8	76	intron29+1253	ctcttaggattgtgtctea G/T taagaagagcagagcaag	1959
ABCC8	77	intron29+1589	cagatccagcttctgttaa A/G cagctcagctcagggccaaa	1960
ABCC8	78	intron29+2322	gcccctcacactctataac G/A cgcacatgccctgatgcaca	1961
ABCC8	79	intron29+2348	atgccctgatgcacacat T/C ttcaacacgcacttactcta	1962
ABCC8	80	intron29+2418	agacacgtcacctcccaca C/T gtctccacctgggggtgtg	1963
ABCC8	81	intron29+2494	tcagtcctcagacacatg C/A cctctctccacgagagaca	1964
ABCC8	82	intron29+2735	gcccgaagcagagtgatga C/T ggcagccaggttgatcaga	1965
ABCC8	83	intron30+386	gctcctggggtccagcctt C/T gcagccctgtgtgtgtg	1966
ABCC8	84	intron33+93	gggttcgcagtcacctgtg G/T ccttcaggccgagggcctc	1967
ABCC8	85	intron33+358	aggagactggggcagagag C/T gaggccaccctgtattgag	1968
ABCC8	86	intron38+54	cccaggacaggaactggct G/C ttgtggcctgactcagtgca	1969
ABCC8	87	intron38+466	aggacattctggcacatgc C/Δ tcatctctctctcaagcc	1970
ABCC8	88	intron38+529	tggcccccacccgggtgtt A/G tccccaccctctgacccgc	1971
ABCC9	1	intron3+38	tgtgtttctcttaagag C/A tattgtttttcccccaaa	1972
ABCC9	2	intron3+305	gctggccttctggttgcag T/A agttgtatttaagaatcag	1973
ABCC9	3	intron3+320	tgcagaagttgtatttaag A/G atcagagctctgtgaggag	1974

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCC9	4	intron3+631	ttctgtggaatcagaggct G/C tctaaatattctcaattt	1975
ABCC9	5	intron3+8644	tggacgcactcaacattt G/G agttattactccttcaact	1976
ABCC9	6	intron4+757	eggetatcatgaacactga A/G tcttagtaaaactctctt	1977
ABCC9	7	intron4+1022	tactgtggaattttttct G/C acagagatattgttttca	1978
ABCC9	8	intron5-1217	cagtggttagatgtttt G/G ttgccatcatctacaatat	1979
ABCC9	9	intron6+(106-107)	tatgagttgttcaaataggc (T)7-9 cagagaattgaatgtttct	1980
ABCC9	10	intron6+1347	tcagtcgtattcctactaaa A/Δ caaaattttgaagtatgt	1981
ABCC9	11	intron6+1618	cttttatttctgtcttacc G/A tttaactaaggttgatata	1982
ABCC9	12	intron6+1835	cttttaataaatgcaactg C/T acacctgtctataaaaaga	1983
ABCC9	13	intron7+407	cctatagaatttttctt G/G tttttctcaaaaaattaaa	1984
ABCC9	14	intron7+423	ttcttttttctcaaaaa C/T taatgtttgttttattt	1985
ABCC9	15	intron8+743	ttctgtagatgaagcttaag A/T gctagattttattgaaaaa	1986
ABCC9	16	intron8+850	ttttaactattgtttt G/G ttctatttttaataaaaaa	1987
ABCC9	17	intron9+585	cgaatttgcgtcttttag A/T aatcttgcataataaaaa	1988
ABCC9	18	intron9+1394	attttttctgttaagt G/C agtgaagagctgactgacg	1989
ABCC9	19	intron12+1167	atttgaagacttttaaat G/A agataattgtgctgtgtct	1990
ABCC9	20	intron12+1195	tggtgtgtgtctatatt A/G ctgaaactatgaattat	1991
ABCC9	21	intron12+2123	ataagtcctctcccgctt G/A attgacittagagctttt	1992
ABCC9	22	intron12+(2653-2656)	caaaaacagaataatgaag TAAC/Δ tattatctaaataaaaa	1993
ABCC9	23	intron13+(3043-3044)	aacatactctctctctct (CTCTTT) aagtcataatattagat	1994
ABCC9	23	intron13+(3043-3044)	aacatactctctctctct (CT) aagtcataatattagat	1995
ABCC9	23	intron13+(3043-3044)	aacatactctctctctct aagtcataatattagat	1996
ABCC9	24	intron14+85	ttctgtgaagtgctccaaa T/A ttgcttttaaatgtttt	1997
ABCC9	25	intron14+275	agtgctacatgtattttt T/C ggtattctatgttttcaa	1998
ABCC9	26	intron14+453	ctcatttcaacttggtat T/C tggactctcccaggcttg	1999
ABCC9	27	intron14+3709	atccctagtgatgacact G/A agcttgcctccactttct	2000
ABCC9	28	intron14+3813	ctgatttatatttagat G/T ttccaagttcagacatca	2001
ABCC9	29	intron14+4000	tttttactcaatgtagc A/Δ ccaaatcagaaggtgacatt	2002
ABCC9	30	intron16+1466	atccacgtgatttaattac A/G ttgttagctgtgcaacca	2003
ABCC9	31	intron16+5357	attttgaaggaattata T/G aaccttccacaactgaatt	2004
ABCC9	32	intron17+1368	aatcctgtgtttttttt T/Δ ctttttcttttcagtagg	2005
ABCC9	33	intron20+98	aagtaactcaaggaagatg G/A ttaactgtgaactgtaa	2006
ABCC9	34	intron22+28	ctcatagtccaagagctt G/C gagcccaattcagaaggtt	2007
ABCC9	35	intron22+194	tgaacctataaattctat G/Δ ccatctttggtgagtgca	2008
ABCC9	36	intron22+1370	ccagggacaaaagaagatg G/T gtaacttaaggattggac	2009
ABCC9	37	intron22+1487	agcaagccaggaaggaagtc G/G attgaattgtattagaat	2010
ABCC9	38	intron23+(455-462)	atagccatgaaggaatga AATTAGAA/Δ tgccatttgt	2011
ABCC9	38	intron23+(455-462)	tatgtttcag	2011
ABCC9	39	intron24+(460-465)	aactctttcttctatctg TTTAAAA/TTTTAA gcaagccttg	2012
ABCC9	39	intron24+(460-465)	aaggagagtg	2012
ABCC9	40	intron24+595	gcctgcaaaaataatgaaga A/G acaactctgtctgacattga	2013
ABCC9	41	intron28-926	aaatatttcagaatttggg G/A tgtgagcattgcccctat	2014
ABCC9	42	intron29+2692	cttgaagtctttttttt T/Δ aaagtaatgaatttctaa	2015
ABCC9	43	intron29+5464	agacaacactgctttttt G/A ttttcaaatcaacgacag	2016
ABCC9	44	intron29-1830	aactggtcgaaggaaaaa A/T tcatattgtctgaattttt	2017
ABCC9	45	intron31+102	tgcttttcttccacttca G/A tatccagaataactctctat	2018
ABCC9	46	intron33+877	aecatggactatagtaaat A/G tagtttttttgggttcaga	2018
ABCC9	47	intron36+1281	aatttcaactttttttt T/Δ gcaggagatattttgcaaa	2020
ABCC9	48	3'flanking+197	aattgagctcatgctgtgt T/G ttcaaatatatacatgcaaa	2021
CES1	1	5'flanking-983	tatttctttagccagcgta T/C caagctgtgttttagtaatt	2022
CES1	2	5'flanking-814	tcacattgcttgcacacac A/C cctactgctctccacccta	2023
CES1	3	5'flanking-248	agtctgcaaggtgacacc G/Δ ttatgccacaagcagttggg	2024
CES1	4	intron1+22	tgaagtccttgaagtcaaa T/Δ atgcggggcaacttttgaaa	2025
CES1	5	intron1+30	tcgaagtcacaatgctggg G/T cacttttgaatctctgtt	2026
CES1	6	intron1+1662	aagggaatccctgagctag G/A atgaccagccagtggttc	2027
CES1	7	intron1+1726	cctccctgaagtcctcagca A/C tcttagctgttctctcgcc	2028
CES1	8	intron1+2716	tgcttccaaggaagtcate T/G cagtatttttgaattagc	2029
CES1	9	intron1+(2747-2749)	tgttaattgacaacaacaca AAA/Δ gaagaagctaaatttga	2030
CES1	10	intron1+3288	ttatttgcatttaagaaa A/Δ ctcaagcgttagcttgcca	2031
CES1	11	intron1+3691	gagaatttgggacccccct T/G ttcatctctcatccagcat	2032

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
CES1	12	intron1+3819	tccttctgcttattttt A/G gctggatgttttatgcctc	2033
CES1	13	intron1+3880	aaccagctcaatgggttagg G/A aggcattgatcgtcatccc	2034
CES1	14	intron2+74	gagtcaaggcagtcctcga T/C gggctgacctttgtctg	2035
CES1	15	intron2+552	atggaagggtgtccatcca C/A cctggccaaagctgggaagaa	2036
CES1	16	intron2+885	cagtatttagatggttaag T/C attatgaigtaatatgt	2037
CES1	17	intron2+2001	ttggcatgcaaggctgcaa G/A actcatgtagaatcactcc	2038
CES1	18	intron3+2119	cgctgagtcgatgaatagtc T/G aggcctgagggtgatggag	2039
CES1	19	intron4+127	taaggcatccagccoccttc G/A taattggacactacccccc	2040
CES1	20	intron4+347	tcctgcatgacacttagcag T/G cagccagcagggtgaaggtt	2041
CES1	21	intron4+(1984-1985)	tggtgctggaaggtctgc (C) tgacatctgtctcccccc	2042
CES1	21	intron4+(1984-1985)	tggtgctggaaggtctgc tgacatctgtctcccccc	2043
CES1	22	intron5+766	gggtggcagagggtcagc T/C cactactgattcctcagtc	2044
CES1	23	intron5+825	ggagtagatcagcctgaa T/G agcgagtgagtcactgaccc	2045
CES1	24	intron5+828	gtagatcagcctggaaag C/T ggtgagtcactgacccac	2046
CES1	25	intron5+868	ctcctgcatgaactctcc T/A cccctccactctgctcag	2047
CES1	26	intron7+68	acttctcattcagctgtc C/G tcttggccaggagcagtttc	2048
CES1	27	intron7+681	cctccaatcaacaatcca A/G ttatgcctctgtctagtt	2049
CES1	28	intron7+885	aggaactatccaagagaaa T/C acattcatatacttcgacgg	2050
CES1	29	intron7+2151	gtcgtgtaactgaatct C/G aggagttgaggttcaggc	2051
CES1	30	intron7+2470	atatgatatacgaattcac G/A gagtgtgagggaagacct	2052
CES1	31	intron8+128	cgtgtttgtttctgagccc A/C gagagggtgagtcactcacc	2053
CES1	32	intron8+2618	cctgatggcaacacatggt T/G gggctctctaatctgtga	2054
CES1	33	intron8+2665	aaaattattcatcaagggt G/A aaacctaaatgaagacatg	2055
CES1	34	intron8+3785	ccatggcagtgccatgcc G/A gtctatggactggtctcac	2056
CES1	35	intron8+3791	cgcatggccatgccgtcta T/C ggtactggttcacccctcag	2057
CES1	36	intron10+222	gtggcctggagaagctgcat C/T gctcccccgggctggtgt	2058
CES1	37	intron10+230	gagaagctgcatgctcacc A/C gggcctggtgtgacatttt	2059
CES1	38	intron11+1177	ctagcaggtgccctgacaca C/G ctttgacacaggaaggagcag	2060
CES1	39	intron11+1311	ggcctatgctctgctgtga A/G ctatatatagagttcccatc	2061
CES1	40	intron11+2025	ttctcatttggagtgctaa G/A ttaaaattgacataacact	2062
CES1	41	intron11+2029	catttggagtgctaaatta A/G aaattggcataaaccttcca	2063
CES1	42	intron11+2317	cattcacaaaagctcttct T/G ctatggtgtgctctgagtt	2064
CES1	43	intron11+3887	caaatatttggctctaatto C/T gcttccactcagacagcta	2065
CES1	44	intron12+2311	ggcctctgggcatctcact G/A tgcagctttaggcgccttgc	2066
CES1	45	intron12+2331	gtgcatgcttaggcgccttg C/G ggcctctgttttttcagaa	2067
CES1	46	3'flanking+71	aacggtgatgaagagagcga T/C gtagaaggaaaggtgcttt	2068
CES1	47	3'flanking+362	ttgcacgtgacttaactgacc G/A ttgcacaggcctgcaacacc	2069
CES1	48	3'flanking+581	atttctggattctgttagta C/T gtagaagcctctaaagcatg	2070
CES1	49	3'flanking+1348	aaatctctgctggagaga G/C agcaagcatgcagatcaac	2071
ABCB4	33	intron22+767	acagtggtgctgcataga A/Δ cctgtgcaatccaccagca	2072
AADA	23	intron2+46	tgtcacgtgagtgattcgca A/G acatttlaactaagtttcag	2073
AADA	24	3'flanking+208	aatgctaaaaaasasasaa A/Δ tcactgtggtactttggaga	2074
ABCA4	1	5'flanking - 1005	tgccatcataagcagaact A/G tctctctctcttggagct	2075
ABCA4	2	5'flanking - 819	gtctagagcttttcaagag A/T acacattctgagatttgagg	2076
ABCA4	3	5'flanking - 680	agcccccacccattgcagg G/A tggatgacagtaatggcc	2077
ABCA4	4	intron1 + 208	tgcccttcccaggaaaggt G/A ttctctgtctcagccaca	2078
ABCA4	5	intron1 + 234	ctgtctcagccacatgaaa A/G tcttttgcctaccgtcctg	2079
ABCA4	6	intron1 + 510	agctcacgatcaagtcacag T/C ttaactggacacattattt	2080
ABCA4	7	intron1 + 1527	gcttaacaaccagctcaaaa G/A agagcagcatggacacgct	2081
ABCA4	8	intron1 + 2077	caggactgtgctgtgccc T/C aaatgagccattcctgtg	2082
ABCA4	9	intron1 + 2174	ccctctcaatctggccttc G/C ctggcatgggtgagcactc	2083
ABCA4	10	intron1 + 2246	gtccccaggagatggagcc A/G ctgggctgaggcccttggc	2084
ABCA4	11	intron1 + 2364	ttctgtctggcagcctccc G/A atgctcccccctgtctacc	2085
ABCA4	12	intron1 + 4243	ctccctgggtatgctgta C/G gcagttaagcgtcaaggaca	2086
ABCA4	13	intron1 + 4287	atgccctctgggagggga A/C gctgagcatgattttggaag	2087
ABCA4	14	intron1 + 4309	ctgagcatgattttggaagc C/T ggcagaagaggtatttga	2088
ABCA4	15	intron1 + 4416	tgacgcaaccgcccgcgc C/T ccgcaasacacacact	2089
ABCA4	16	intron1 + 4996	tttcccttggaacaggcag G/A ccaagctgctgtgcccctc	2090
ABCA4	17	intron1 + 5007	aacaggcagccagctggc T/C ggtccctcctctgatacaca	2091
ABCA4	18	intron1 + 5080	gtgtgtgctggtttcttag C/G aagcaccatggttccagtt	2092

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCA4	79	intron11 + 7136	gacttcccaacttacccttag T/C ggagctgtatgacacatagaa	2153
ABCA4	80	intron11 + 7180	acgctcataaagcttctct G/A ggctgtaaaggttgaaattt	2154
ABCA4	81	intron11 + 7701	gttagacgcaggcattacct C/T gtggctttgccccagtgta	2155
ABCA4	82	intron11 + 8073	ggggtgtttgccacatcca T/C tggcattttctcaaaaggaac	2156
ABCA4	83	intron11 + 8586	cagctgctgcgctggagag G/A gctcaaacctttccgccag	2157
ABCA4	84	intron11 + 8893	agcaaatgaccccttgact C/T cttttccactagtgtgct	2158
ABCA4	85	intron11 + 9257	gaatgaggtcactgtctga T/A ggcaggtggttcccatga	2159
ABCA4	86	intron11 + 11234	cccaaatattttgttttc G/A ttttaggaattaaattcag	2160
ABCA4	87	intron11 + 11641	aagaaacaaacatttatga C/G aacttttggtgtgtgacctg	2161
ABCA4	88	intron11 + 11808	tggattttcttaagaata C/T caattccatttcttttaac	2162
ABCA4	89	intron11 + 11923	aagatcattattaatctc A/G tcagcgtggtgtcacttaag	2163
ABCA4	90	intron11 + 12055	tgagaacattccatgggccc T/C gcccccaggcagtgaggct	2164
ABCA4	91	intron12 + 305	tcacocctgtgtcgggggt G/A tgagtgaactatccaaagccc	2165
ABCA4	92	intron13 + 1461	ttgggtttcagtgtcagcat G/A tagctgtctactcagatccc	2166
ABCA4	93	intron14 + 1237	aaggccaccaagtcttaag A/G gatgaggaggagcgtgagc	2167
ABCA4	94	intron14 + 1268	ggagctgagccctgtctct T/G atctaggtttccctgttct	2168
ABCA4	95	intron14 + 1309	ttccatcctcagctgtct T/C cttttccagttaccaacatg	2169
ABCA4	96	intron14 + 2979	tcacctgtgtgtgtgacaaa C/T ctgacaaaatcaagtata	2170
ABCA4	97	intron17 + 23	gagtcctttaaaacacaaat C/G ttaattgtttgaaatcaactc	2171
ABCA4	98	intron17 + 204	tgctgggcccgtgtgtatca T/G gaatggcgtgatcagtgatga	2172
ABCA4	99	intron17 + 715	gggactccctagagctgaa G/A tactctccatctgtttgtt	2173
ABCA4	100	intron18 + 1282	ggaagtgaagaacccaagc C/T gcttcagaaattcatgagg	2174
ABCA4	101	intron18 + 1531	gtctacoccttaggaccatt G/A taagagtacattggggtaat	2175
ABCA4	102	intron19 + 1802	actgctcacccaggaggcaa C/A gccctgagtcagtcaccgaa	2176
ABCA4	103	intron20 - 195	ocagattttccattgtatg G/A atgaactatgtaagccatcc	2177
ABCA4	104	intron23 + 755	ctgctcccccgtgggttcc C/T tatgtccatccacgggggag	2178
ABCA4	105	intron26 + 497	ctgagttaggtctagatgg G/A acactttgtagaalgagga	2179
ABCA4	106	intron26 + 702	tatcaaatataacacagacg T/G cagctcctctggccccttga	2180
ABCA4	107	intron27 + 156	cctgctttccaaaccccttat C/T ttagttcttggtaaacatga	2181
ABCA4	108	intron27 + 385	tttaagaacagtgagtcac G/A tgacttgcctttgaaatgc	2182
ABCA4	109	intron28 + 299	gacatgccaatcagaccacg C/T gagtgttcaggcagcctacc	2183
ABCA4	110	intron29 + 168	ctccttcacacttgtgtgc A/G gggacattcaactcctcta	2184
ABCA4	111	intron29 + 497	gctgtcaataaggaccacaa C/T agactaatttcaaatcctc	2185
ABCA4	112	intron29 + 567	agctgttaggataaaaagg G/A agacaaaacagtcacacaago	2186
ABCA4	113	intron29 + 577	aataaaaaggggagacaaaac G/A atccacaagctagagatggt	2187
ABCA4	114	intron30 - 2494	aatcacagctcatctgtgc A/G tcataaggatcccaaaagaa	2188
ABCA4	115	intron30 - 2169	aatgtacagccaagagtcct A/G gaaaaggcagggccgttcc	2189
ABCA4	116	intron31 + 535	ctactgtgaattatctct T/G tgatcactgcccctttgagat	2190
ABCA4	117	intron31 + 957	gagttctcagcagcaaatct C/A cagtatgaattttgattt	2191
ABCA4	118	intron32 + 445	tcagagggttagaacctca C/T caagtggagctcaggagcc	2192
ABCA4	119	intron33 + 48	aggatttttgacttgcttaa C/T taccatgaatgagaactct	2193
ABCA4	120	intron35 + 129	tgtttagtcaggcacatatg A/G acatccgactttcaataag	2194
ABCA4	121	intron35 + 209	ttcccccacatttatgtgg C/A aagtaagttacatttggtt	2195
ABCA4	122	intron36 + 3209	ttgaggcctccacacccac G/A gcaggttgcctcctggaggaa	2196
ABCA4	123	intron36 + 3542	cttggcagtgaggtagggca T/C ggggtgggttagggagcta	2197
ABCA4	124	intron37 + 304	ctggggcagccattcccca A/G cccctcaccagctctgact	2198
ABCA4	125	intron37 + 525	taaatttgaatgagtaatto A/G tccatctcggcctcagtttc	2199
ABCA4	126	intron37 + 766	tgttcaggtctggagacccc T/G cctatgaattgtacaggct	2200
ABCA4	127	intron37 + 856	aaaccccatgaagtgtca A/G ggcaggcatcattatctcca	2201
ABCA4	128	intron38 + 62	tagtagagtatgtttgttc G/A agcagagccaggggcaagca	2202
ABCA4	129	intron38 + 761	tccttggccaagttatctt G/A atgaagagactgggtgtct	2203
ABCA4	130	intron38 + 1315	cagagtcagactctggaag G/T cggggggataagaacacagc	2204
ABCA4	131	intron38 + 1316	agagtcagactctggaag G/A ggggggataagaacacagcc	2205
ABCA4	132	intron38 + 1526	ccaacatttgcataagcccc G/A ccttcaaaaacctgttctt	2206
ABCA4	133	intron38 + 1561	gtttttcatgttaattatc C/A gatcacacgtctatggaa	2207
ABCA4	134	intron38 + 1562	ttttttcatgttaattatc G/A atacacagctctatggaaa	2208
ABCA4	135	intron38 + 1674	ccagctgaacaccacgtgcc G/A ggtgtgtgtgatataaaca	2209
ABCA4	136	intron38 + 2867	tgcctgctagacaaagggg A/G agctccgcccactagaaac	2210
ABCA4	137	intron38 + 2874	ctagacaaagggaagctcc C/T gccactagaacattgcagg	2211
ABCA4	138	intron39 + 123	gaggggaccttctggggctg G/A aggtgtcctgcagctggag	2212

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCA4	139	intron40 + 1904	gacactgtacagccagccca A/G tctgaccccttttctcat	2213
ABCA4	140	exon41 + 5814	ggaaataaactgacatctt A/G aggtacatgaactaacc	2214
ABCA4	141	intron41 + 122	atttggtccagtttttg T/G aggtcatcatccctgtgt	2215
ABCA4	142	intron41 + 287	tctgcagagcatgggtcag C/T tcgagatgtctactca	2216
ABCA4	143	intron41 + 411	cccttccccccttctct C/A accctgtctcagttctcag	2217
ABCA4	144	intron41 + 443	gttctcagtcgggtttctt G/A tctctgcagattatccg	2218
ABCA4	145	exon42 + 5844	cgtatcttcagatttacc A/G ggcacccccagccagcag	2219
ABCA4	146	intron43 + 328	ttttagcctattccatcc A/G aatgcaccattgttccat	2220
ABCA4	147	intron43 + 345	taaaatgcacacattgttc C/G cattaccccccacacat	2221
ABCA4	148	intron43 + 370	acctcccccacacattttt A/G caaacgtttcaggggttt	2222
ABCA4	149	intron43 + 376	ctccacacattttacaaa C/T gtttcaggggtttactgag	2223
ABCA4	150	intron43 + 670	ttaaacagactggcccta T/G ggcagagacagagagatga	2224
ABCA4	151	intron43 + 701	ggagagatgagctctcactc A/G tctgctcttcttcgtctc	2225
ABCA4	152	intron43 + 822	gttaggtgtcgtgacatct G/A tccagcatctgttgaactg	2226
ABCA4	153	intron43 + 915	ggcagagcagctcctgagca C/T gcttcaatgctcagcagg	2227
ABCA4	154	intron43 + 1242	actgagctggagctagaaa G/T aaactataggttaagacac	2228
ABCA4	155	intron43 + 1871	tagagaagtttacttccat G/A ggcacatgcatctttcta	2229
ABCA4	156	intron43 + 2036	ttgagggctactcagtaatt G/A cttttttcttcagatttt	2230
ABCA4	157	intron45 + 178	gtgtttgttcacacagctc C/T ggagaaaaaacagtcagg	2231
ABCA4	158	intron45 + 193	ctccggagaaaaaacagtc C/T ggcacagccctgactggga	2232
ABCA4	159	intron47 + 238	cccaagctctcgtatgggc A/G tctgacagagcatgcag	2233
ABCA4	160	intron47 + 269	atgcatgcagacccctgctg G/A gatggggagggctctacc	2234
ABCA4	161	intron47 + 326	accattatctcaacagatc C/G gggagccttgccctattac	2235
ABCA4	162	intron47 + 715	aagtcaactaagctgttgt G/A ggaggaacagcacataccc	2236
ABCA4	163	intron47 + 734	tggggagaaacagcacataac G/T cacttatctatctgaggt	2237
ABCA4	164	intron47 + 931	ggacactgcatagatata T/C agaaatagcagcatgtcagg	2238
ABCA4	165	intron47 + 1260	acactctctgtggaccatc A/C ctcatccaagagaggttaac	2239
ABCA4	166	intron48 + 1663	tctcgtctctctcttacc C/T aggtgttgttaattttgt	2240
ABCA4	167	intron49 + 127	agagagcccccacacacca C/T ggtcctaccaggtcccccac	2241
ABCA4	168	intron49 - 1545	gcagtttaattccaaactttt C/A tcccttatggatgatca	2242
ABCA4	169	5'flanking - (1441-1400)	gtaaatcagttgaatcag (TCA)14-16 atttttcagctgttctctg	2243
ABCA4	170	intron1 + (4712-4720)	ggggggcgggactatagcc (A)8-10 cagcctaattcaaggtgag	2244
ABCA4	171	intron1 + (7295-7304)	ttgttggtttgcaatggat CACAGTCAT/Δ ttattcactc	2245
ABCA4	172	intron2 + (951-952)	cctgtccatcagactcttct TT/Δ accctccccggaggccca	2246
ABCA4	173	intron3 + (2642-2653)	cctgggtgcagagcagat (A)10-12 tagcatgatattattact	2247
ABCA4	174	intron4 + 5202	cacaaagcatctgacacccc C/Δ atocagccctgcttaacttt	2248
ABCA4	175	intron6 + (3029-3044)	cactaanaacaaasatttac (A)15-18 cctgaagaattgcaggca	2249
ABCA4	176	intron6 + (5138-5139)	ttcatgacagatcagatgtt (G) cttttatgatttacaaga	2250
ABCA4	176	intron6 + (5138-5139)	ttcatgacagatcagatgtt cttttatgatttacaaga	2251
ABCA4	177	intron6 + 5985	tttcttttttaaaaccccc C/Δ agactaggagaaggtctgtc	2252
ABCA4	178	intron6 + 6094	gggacggacagaaaaagacc T/Δ agtttctgttgccaaaga	2253
ABCA4	179	intron6 - 161	tattttttcaatnaataaa A/Δ gattttttgtttcaaaag	2254
ABCA4	180	intron7 + (809-810)	ggcccgatgtgcacactga (TG) tctggaaaagttagagaaga	2255
ABCA4	180	intron7 + (809-810)	ggcccgatgtgcacactga tctggaaaagttagagaaga	2256
ABCA4	181	intron8 + (472-484)	atcttccccacatttacta (T)10-13 ggtcttctatgggttaaagg	2257
ABCA4	182	intron9 + (48-71)	gtcccctggaccccccagaa (GT)11-13 gagagagatgtgccttctg	2258
ABCA4	183	intron9 + 554	ataggggcagaaaagacaca A/Δ ccaaaagttctctctcactt	2259
ABCA4	184	intron10 + 11	catgatcagatgaaggggg G/Δ ttgaggtatggggggggg	2260
ABCA4	185	intron11 + 4242	ggagaggaatgctgttagt G/Δ cctcctgaatagggcccg	2261
ABCA4	186	intron11 + (13743-13753)	gtctcttttgggtgtagg (T)9-11 cctctccaggagaagaaaa	2262
ABCA4	187	intron13 + (636-637)	cggttgcaggttgggggg (G) ctcatgttcattatagatg	2263
ABCA4	187	intron13 + (636-637)	cggttgcaggttgggggg ctcatgttcattatagatg	2264
ABCA4	188	intron18 + (569-570)	tgtctccctcatctctctc TT/Δ aaactagttctgattttctc	2265
ABCA4	189	intron20 - (304-297)	tataacctgactttttttc (A)7-9 ggattgtctttttaacata	2266
ABCA4	190	intron22 + (1236-1246)	gtcgaattagttcccttggg (T)9-11 agttaactcctgattttgc	2267
ABCA4	191	intron26 + (4626-4635)	gataatcaatgctgtaaggg (A)9-10 tgcattagagatccagacc	2268
ABCA4	192	intron33 + (115-116)	taaaacgtcttctttttt GT/Δ ttcatgttttttagggccc	2269
ABCA4	193	intron36 + 1078	taagcagctatcacttaaca A/Δ tacaataccagagattatca	2270
ABCA4	194	intron37 + (290-291)	ccttgaccaaagcctggggg (T) cagcattccccacccttc	2271

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCA4	184	intron37 + (290-291)	ctttgacaaagcctggag cagcatcccaacccctc	2272
ABCA4	185	intron38 + 896	ataaaagagagagaaasa A/D gaggcagctgcagagac	2273
ABCA4	196	intron38 + (1209-1210)	atggacccctgagactct CT/A ttccagactctttagatt	2274
ABCA4	197	intron38 + 1322	atcttgaaagagcgggg G/A atagagacagcccccga	2275
ABCA4	198	intron38 + 3107	agccccacctgctgaag A/D agggagctgggttcccc	2276
ABCA4	199	intron40 + 152	tttttcaaatatcaagct A/D agagctagctgaatagg	2277
ABCA4	200	intron43 + 330	ttatgactttctctaaaa A/D gacacatgtctccatga	2278
ABCA4	201	intron43 + 1358	tttttttgccatctctct G/A tttagctctttttcttg	2279
ABCA4	202	intron43 + (1305-1306)	ttctctctgagagagaa AAAG/A ccccaatgcccacgaccta	2280
ABCA7	1	5'flanking - 1598	agaaatgttgcacctctccc C/T tctgcatctctctcagag	2281
ABCA7	2	5'flanking - 1594	aatgttgccacctccct C/T ctgcatctctctcagagcc	2282
ABCA7	3	5'flanking - 1180	gccccagctgagagagac G/A tggcccaatagagagctcc	2283
ABCA7	4	5'flanking - 450	atgctgctgctgctctcc A/G gctgagccactgctctctc	2284
ABCA7	5	5' untranslated - 9	ctctctctgctctctctccc G/A ttccagctctctctctctc	2285
ABCA7	6	intron5 + 31	ccccagctgagagagagac G/A ttctctctctctctctctc	2286
ABCA7	7	exon + 543	ctgctctctgagagagagac A/G gctgagccactgctctctc	2287
ABCA7	8	intron8 + 103	ccccagctgagagagagac A/G ttgagagagagagagagag	2288
ABCA7	9	intron8 + 166	ttcagagagagagagagac C/T gctgagagagagagagag	2289
ABCA7	10	exon8 + 955	ccccagctgagagagagac A/G cctgagagagagagagag	2290
ABCA7	11	intron8 + 421	tttttttttttttttttt T/A taagagagagagagagag	2291
ABCA7	12	intron8 + 443	tttccagctgagagagagac G/A ttccagctctctctctctc	2292
ABCA7	13	intron8 + 447	ccccagctgagagagagac C/T aaatctgagagagagag	2293
ABCA7	14	intron8 + 448	gagctctgagagagagagac C/T cctgagagagagagagag	2294
ABCA7	15	exon10 + 1184	gagagagagagagagagac A/G cctgagagagagagagag	2295
ABCA7	16	intron10 + 10	tttccagagagagagagagac T/G gctgagagagagagagag	2296
ABCA7	17	exon11 + 1386	cttgcctcccccagagagac G/A cctgagagagagagagag	2297
ABCA7	18	intron12 + 115	gagctctgagagagagagac T/G cctgagagagagagagag	2298
ABCA7	19	exon13 + 1424	cttgcctcccccagagagac A/G cctgagagagagagagag	2299
ABCA7	20	intron13 + 55	gagctctgagagagagagac A/G cctgagagagagagagag	2300
ABCA7	21	intron13 + 78	tttccagagagagagagagac C/A gctgagagagagagagag	2301
ABCA7	22	exon14 + 1851	cttgcctcccccagagagac A/G gctgagagagagagagag	2302
ABCA7	23	exon16 + 2153	gagagagagagagagagac A/G cctgagagagagagagag	2303
ABCA7	24	intron16 + 34	tttccagagagagagagagac C/G gctgagagagagagagag	2304
ABCA7	25	intron17 + 8	gagagagagagagagagac A/G cctgagagagagagagag	2305
ABCA7	26	intron18 + 181	tttccagagagagagagagac C/T gctgagagagagagagag	2306
ABCA7	27	exon17 + 2385	tttccagagagagagagagac G/A gctgagagagagagagag	2307
ABCA7	28	exon17 + 2421	tttccagagagagagagagac G/A gctgagagagagagagag	2308
ABCA7	29	intron20 + 166	gagagagagagagagagac A/G gctgagagagagagagag	2309
ABCA7	30	exon21 + 3027	cttgcctcccccagagagac C/T gctgagagagagagagag	2310
ABCA7	31	intron22 + 1388	tttccagagagagagagagac C/T gctgagagagagagagag	2311
ABCA7	32	exon23 + 3417	tttccagagagagagagagac C/G gctgagagagagagagag	2312
ABCA7	33	intron23 + 147	tttccagagagagagagagac G/A gctgagagagagagagag	2313
ABCA7	34	exon26 + 3598	tttccagagagagagagagac A/G gctgagagagagagagag	2314
ABCA7	35	exon28 + 4046	tttccagagagagagagagac G/A gctgagagagagagagag	2315
ABCA7	36	intron30 + 81	tttccagagagagagagagac A/G gctgagagagagagagag	2316
ABCA7	37	exon31 + 4239	tttccagagagagagagagac A/G gctgagagagagagagag	2317
ABCA7	38	intron32 + 1	tttccagagagagagagagac G/A gctgagagagagagagag	2318
ABCA7	39	intron33 + 54	tttccagagagagagagagac G/A gctgagagagagagagag	2319
ABCA7	40	intron34 + 245	tttccagagagagagagagac G/A gctgagagagagagagag	2320
ABCA7	41	exon36 + 5057	tttccagagagagagagagac A/G gctgagagagagagagag	2321
ABCA7	42	intron38 + 65	tttccagagagagagagagac A/G gctgagagagagagagag	2322
ABCA7	43	intron40 + 154	tttccagagagagagagagac G/G gctgagagagagagagag	2323
ABCA7	44	intron46 + 277	tttccagagagagagagagac T/G gctgagagagagagagag	2324
ABCA7	45	exon41 + 5592	tttccagagagagagagagac T/G gctgagagagagagagag	2325
ABCA7	46	intron41 + 266	tttccagagagagagagagac T/C gctgagagagagagagag	2326
ABCA7	47	intron41 + 389	tttccagagagagagagagac C/T gctgagagagagagagag	2327
ABCA7	48	intron41 + 891	tttccagagagagagagagac C/T gctgagagagagagagag	2328
ABCA7	49	intron41 + 944	tttccagagagagagagagac C/T gctgagagagagagagag	2329
ABCA7	50	intron41 + 988	tttccagagagagagagagac C/G gctgagagagagagagag	2330
ABCA7	51	intron41 + 1001	tttccagagagagagagagac A/G gctgagagagagagagag	2331

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCA7	52	intron41 + 1051	actcatgctggctccacca C/T accatggccccgcccatcac	2332
ABCA7	53	intron41 + 1131	tgcctctgccccatgccatt A/G tgcctctgctccacactcaa	2333
ABCA7	54	exon44 + 5985	gaagcgtctcgtcgcgcct G/A gccatcatggtgaatggcg	2334
ABCA7	55	intron44 + 201	ggcgaggaccaggagggct G/C agccggggctctgggtgg	2335
ABCA7	56	intron44 + 233	ctgggtgatttagaagaca C/T aatcagggtgctgtggagt	2336
ABCA7	57	intron44 + 313	agttaggaggaggcctggtt A/G gggggggggccataggaaa	2337
ABCA7	58	intron44 + 337	ggcggggccataggaaagt G/C ggcgggggtattttgtgt	2338
ABCA7	59	exon45 + 6133	tggcgggcgggttccctggg G/T cggagctgcggcggcacat	2339
ABCA7	60	exon45 + 6159	ctgcggaggacatggagg C/T cgcctgcgttccagctgcc	2340
ABCA7	61	intron45 + 27	acggcgccggggtcgggctg G/C gggaggcgggctggggcca	2341
ABCA7	62	3'untranslated + 6580	aaggctggaggagagccg G/C tggtaaacctgtgcatgt	2342
ABCA7	63	3'flanking + 108	caagctgagtggtgcacatc G/A ggcgaagtgcggttcctag	2343
ABCA7	64	3'flanking + 376	cttacaggagcccggtgtcc C/T gggacacagccagggccgg	2344
ABCA7	65	3'flanking + 687	cagcaggagagacttggggg G/A gggagagaggttccactgc	2345
ABCA7	66	3'flanking + 688	agcggggagacttggggg G/A gggagagaggttcacactgc	2346
ABCA7	67	3'flanking + 1169	cctcagctgacccacttca C/T ggggctgcaggcgggtgat	2347
ABCA7	68	intron9 + (398-422)	ctgtaactaccagctctgc (T)22-26 aagagatggagctcactct	2348
ABCA7	69	intron12 + (175-184)	gggactctgagggtctgtt (G)8-10 actctgggggtctggggcc	2349
ABCA7	70	intron30 + (81-87)	ccctctgggactctccgg (C)6-7 ggcctcagctcccttcc	2350
ABCA7	71	intron34 + (349-361)	agaaagagaaagagagaaag (A)12-14 cagaatgtgctttgggtga	2351
ABCG1	1	5'flanking - 1772	cctgggcttcagcaggggcc T/C cacacotgcaatgggtcct	2352
ABCG1	2	5'flanking - 1754	cctcacacctgcaatgggt G/T ctggggagaggggtgcagtg	2353
ABCG1	3	5'flanking - 1450	tcacaagcccgatttgggt T/C ttttgggctcttttggat	2354
ABCG1	4	intron1 + 4	ctgggtggaggaagaaagta G/A gggggcggctcttttgt	2355
ABCG1	5	intron1 + 576	agctcaggaggtgtctgaa C/T gccacacagtcaggagttt	2356
ABCG1	6	intron1 + 1426	aattctcttcttaacttca A/G gaattttttatagaasat	2357
ABCG1	7	intron1 + 2342	agagcctgcaatggggccgc G/A agggacgtcccatgactca	2358
ABCG1	8	intron1 + 2399	gggggttgacagacagat A/G tgtctgtctgttccagctg	2359
ABCG1	9	intron1 + 2406	tgacagacagatatgtctg C/G tgtgttcagctgtcggtt	2360
ABCG1	10	intron1 + 2911	ccctctctgtgccactgt G/C tccaacacacagcctgtct	2361
ABCG1	11	intron1 + 4363	tataatagattcctagcaga A/G aacataattgtgagaggaac	2362
ABCG1	12	intron1 + 4752	gctttcagagccattcaca C/T aagggtctctttttatagg	2363
ABCG1	13	intron1 + 5026	ccaggtctgtgggtttcag G/A ccaaaagggcgctgcaag	2364
ABCG1	14	intron1 + 5532	gggttaaatattccggcg C/T gccaaagtcaattatctga	2365
ABCG1	15	intron1 + 5681	gctaaagtgcattggaagca T/C catgaataatctcttcagg	2366
ABCG1	16	intron1 + 6290	tcacagcagattcatgag T/A gaattgttagcccgctgt	2367
ABCG1	17	intron1 + 6386	agatgctccctccagccag C/T acattttctccctgagca	2368
ABCG1	18	intron1 + 6758	acctgcattgtgggtccccc C/G ctgccttctctctgctt	2369
ABCG1	19	intron1 + 7029	tgggtcagattaaatatc C/T tgaaggactaaaccgtaaa	2370
ABCG1	20	intron1 + 7176	ttgtcacaatttgaaasaa C/G gcaaaagatgggtttcag	2371
ABCG1	21	intron1 + 9243	gcctgagagcgtggcagta G/A gaaggctgccagtgaggac	2372
ABCG1	22	intron1 + 11224	ctctgtttgagaggaaat G/A ggcagcatcattttgcaac	2373
ABCG1	23	intron1 + 11371	ggcctctcttggagccctt T/G tctctccagccctgctct	2374
ABCG1	24	intron1 + 12420	gggatttgaatctcaaac T/C ctgagctctgtctttccac	2375
ABCG1	25	intron1 + 12484	gggttctcccaagagaat G/T tttgtatgttcttttctg	2376
ABCG1	26	intron1 + 12955	ctgggttgggtggagccac A/G gttccacactattggcagg	2377
ABCG1	27	intron1 + 12985	ctattgcaggtctgcaaca T/C ttttttggatttgcataa	2378
ABCG1	28	intron1 + 20041	acatggcgggttcccttct T/C cctcggaatggcctggaatt	2379
ABCG1	29	intron1 + 20046	gcoogcttcccttcttctc G/A gaatggcctggaattcagtc	2380
ABCG1	30	intron1 + 21058	acaagactlagaatttgacc G/A tgattttaaactattctaa	2381
ABCG1	31	intron1 + 26189	ttcttggatgtggccatgca C/T ggggcaagggttggatg	2382
ABCG1	32	intron1 + 27453	atcatgtgttgggggaaa G/C ctgggacccacttggtaga	2383
ABCG1	33	intron1 + 28098	cagggaaggagacagctgtg G/C tctgttagagttaggccg	2384
ABCG1	34	intron1 + 29670	ccttcagttgtaataggag A/G agggcgcaagaggagctg	2385
ABCG1	35	intron1 + 29810	attgttctctgtgtttgt T/C tgtttgactttcccttaa	2386
ABCG1	36	intron1 + 36220	cagaacctgtgtgtgtg C/T aggttagaggaggttttt	2387
ABCG1	37	intron1 + 36341	aaacagggttgggtctcc G/A taaggacaggagaccttcc	2388
ABCG1	38	intron1 + 36370	aggagaccttccacatct G/A gcaagaattctctttttc	2389
ABCG1	39	intron1 + 36662	cagactaatgcacattct G/A gattgagctgactgtatga	2390
ABCG1	40	intron1 + 36914	tgtaaaagatggagaagac A/G cagtgtcgttctgtgtgag	2391

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCG1	41	intron1 + 37029	tgtgactcatggccctctgcc A/G ggggactgggctggccctgc	2392
ABCG1	42	intron4 + 1186	tgaagaagaatggatgagt G/A gaaccosaaagagagaaat	2393
ABCG1	43	intron4 + 1200	aagaaaatggatgagtgaa A/C ccaaaagagagaaatgtgg	2394
ABCG1	44	intron4 + 2041	aagcagagggttttccaccc G/A gagactcaagagctgtccc	2395
ABCG1	45	intron4 + 2490	gtgtgaagtagagctgagc A/T cacggggagccctccatcc	2396
ABCG1	46	intron4 + 2552	atggccttggggcactgcct G/A ctgtgcccagccagctt	2397
ABCG1	47	intron4 + 2822	cagcagactccgtgctgag T/C cacagaaagccagcccttg	2398
ABCG1	48	intron4 + 2850	agccagggcccttggcctgcc G/A gagctggaagaccagaaaca	2399
ABCG1	49	intron4 + 2919	gcctccagagtagtactaca C/T gggaccggagggcagatggc	2400
ABCG1	50	intron4 + 3506	ggcagcctgggctgcccaga T/C cctccctggagcccccgcg	2401
ABCG1	51	intron4 + 3538	cgcccgccrfaagcccccag G/A ggggctggagctacaagtg	2402
ABCG1	52	intron4 + 3554	ccagggggctggagctaca A/G gtgaccttgaggtttttg	2403
ABCG1	53	intron4 + 3721	ccagctcatggcaggggtg C/T gggggaaagccaccacag	2404
ABCG1	54	intron4 + 3852	ccacagagccactcagtcgg C/T caagagcgtgcccagctgt	2405
ABCG1	55	intron4 + 3921	gaagaccagcagctgatgcc A/G gctgggaagggctctgcc	2406
ABCG1	56	intron4 + 3979	accaccagcctttccaga C/T agccttccagagctgtttc	2407
ABCG1	57	intron4 + 4291	gagccgctggagtggttcc G/A ctgtgatggctcccaggg	2408
ABCG1	58	intron4 + 4922	gaaccaccagaaattgtgc A/G tctctcagtgctcattca	2409
ABCG1	59	intron4 + 4988	tattgactggacacttctc C/T gtatgggactgggctagg	2410
ABCG1	60	intron7 + 672	atcagtaaacggtcactaac G/A gatcgtgatgagggccg	2411
ABCG1	61	intron7 + 840	atttcttctcactgctg T/C ctgaccagagagcggaggt	2412
ABCG1	62	intron7 + 891	tggccactgttgggtgt G/A ggtaccagagggccctgga	2413
ABCG1	63	intron7 + 997	tgtgctctgtttgtgctt C/G atctagggagtggtggcc	2414
ABCG1	64	intron9 + 1616	ctggaggagaaagcagata A/C agtctagcgtgctgtcac	2415
ABCG1	65	intron9 + 1630	aggataaagctaaagactg C/T tgcacagagtcagggtcc	2416
ABCG1	66	intron9 + 1674	gcttccaaagccgcacccg G/T gttgttctctgagccagga	2417
ABCG1	67	intron9 + 1689	ntccgggtttctctcagc C/T gagagggcttggagaaagc	2418
ABCG1	68	intron10 + 446	tggctgacagtgaaacacgc G/A gctgcttctcagaacttta	2419
ABCG1	69	intron10 + 581	atgcagagtttcaagagg C/G agactcaggaagagtaagcc	2420
ABCG1	70	intron13 + 243	accggagagccatggcagg A/C ccaagtgttctggacgttgc	2421
ABCG1	71	3'untranslated + 2370	gccttcagctgagtgctgc A/G cagtcagatgtctgggca	2422
ABCG1	72	3'flanking + 1124	ctcagaactacatcagtgga G/A gtcagtgttgaacggcca	2423
ABCG1	73	3'flanking + 1252	atggggccacagccctgcc T/C cagaagcagcttggctctc	2424
ABCG1	74	3'flanking + 1433	ggggagagcgttgggaacc A/G tggggctgttggtctgaa	2425
ABCG1	75	3'flanking + 1513	tgaaggtgaactgagtag G/C tgaagattctcagttgacg	2426
ABCG1	76	intron1 + (19909-19944)	ccgatgagggggatggg (CACCAGGCAGCAGACTCTGA TGAGGAGGGGAGGGGG)caccagggccagacttga	2427
ABCG1	77	intron1 + (19909-19944)	ccgatgagggggatggg ca	2428
ABCG1	78	intron1 + (25136-25137)	ccagccagcagactctga	2429
ABCG1	79	intron1 + (25136-25137)	catgaacttgcctgaccata cccctgaggagctagggt	2430
ABCG2	1	intron1 + 152	tcatttgaagtggtatgc G/A gtttaaaactgacagttaa	2431
ABCG2	2	intron1 + 614	agctagtcatataataac G/A ccagagtagtaagggagga	2432
ABCG2	3	intron1 + 10002	cctcatgaatggatcatg T/A cccaacatctctcttctgat	2433
ABCG2	4	intron1 + 10123	aaagtgttcccttgggtgc G/A tataccaaatccctgcata	2434
ABCG2	5	intron1 + 10768	ataggataattgagacag G/A gctcgaagaaactctcagga	2435
ABCG2	6	intron1 + 10791	ctgaagaaactctcaggaaa T/C gaaatagttccctgcttt	2436
ABCG2	7	intron1 + 10792	tgaagaaactctcaggaaat G/A aaatagttccctgctttta	2437
ABCG2	8	intron1 + 14183	tcacttaaggcttgcagg T/G gctcaggcaccagaaagaga	2438
ABCG2	9	intron1 + 14934	aaagtgtctttaaatttcc A/G tcttgagtcagtgactatt	2439
ABCG2	10	intron1 + 14955	tcttgagtcagtgactatt G/T aaattcagcgaataagttat	2440
ABCG2	11	intron1 + 17251	clgttgggaacagcaactc A/C atcataggcagagagaaagt	2441
ABCG2	12	intron1 + 17347	atttcaaacctgtttccaa G/A ttgttaagctcatcttaagg	2442
ABCG2	13	intron1 + 17626	gaaggtgcatacaacttcc T/G acataaagcttggagctata	2443
ABCG2	14	intron1 + 18271	aaatgaagctgcicattgcc A/G cacatttaaaatggacttg	2444
ABCG2	15	intron1 + 18369	ctattgctttctgtctgca G/T aaagetaaaactctccaga	2445
ABCG2	16	exon2 + 34	algtcgaagttttatccca G/A tgcacaaggaacaccaat	2446
ABCG2	17	intron2 + 36	tgaanaagacagcttttta A/G tttaactacagtgaacctca	2447
ABCG2	18	intron2 + 4230	caaccctaattggaggcc C/T gggcgtgtgtatggaaag	2448
ABCG2	19	intron2 + 4518	gttgacagacttttatgtg A/C gggcactgacctgcatgca	2449

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
CHST1	3	intron1 + 3900	gcctgcccccactccaga C/G ttgcggccctccagccctt	2509
CHST1	4	intron1 + 6520	ccctccccagaggagctgg C/T acactggggcctgtgtgt	2510
CHST1	5	intron1 + 7534	attgtgtgtgctactgc T/C cacatggaagatgcttag	2511
CHST1	6	intron1 + 7911	ttttcctlagaagaaaaa G/A ccttgcgtttttatgcatt	2512
CHST1	7	intron1 + 7963	aaaactcattcggggatta G/C tctgctactgcacgacta	2513
CHST1	8	intron1 + 9173	ggcgtgccacagatcaggcc G/A agtggggagacagaatgcc	2514
CHST1	9	intron1 + 9701	cccagaattctgaalacagc A/G gcgatgacgggactcagg	2515
CHST1	10	intron1 + 12132	aacagatccacaggaccaga C/A agcaaggagggaacatgc	2516
CHST1	11	intron1 + 12465	atgcagagaggggcttggc G/A caaaactgtaactgagata	2517
CHST1	12	intron1 + 12561	atgcicctcgttccacttgc G/A ctttgatttcagatctgc	2518
CHST1	13	intron3 + 529	ccatgtgtcaggggctct T/G catgtcagggatggggt	2519
CHST1	14	intron3 + 617	agggagcaggggaaggga C/A cacttggaactggcgcc	2520
CHST1	15	intron3 + 796	agagagctccagcagctgtc C/T gggcttaactcctgggtg	2521
CHST1	16	intron3 + 818	caggttaaatcctgggtgc A/G agaatgtttgtcagctcc	2522
CHST1	17	3'flanking + 762	ataactggtagcagtttact G/C gtgtctacactggcagaa	2523
CHST1	18	intron1 + 7874	tttccctctggctgctct T/A cattttcactcatttt	2524
CHST1	19	3'flanking + (335-349)	caacactgccacactggcta (T)12-15 gatttttctgagagcggg	2525
CHST3	1	5'untranslated - 294	tccagcgtgccagcggcc C/G gcagcgtctcactccctccg	2526
CHST3	2	intron1 + 96	gcgtccagggcggcggcca G/A cctttggggagggggggg	2527
CHST3	3	intron1 + 4467	agagagagggggggcagga C/G gtagcagcaggggggggta	2528
CHST3	4	intron1 + 4853	ggatgagcaatgccacgtg A/G tccctgccaccttccacag	2529
CHST3	5	intron1 + 4965	tccactgagagggggacaca G/C tggccaggagcggagttgg	2530
CHST3	6	intron1 + 5046	gggtgtcactctttttgc C/T ctggtccatccagcgtct	2531
CHST3	7	intron1 + 5300	ccctttcttctaaaggct A/G aagagatgacagatgtctgc	2532
CHST3	8	intron1 + 5354	agcgtgtgactccacagcg G/A ggttgggggtggccctggc	2533
CHST3	9	intron1 + 5428	gacacgtgttcagccctct G/G tctattgtcccaaatctggc	2534
CHST3	10	intron1 + 5621	ctgtggttccctgggacct A/G ggaattttatcactgatt	2535
CHST3	11	intron1 + 6555	gggtgtggtcactctggag G/C tctgtgttcctttgttgc	2536
CHST3	12	intron1 + 6990	aaacacactgggcacccccc G/A tcccgcactgtgactacac	2537
CHST3	13	intron1 + 7133	ctggggccctgtccacagg T/G ttgtgtgtgtgagagccc	2538
CHST3	14	intron1 + 7161	gtctgagaggcccccagaa T/C agaatctagaaactggcag	2539
CHST3	15	intron1 + 7199	cagtcacgaagcagtgctac C/T caccagagatgaagaactg	2540
CHST3	16	intron1 + 7316	cttgcacttggttgaatgc C/T tgggggtcgtgtgccagga	2541
CHST3	17	intron1 + 7967	gacaggaaaccccccagag T/G gatgtctggccctgtgact	2542
CHST3	18	intron1 + 11412	gttgcactttgtacttct T/G tgcactgactgtctttgt	2543
CHST3	19	intron1 + 11591	ccctggaggggcctactgc G/A gcttacttactccagcatg	2544
CHST3	20	intron1 + 12541	ccccacacacatgaatgg G/C ccagcccccagcctgcgcct	2545
CHST3	21	intron1 + 12672	gtggccacagctgggact G/C ggttcggggatggcaagg	2546
CHST3	22	intron1 + 14809	ggatgtgtgggtttggct C/T ggccttaaggatgggtga	2547
CHST3	23	intron1 + 16161	gatgtgttgaagcattgt G/A ttgggtcttttaaccacc	2548
CHST3	24	intron1 + 16385	tatttagcatgtggtttca A/C ctltctgtttttcaagg	2549
CHST3	25	intron1 + 33638	gaattgggcaagctcttgg G/C catgaatctgtgtatgtc	2550
CHST3	26	intron1 + 33878	agcaagaagtgtctctccc C/T acagcccccacacaggcataa	2551
CHST3	27	intron1 + 34690	agcacacatggagctttccc G/A cagtgtgttccagctccc	2552
CHST3	28	intron1 + 35145	aggaagccgaagccttact T/G cttgggacttgcctgacct	2553
CHST3	29	intron1 + 35340	ttgtgaattgttcccaagt T/C agtggcctgtgttgcacag	2554
CHST3	30	intron1 + 35436	gccactcatgtatggagaa T/G tgcctttttttctctct	2555
CHST3	31	intron1 + 36150	ccatagaaaggcctggcct G/T aggaagccagggaagcaga	2556
CHST3	32	intron1 + 36194	gttggggaggccagcagg G/A gttgggctctcagggagg	2557
CHST3	33	intron1 + 36561	ctctgtgtttgtctcaat A/G tgcagagtgtgcccacaaac	2558
CHST3	34	intron1 + 37602	ctggaaacagcaactaaaaa A/T agaatgttccctggagg	2559
CHST3	35	intron1 + 37725	aggtagccaggcagctccc C/T gaccgcacactgctttt	2560
CHST3	36	intron1 + 37734	cgagctcccccagccgca C/G ctgccttttaaccccttccc	2561
CHST3	37	intron1 + 38208	gccattctagatggagttc C/T gactttgggtgttgca	2562
CHST3	38	intron1 + 38219	cgaagccacactttgggg T/C gcttcattctgggaaggga	2563
CHST3	39	intron2 + 255	ctacagctgttaaagattag A/G caagataactaaattcttg	2564
CHST3	40	3'untranslated + 2202	acaccctcagaggacctgtg G/A ttaacatttgttaggtatt	2565
CHST3	41	3'untranslated + 2569	agcctcatctgggtggg C/G caagaggaagtcacaggtg	2566
CHST3	42	3'untranslated + 2717	cttgaattcctcttagggc C/T ctgggaagagattgtctta	

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
CHST3	44	3'untranslated + 2800	gcttggctgtctttctgttt C/T atggctgtgttttgccttt	2569
CHST3	45	3'untranslated + 3283	ccgagggctgcccgctctg C/T ttctgtttctggacaatt	2570
CHST3	46	3'untranslated + 3327	ctgtcagatcacggccattg T/C aaaccacaggggtgcattt	2571
CHST3	47	3'untranslated + 3787	gttcccaatgtggaggtcgg A/G gggctggagctggggggg	2572
CHST3	48	3'untranslated + 3860	ggccctgtctaattgtggacag T/C agactttatccctcttctt	2573
CHST3	49	3'untranslated + 4915	ccagatgtcatagaagcca G/A tctctgtcacatacaccgca	2574
CHST3	50	3'untranslated + 4993	taaagcaattttggctttt G/A tcttctgcaatacagcac	2575
CHST3	51	3'untranslated + 5223	ggagggagcttcagcaggag G/A tcttcccaagaggttga	2576
CHST3	52	3'untranslated + 5370	tcataactgtaatcccagca G/T ttggggagcccaagggtggg	2577
CHST3	53	3'untranslated + 5545	ccattcccaagtcagaaag T/C gaagccagatclcaaggct	2578
CHST3	54	3'untranslated + 5859	caaaagcacaaagcagaatt G/C gcaacttcacttgcctca	2579
CHST3	55	3'untranslated + 5870	cagaattggcaacttcc T/A tgtctcaaggtctccaagat	2580
CHST3	56	3'untranslated + 5971	ttccaaggctacagacatgg C/T gcaactctcacaggcctagc	2581
CHST3	57	3'untranslated + 6208	attcatgtctgcatgttac G/A agacaccccttcacggca	2582
CHST3	58	3'untranslated + 6223	tacgagacaccccttcac G/A gcaacttcacttgcctatg	2583
CHST3	59	3'flanking + 281	agcagaggtgttggccag C/T ggtcaggggctggggatg	2584
CHST3	60	3'flanking + 997	aactcttaagattttgagc C/T ggtgctgtatcccaacct	2585
CHST3	61	intron1 + 22595	cggagcgggaaabaa A/ Δ gaataagaagaaaggct	2586
CHST3	62	intron1 + (35423-35424)	gctcatgtcacagccactc AT/ Δ gtatggagcaattgccttt	2587
NDUFV1	1	intron3 + 670	ctgggtgagtggtggcca T/C ggaattgaagaccagtcct	2588
NDUFV1	2	intron6 + 160	tgctcggggccagccctga C/G catgctccttttggagcc	2589
NDUFV1	3	intron9 + 27	accaccccttctgctagcac G/A gagggtgggtgcatcaagg	2590
NDUFV1	4	3'flanking + 1111	tgtaggctgaggtcagcccc A/G atccagtcacagccccc	2591
NDUFV1	5	3'flanking + 1658	gaatcggaagtgtctgtg G/A gcaaccaccatgctccggc	2592
NDUFV1	6	3'flanking + 1713	gatctgggagggaggtaca C/T agggctgagctgggtgaag	2593
NDUFV1	7	intron4 + 214	tgggtaaattttttttt T/ Δ gcttcaaaatagattt	2594
NDUFV1	8	3'flanking + (772-774)	tgaactcgggttcagggtc TTC/ Δ ctgtgaacactgttttga	2595
NDUFV2	1	intron1 + 526	ggaaatgtcgtctaataaa C/T ggtatcaactaactctga	2596
NDUFV2	2	intron1 + 6689	tcgttgatgtgtattgt T/G tgaacaacagaagaattca	2597
NDUFV2	3	intron1 + 14767	ccaaatgcctgcccagag C/T gtggcaggaaggtacacag	2598
NDUFV2	4	exon2 + 86	aaggaaattgcataagacag T/C tatgcaaaatggagctggg	2599
NDUFV2	5	intron2 - 29	cagaagatcttactcttaa T/G gaagctggatacaactttt	2600
NDUFV2	6	intron2 - 168	tttactttgtaactact T/C atcaaatgtgttttggcca	2601
NDUFV2	7	intron4 + 677	aaaccacatctcttattg G/A tgaatgaatcacataacca	2602
NDUFV2	8	intron4 + 2295	tatgattcaacttcaaaag A/T gtattgtatgaaataga	2603
NDUFV2	9	intron5 + 102	caactctgcccattattg G/A atctgtacttacctagta	2604
NDUFV2	10	intron7 + 5466	tgtgaagaggcttaagata A/C caaatgctcagctttcagga	2605
NDUFV2	11	intron1 + (13562-13563)	tactcttaaatattcctt (CTT) ttattataagatacagct	2606
NDUFV2	11	intron1 + (13562-13563)	tactcttaaatattcctt ttattataagatacagct	2607
NDUFV3	1	5'flanking - 606	aatttcgactaacgttggg A/G cgaactotttgcataataaa	2608
NDUFV3	2	5'flanking - 222	cgccgcgccccgccagc G/A cccagcgccccggggcac	2609
NDUFV3	3	5'flanking - 111	tggcccaagggagggcactt A/G gccctactgggtgcgcgc	2610
NDUFV3	4	intron1 + 137	ttggccgtgaccccgctc C/T ctggcccgagactgaccgc	2611
NDUFV3	5	intron2 + 152	tatacaagcacagatcta T/C aacagattttgaccaaaaa	2612
NDUFV3	6	intron2 + 6304	ttcacagatgaaggggtcc G/A aaattttgtcaagaagac	2613
NDUFV3	7	intron2 + 6433	tcgcttgccttctcctc T/G tccagctcctctgattctga	2614
NDUFV3	8	intron2 + 6563	ccittgaaacagagccccc C/T gattacagatcagcaaaa	2615
NDUFV3	9	intron2 + 9819	actatcttctgtggcctgc G/A cagagccaccttgccagc	2616
NDUFV3	10	intron2 + 9858	aggatgccagctcttaaat G/A agacatogtttttgcctaa	2617
NDUFV3	11	intron2 + 11673	cttgtagtgaagccctgt A/G tgtgagccaagtcatcata	2618
NDUFA10	1	5'flanking - 1734	tgcaccttgaaactgtttact T/C tctgtabccatttaacct	2619
NDUFA10	2	5'flanking - 1492	aaaacatccagcacaacagg T/C tggaggaattacgtctcg	2620
NDUFA10	3	intron3 + 370	aagactgtcatgtgccctg G/A agacagagatgtgggtgcca	2621
NDUFA10	4	intron3 + 2485	ttgtattttctttctctg G/A aatgcagtgatcagttgaca	2622
NDUFA10	5	intron4 + 236	ctgtgaagcagattggagc C/T ctggacctcaacacacgca	2623
NDUFA10	6	intron4 + 1742	tgtcggcatctgctgagtg C/T tgcgtgaactgtgagactgg	2624
NDUFA10	7	intron4 + 2090	ggctgggggaagcagatca T/C gttggctgaagacaggtgg	2625
NDUFA10	8	intron4 + 3054	cagctgattactactgaa A/C cgggataagtcagcttgat	2626
NDUFA10	9	intron4 + 3066	ctactgaacgggaataag G/T agctgatgatttcagctg	2627
NDUFA10	10	intron4 + 3377	gtcacggttaastgtct G/A tttaactctgtgaagtagc	2628

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO
NDUFA10	11	intron5 + 46	aagcatctctatttgaatg T/C agatcagcactaaagccct	2629
NDUFA10	12	intron8 + 1465	gcacgcgccagttcctgta C/T aggcctcatatccagcgtgc	2630
NDUFA10	13	intron8 + 1809	cctggaggccacaggtggc C/A ggggcactcaacttccctct	2631
NDUFA10	14	intron8 + 11226	gttgtgactgtgtgggc A/G tctacactctcgggctgcag	2632
NDUFA10	15	intron8 + 11319	atcttgcccttccctcctgc G/A tctgttcaggctgaatcct	2633
NDUFA10	16	intron8 + 11386	ccataatcctagctgaacc C/T tctttttccctgtgaccc	2634
NDUFA10	17	intron8 + 12301	acataattattgttaacatg C/T cgttaccagtgacattcct	2635
NDUFA10	18	intron8 + 13361	ccagggccactgattgctt G/A cattttctagcattttctta	2636
NDUFA10	19	intron9 + 183	tttctgtgtggagctgat G/A agtctctcagtgacagccc	2637
NDUFA10	20	intron9 + 6669	aataaiaatgaccctttctg G/T aaattctagaattcctttt	2638
NDUFA10	21	intron9 + 8028	gaggacattccacagaact G/A tgcattatagagcagaggt	2639
NDUFA10	22	intron9 + 10742	ctggggagaggggtgggc C/G agttcagccagcactgggt	2640
NDUFA10	23	intron9 + 10985	agaaagggttacacaggagc A/G cactttcagggagtggt	2641
NDUFA10	24	intron9 + 10989	agggttacacaggagcac C/T tctcaggagtggtgtgagc	2642
NDUFA10	25	intron9 + 12601	ctgtgaatcctctcacctgc G/A tgaaggccctggctcctct	2643
NDUFA10	26	intron9 + 13908	cacattgttatgaaccaag C/T ctggaattcagtgtagaaga	2644
NDUFA10	27	intron9 + 13911	attgttatgaaccaagct G/T gaattgcagtgtagaaga	2645
NDUFA10	28	intron9 + 14064	tcttgactattagaaccct A/G tcagataaatttaaacag	2646
NDUFA10	29	intron9 + 14184	tggctttgttgggaacagc G/A agagatacagaaccgaggt	2647
NDUFA10	30	intron9 + 16487	cttgaagctgactgttccct C/A cttgaagctgactgttccct	2648
NDUFA10	31	intron9 + 16779	gccagcgtgactgtttag G/A ttctctatgacattcagacc	2649
NDUFA10	32	intron9 + 17663	ttccaaatcacccagaaact T/G tgcagtattttgaagctct	2650
NDUFA10	33	5'flanking - (1668-1659)	gtaaatgttttaactaga (C)9-11 ttctaacaacaggtataaa	2651
NDUFA10	34	5'flanking - (1355-1334)	ctgtatccatttgaaggcac (A)15-21 tgcagaagaaacagggcaca	2652
NDUFA10	35	intron1 + (46-61)	tggcgggtggcaggtggc GGGGTGGCGGGGTGGG/Δ gag	2653
NDUFA10	36	intron4 + 2486	ctcactggaaattttttt T/Δ aatttaatttlaaatttt	2654
NDUFA10	37	intron7 + (1600-1601)	cacttccattctgactgtta (A) cgggtgacttcttctgccca	2655
NDUFA10	37	intron7 + (1600-1601)	cacttccattctgactgtta cgggtgacttcttctgccca	2656
NDUFA10	38	intron9 + 1054	ggcgtgctgttttccctt A/Δ tctgtcctgttacagctgtg	2657
NDUFA10	39	intron9 + (8161-8172)	tttctcgtttctggagac (T)10-12 aatgtgaasattgtgtt	2658
NDUFA10	40	intron9 + (8646-8647)	aattccccctgttctct (TT) ctgtagacattttaaccta	2659
NDUFA10	40	intron9 + (8646-8647)	aattccccctgttctct ctgtagacattttaaccta	2660
NDUFA10	41	intron9 + (16503-16523)	ccttcttgaagctgactgt TCCCTCCTTG	2661
NDUFA10	42	intron9 + (17905-17936)	AAGGTGATGCT/Δ gtccaggtgactgtctagga	2662
MGST1	37	5'flanking - 1376	caaatatgttatcatgta (CA)12-18 tcttcatgaaaactctttc	2663
MGST1	38	intron1A + 147	ttataaatgtttattcaat T/G aaaccaactgtcaattct	2664
MGST1	39	intron1B + 36	cctggagattttaaatttct G/A cgaagattttaaacaact	2665
MGST1	40	intron1C + 456	ggagaaaggagccagatga A/G agggtagcagcagggagg	2666
MGST1	41	intron1C + 719	ccccttggagcgttctcac C/T tctgccccacttccccgtc	2667
MGST1	42	intron1C + 985	gcccgaagcattgtctgtat A/G gcaccagggcctccagtgg	2668
MGST1	43	intron2 + 3083	cgatgaasatttttctaccg C/G ttgttttagagtgtgtct	2669
MGST1	44	intron2 + 3106	aaaaaatlttagatatggg T/G actccctatgttgcacagc	2670
MGST1	45	intron3 + 1703	ttccatgttggccaggtg A/G tcttgaattcttgggtcaa	2671
MGST1	46	intron3 + 2557	ttcttcttcaagaagaagtc T/G gtgcagatctttagcacaca	2672
MGST1	47	intron3 + 3032	tccgacatcttcccttcca T/C tttaaagtiagactttttt	2673
MGST1	48	intron3 + 3045	agagcattttagaatatt C/A ctttaaaggttaggaataa	2674
MGST1	49	intron3 + 3289	atatattccctttaaagta G/G agaatcccttcaactgaga	2675
MGST1	50	intron3 + 3885	ggtttatagtgttcccccc T/A ccccgcccccaaaagccca	2676
MGST1	51	intron3 + 3978	gaagctgccgtccaggaag G/C agtctgtgttggagagag	2677
MGST1	52	intron3 + 4298	ggaaagctgggaactgtt G/T cctggacagagttctcaaa	2678
MGST1	53	intron3 + 4519	tgtcaactcgtaacacagg G/T gtagaagtgacattgttt	2679
MGST1	54	3'untranslated + 603	tttaatagaaatgtattc C/T tgtcttttcttccatctc	2680
MGST1	55	3'flanking + 147	gggtaaaccattttgata T/G tagcattggcaatctctgt	2681
MGST1	56	3'flanking + 237	tattgttttcttctct C/T tgttttcttctctgaaa	2682
MGST1	57	3'flanking + 1318	cagcagtttttctatga C/T aagacattctccaataact	2683
MGST1	58	3'flanking + 1331	tggctctgtgtcatgaaca T/C gaacgctgcacggcgaac	2684
MGST1	59	intron1C + (904-923)	atgaactgcacgcgtgcac G/A cgacacacacacacacaca	2685
MGST1	60	intron1C + (3433-3434)	tccgattatcttgttaatt (A)18-20 ggcasatcagtcasatttg	2686
MGST1	60	intron1C + (3433-3434)	cccttcaactagaaaca (AA) gcagacattaaatgttac	2686

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
MGST1	61	intron1C + (3433-3434)	cccttcaactagaaacaa gacgacacattaaatgttc	2687
MGST1	62	intron1C + 5146	actatttcaatttttttt T/Δ gacggggagacagagcttc	2688
MGST1	63	intron2 + (552-563)	cccagcattataagaatgac (T)9-13 aagtcagatgtggggggg	2689
MGST1	64	exon3 + (172-173)	tagcatttggcaaaagagaa AA/Δ tgccaagaagtatcttcgaa	2690
			agaaacatggatgtctgaaa TTGACA/GTCCAATAT cactg	
MGST1	65	intron3 + (152-158)	cacttgaatgtgtg	2691
MGST1	66	intron3 + (2198-2200)	ggattttagattcctcccta CTA/Δ ttcttccgaccttccaccc	2692
MGST1	67	intron3 + (2571-2580)	tttccatttttaagtlagac (T)9-10 cactctctctgttacttcag	2693
			tcctctcatgtctctatgt (GAGATGTTG	
MGST1	68	intron3 + (4682-4683)	TGGCTCACAT) agtcaccccttttggagac	2694
MGST1	69	intron3 + (4682-4683)	tcctctcatgtctctatgt agtcaccccttttggagac	2695
MGST1	70	3'flank + (1359-1360)	acacacacacacacacacac CC/Δ tgcctcggagttggcact	2696
MGST1	71	3'flank + (1889-1891)	ttagaatagtttctaactat ACT/Δ ttactcccagagagcctt	2697
HMG17L1	1	3'untranslated + 864	ctttcgtattttgtatgac G/C gttgaagaaggagttgaa	2698
UGT2A1	1	5'flanking - 1602	ataacatcttctgcagagaa A/C cttaaatggaatccactca	2699
UGT2A1	2	5'flanking - 1480	taacagattatctttgtgt G/C ggagagcttagaagagacat	2700
UGT2A1	3	5'flanking - 1406	atttcagaagatttataac A/T tgaagaaggtcactctgtt	2701
UGT2A1	4	5'flanking - 1388	acatgaagaaggtcactctg C/T ttattcacagacatgtcat	2702
UGT2A1	5	5'flanking - 935	aaattatcactctcttgg G/A cagtggtttcttttcttgg	2703
UGT2A1	6	5'flanking - 287	cctgaatgtagagttgagat G/A tacagaagctttatccaatt	2704
UGT2A1	7	5'flanking - 128	gagaagtaagacacattacc C/T ataactctgaatatctcta	2705
UGT2A1	8	intron1 + 535	cattgatccgggtgattat C/T catgctaagcttatttaatt	2706
UGT2A1	9	intron1 + 642	tatattgatcatgttgatc A/C ttatcacatatttctcta	2707
UGT2A1	10	intron1 + 1221	ttttatctaataagcaatt C/G aggcaccatcaagggaat	2708
UGT2A1	11	intron1 + 1448	agtgcttaccaggaacatc C/T acatgacagctctgtgctgg	2709
UGT2A1	12	intron1 + 2000	gacacattagcttctttct A/G cagatctctgttctaaaca	2710
UGT2A1	13	intron1 + 3118	cttaaaattctttaaagaa T/G cattgcaacaaatttataic	2711
UGT2A1	14	intron1 + 3191	ataaataagacaactcccta A/T gtttactctctgcagtga	2712
UGT2A1	15	intron1 + 3770	atcaccagataatttactct C/T cattaaaggagtaggtatca	2713
UGT2A1	16	intron1 + 4584	tgattggttagaactcttga A/C aaactctctagatcatc	2714
UGT2A1	17	intron1 + 4854	tactctgtccttcttata G/A cctatcacttctgtctgcc	2715
UGT2A1	18	intron1 - 19146	ctgttaaatctctcattcaa C/T ggccacatgtgttaataaa	2716
UGT2A1	19	intron1 - 18346	atggcaatttttggaaat G/A ttaactcccaataatgaata	2717
UGT2A1	20	intron1 - 18218	tatatcatatttttaactta T/G agatagcactagccctaatt	2718
UGT2A1	21	intron1 - 17937	ctccatcaatttggactca C/T catacttattcagcactatc	2719
UGT2A1	22	intron1 - 12585	ttccacacagggacagatca A/G cagaggaattttttctgt	2720
UGT2A1	23	intron1 - 11430	aacaaagggttttttttcta C/G agttctgatgcttagacgtc	2721
UGT2A1	24	intron1 - 10761	ttttaaataatgcatttatt T/G ccactttttaaactatc	2722
UGT2A1	25	intron1 - 381	aaatctctccctctctctc C/T ttcccaggcccaactctac	2723
UGT2A1	26	intron1 - 329	ttcccttctctcttctctc A/G tctctctctcttctctc	2724
UGT2A1	27	intron1 - 41	ttttctctcagcaaacata T/A aagctaatttctccatcca	2725
UGT2A1	28	intron2 + 263	caccttgatactggacttgg T/C gggacagaasaccagatcat	2726
UGT2A1	29	intron2 + 454	agaaagcccatgaaataag G/C cagggttttaggttttaatt	2727
UGT2A1	30	intron2 + 554	aaaaacttttttgggttgc A/T atgttgatttttatttctga	2728
UGT2A1	31	intron2 + 1113	ctgcaggcaagctctagtga A/T ttttattataggaataat	2729
UGT2A1	32	intron2 + 1304	gacaaatcagccatgtttta C/T aatagcagacattatgccat	2730
UGT2A1	33	intron2 + 1305	acaaatcagccatgtttta A/G atagcagacattatgccat	2731
UGT2A1	34	intron2 + 1367	atcgatctaggttttggaa A/C tatgataccaaccatgggt	2732
UGT2A1	35	intron2 + 2074	aaattttttcttagacclat G/T aatcaaggaggcatacagt	2733
UGT2A1	36	intron2 + 2164	attttatlagatataactgg A/C atgtaacaaattttaaagc	2734
UGT2A1	37	intron2 + 2298	taacaatttcagttagcatg A/C gaagagtttcccttatta	2735
UGT2A1	38	intron2 + 2346	tttctgaatgttttgcct T/G catgcttggacttgaatca	2736
UGT2A1	39	exon3 + 922	gtgttggtgtttttctctg G/A gatcaatgttcaaaacctt	2737
UGT2A1	40	intron3 - 217	aagcttgaagtgataata T/C caaaacataatcttact	2738
UGT2A1	41	intron3 - 194	aaacaataatcttactctg G/A tagactatttagtaacagact	2739
UGT2A1	42	exon5 + 1171	acggagtcctatgttggga G/A ttcccatgtttctgatcag	2740
UGT2A1	43	intron5 + 1546	tttttaaattcagaactc A/G gttatgtgtattcttaca	2741
UGT2A1	44	intron5 + 1547	tttttaaattcagaactc A/G gttatgtgtattcttaca	2742
UGT2A1	45	intron5 + 2013	atcatattcattaccctccc G/T ctattattgtatttgaatc	2743
UGT2A1	46	intron5 + 2318	aattttagtctttttctaa C/T ggaagtaacctgtttaa	2744

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
OATP1	41	3' untranslated + 2130	gtcttaagaacclaaaaa C/A ctcttaactcaaatatata	2805
OATP1	42	3' flanking + 57	agtgaactaaagtttttctta C/A aaacaagtgtcgaatcaa	2806
OATP1	43	3' flanking + 572	aatacactatgggtatttat G/A tgtactataaatggaglgag	2807
OATP1	44	3' flanking + 788	atttccataatgatcagatg C/T atcatatgaaaaaagagc	2808
OATP1	45	3' flanking + 1356	agtgactgacataaatggg G/A gcagaggacataatgaggtt	2809
OATP1	46	5' untranslated - (189-188)	attttcactcgtatataaa (A) gcgttccaggattttttgta	2810
OATP1	47	5' untranslated - (189-188)	attttcactcgtatataaa gcgttccaggattttttgta	2811
OATP1	48	intron4 + (725-726)	tgatctttatagcggggaa AA/Δ caggcaagtacgctatggt	2812
OATP1	49	intron4 + (1082-1083)	attgagtcaggaaacaaaa GA/Δ gtttcaaaaatttgaaaaat	2813
OATP1	50	intron4 + 2301	aatgicactgtcttttttt T/Δ atgcagagtgatcaaaagga	2814
OATP1	51	intron9 + (241-246)	attgatgtgcagtgagggt TGTGTG/Δ catgattgctttgtat	2815
OATP2	1	5' flanking - 2574	ggataaggcaacccctatgt A/G tcaactcgcggggggggg	2816
OATP2	2	5' flanking - 2366	aaacataggaaatgcagagc C/T ctgtggggattagagagag	2817
OATP2	3	5' flanking - 2244	tgatgatccagagcttga T/G cattgtgggtatagaacca	2818
OATP2	4	5' flanking - 1723	tcttcagacttcaaaagcc A/G tgaatttcatcagagctgt	2819
OATP2	5	5' flanking - 1180	tgcttatttaacaggcataa T/G ctttgcctcctgagccaga	2820
OATP2	6	5' flanking - 811	tatgtgcataatgtatata G/A gtataagtgatgtatgtgt	2821
OATP2	7	intron1 + 7188	oatcatttgaaatttaaga A/G aaatatgttcagagaaaaa	2822
OATP2	8	intron1 + 7331	gtgaatgaggaaacaaagt T/C ccccttttttctgataa	2823
OATP2	9	intron1 + 7391	agagagatgtgaatgtat T/G tttcggggagatggggaa	2824
OATP2	10	intron1 + 7888	tgtttagtagaagaataac G/A aagcctaaactaaaggag	2825
OATP2	11	intron1 + 7958	tgtctattataaattttt T/A aaaaaagatttctaataat	2826
OATP2	12	intron1 + 7959	tgtctattataaattttt A/T aaaaaagatttctaataat	2827
OATP2	13	intron1 + 8036	ggaaaaaatgggggaaatt A/T atcaaaaggcagctatttao	2828
OATP2	14	intron1 + 9164	acattatattctataaaga G/T agtcagttgaagttaaaagt	2829
OATP2	15	intron1 + 10123	tctgtcttctcactttgt T/G tccagcattgacctagcaga	2830
OATP2	16	intron2 + 193	tgttaagttattctttggc G/A aaatttttgatgcttaatag	2831
OATP2	17	intron2 + 1020	ttagtaaaccttttagccaa G/A tggcagtcataaggaaaaag	2832
OATP2	18	intron2 + 14865	agaggatttaactcotaagag G/T ttattttggctaaagtgcac	2833
OATP2	19	intron2 + 14931	gttagttaataacagaaaaa A/T talcagaaatttaaaaaat	2834
OATP2	20	intron2 + 15417	ttctaaatbaagtaagctaa A/T tctctatattataactacta	2835
OATP2	21	intron2 + 20823	ttgtalaagagatccaaac A/C aattcctactagggaataa	2836
OATP2	22	intron2 + 20852	ctaggggaataaaagcttca G/G taaggaggtgacctaaagt	2837
OATP2	23	intron2 + 20930	atggagagaagcagcaggt G/A ccacagataaatgaagtgg	2838
OATP2	24	intron2 + 21360	ttcaaaagcgtatttttca T/C taagtctttttgtaataaa	2839
OATP2	25	intron2 + 21467	tatatcaccaataacctgtcc A/G gaagatgtgtataagccaa	2840
OATP2	26	intron2 + 21621	tatcaatacttatgaagaga A/G ctactcttcttaactaggga	2841
OATP2	27	intron2 + 22760	ttccccacctctgttgtt G/G tctctttaaacttctcttg	2842
OATP2	28	intron2 + 23199	ctactctgcataacatta C/T aaacttaaggcaattataa	2843
OATP2	29	intron2 + 23218	acaaacttaaggcaattata A/G aaactcaatcatattatct	2844
OATP2	30	intron2 + 23330	gccttgttctgttctct G/A tacttgcctcaactacatag	2845
OATP2	31	intron2 + 23673	ctggagacgttagctcaaac T/C gaggatgaataagacattt	2846
OATP2	32	intron3 + 89	ggtttcaactgggttaaat T/G tctctctcaaggcaatttg	2847
OATP2	33	intron3 + 224	tgtatattttctataatgc A/G caaagatgatgaactgae	2848
OATP2	34	intron4 + 97	cccttaaataggcagttac C/A ttttgagagatacccaata	2849
OATP2	35	intron4 + 568	ttcatgtaccaattgtggc A/G acgtatttccaggcaacaag	2850
OATP2	36	intron4 + 599	aggcaacaagatgaagaag A/G aaagaataaagaagcaacaaa	2851
OATP2	37	intron4 + 753	aaatagacattatttccag T/A taccaggttccgggttaaa	2852
OATP2	38	intron4 + 781	ttcccggttaaaaaatccaa G/C tatatattactgtgaaggaa	2853
OATP2	39	intron4 + 1196	aaggaccacaactctagatca G/T catgtcttaaatatgccat	2854
OATP2	40	intron4 + 1229	tatgcataatgtgtgacac T/C ttgcacctgtatttctac	2855
OATP2	41	intron4 + 1623	catctgttgaaatggatta G/C attttatttttactacatt	2856
OATP2	42	exon5 + 388	atttcaagaactaatatc A/G atttcatcagaasatttcaaca	2857
OATP2	43	exon5 + 452	taattcaatttttactacta A/G tagagcatcacctggagatg	2858
OATP2	44	intron5 + 165	ttatatacacagttgcccc A/T ttacacacacaggtttaaac	2859
OATP2	45	intron5 + 189	acaacacaggtttaaactac G/A cgttttcaacttctatgcaaa	2860
OATP2	46	intron5 + 191	aacacaggtttaaactac G/A ttttcaacttctatgcaaat	2861
OATP2	47	intron5 + 507	atataactttgtcttctatg C/T aaaggcaaacgtttatct	2862
OATP2	48	intron5 + 520	ttcatgtcaaaaggcaaac A/G ttatctatttaaaagattt	2863
OATP2	49	intron5 + 856	agcatgtataacctaatag A/G ataaacacacaaaaagaaa	2864

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
OATP2	50	intron5 + 1157	acagataattttacttgg T/C gtgttttctgtatgatg	2865
OATP2	51	intron5 + 1226	ccttgattgtaatactccc A/C catgccaaaggtggggccag	2866
OATP2	52	intron5 + 1228	ttgattgtaatactccc A/C tggcaaggtggggccaggt	2867
OATP2	53	intron5 + 1304	actgttctcgttgtaata G/T aagtctcacaagctctgatg	2868
OATP2	54	intron5 + 1348	ttataaagagagttccct G/A caaaagctctcttgcctgcc	2869
OATP2	55	intron5 + 1407	ttgtctctctctctctcc G/A ccatgatttgaggccccc	2870
OATP2	56	exon6 + 521	gtcatatcatggatata T/C gtccatggtaaatgtcttc	2871
OATP2	57	exon6 + 571	gggagactccctatgacca T/C tggggtttcttacttgat	2872
OATP2	58	exon6 + 597	ctttcttcatatgatgatt C/T gctaaaggaagcattcttc	2873
OATP2	59	intron7 + 33	agaaacaggtaccatgata G/T gtcttctcagcacatgc	2874
OATP2	60	intron7 + 267	caaaataaccaaatgtaaa T/A gtctcctcccaaatgact	2875
OATP2	61	intron7 + 1260	gtactctcactttctctgc A/G tttaacttgtaaaacttt	2876
OATP2	62	intron7 + 1386	agtctcaaatatagccaa G/A agcatgctttattgtaac	2877
OATP2	63	intron7 + 1472	ctttccacatgacgaatg G/A catgttttagcaataata	2878
OATP2	64	intron7 + 1697	tttcatgttcaattttag C/A atatgctttagatgctac	2879
OATP2	65	intron7 + 2273	tttccactctctctagcc C/T gattatgaccttagttact	2880
OATP2	66	intron8 + 207	gtggaaagagattaggttg T/C acttttagcagggaagac	2881
OATP2	67	intron8 + 546	tccggaaagtcttcccta T/C gtaattagatgaatttat	2882
OATP2	68	intron8 + 565	gttaattagatgaatttat A/C ttgtgtaattatctatcta	2883
OATP2	69	intron8 + 668	taagtaatgaatttaggt G/T catcagcetttgacagtgc	2884
OATP2	70	intron8 + 739	tggagaccattagagtgca A/G taacaaaggaagatgactg	2885
OATP2	71	intron8 + 2193	tgatcacagatccaaatgac A/G taatttctaccatgaacga	2886
OATP2	72	intron9 + 112	atttttagtaacagggata G/C tataattttctgtatctt	2887
OATP2	73	intron9 + 266	tttaggttagtctctgata A/G ttgactctataatttagt	2888
OATP2	74	intron9 + 305	tgttaagatctgagacaaac C/G cttttgtaattataactt	2889
OATP2	75	intron9 + 888	eggttctgtatgtttttta T/C aaatgacaaagatatata	2890
OATP2	76	intron11 + 10224	tacactgttccataaaaa T/C tctctatcttcttctagt	2891
OATP2	77	intron11 + 10359	attatagattcaactggag G/C ttcccttaacttttagccta	2892
OATP2	78	intron11 + 10916	ctttatagaaagaatcca G/G aaaaactttttactctttt	2893
OATP2	79	intron11 + 10997	aatatattagtgtgaacaa T/C gagacttctactaatata	2894
OATP2	80	intron11 + 11018	gagacttctactaatata G/A caatgtatttgcagccctgt	2895
OATP2	81	intron12 + 442	aacattccaaaacttttct C/T gactcagcagcagctttta	2896
OATP2	82	intron12 + 445	attccaaaacttttactga C/T tcacagcagcagcttttata	2897
OATP2	83	intron12 + 447	tccaaaacttttactgact G/A acagcagcagcttttata	2898
OATP2	84	intron12 + 907	aattgaagaagcgtggcaga T/C tgaacactatgaaagag	2899
OATP2	85	intron13 + 65	tatatatatatatata C/T acacacacatcatatetta	2900
OATP2	86	intron13 + 870	aattcgtggttctcttct G/A atgtatccaactctgtggcac	2901
OATP2	87	intron13 + 1935	taaaasaaaaaagcttgc T/C ttacagcaattggagccag	2902
OATP2	88	intron13 + 2261	aacgaatcctccaaatttt G/C aacttttatttaacaaa	2903
OATP2	89	intron14 + 248	tcaaggataataaccaactt G/A tcaaaatcagagataatag	2904
OATP2	90	intron14 + 2463	attgtttactaatatgaa C/G cttcttcaagccttcttt	2905
OATP2	91	intron14 + 2857	tcatcatgtatttccaggac A/T cctggcaagatgctctcag	2906
OATP2	92	intron14 + 11458	atctccagaggtcgtctgt C/T tcccaaaagtcactgaccc	2907
OATP2	93	3'untranslated + 2243	ataaaaaaacaactgtgg T/C agaaaaatgagagtactca	2908
OATP2	94	3'untranslated + 2404	tcttaaaaaaacaatggt A/G tctacaggttagaggttaa	2909
OATP2	95	3'untranslated + 2515	cagagtttgaactataatc T/G aaggcctgaagcttagcttg	2910
OATP2	96	3'untranslated + 2539	gcctgaagcttagcttgggt A/G tatgtcaaatatctctgt	2911
OATP2	97	intron1 + 457	taattggcaaacataaaaa (A) cagggtctcaagtcacat	2912
OATP2	98	intron1 + 457	taattggcaaacataaaaa cagggtctcaagtcacat	2913
OATP2	99	intron1 + (7537-7538)	gatcagcattacaaccaaga (G) atggagaatgacattcagga	2914
OATP2	100	intron1 + (7537-7538)	gatcagcattacaaccaaga atggagaatgacattcagga	2915
OATP2	101	intron1 + (10032-10035)	ttgtgattctatattactt AGT/Δ gtttcaatttctctccaca	2916
OATP2	102	intron1 + (10058-10061)	ttcaatttctctcccaaa TTTA/Δ ttttctatttaattgta	2917
OATP2	103	intron2 + (413-423)	acttatttaaaattctttt (A)11-13 caaaaaacaggtttlaaaa	2918
OATP2	104	intron3 + (1595-1603)	tggcaagtaattcaagtc (T)8-10 gtttttaaaacaaactttca	2919
OATP2	105	intron4 + (10-23)	ttcatgggtgtaagttgtt (A)12-14 cctctgtgccactatcagta	2920
OATP2	106	intron5 + (1567-1572)	gtgataaattacttctga CTTGTA/Δ aattaaaaaataaagtag	2921
OATP2	107	intron5 + (1577-1585)	attacttcttctgttaatt (A)9-10 taagtataaatttaaggt	2922
OATP2	108	intron8 + (1939-1941)	ttcttactctcttctact CTT/Δ atttcaagcagatgcaactg	2923
OATP2	109	intron10 + (3077-3078)	aaattctttatctactttt (CTT) ttccctcttctctgctttc	2924

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
OATP2	110	intron10 + (3077-3078)	aaattctttatctactttt ttcctctttctctgttcc	2925
OATP2	111	intron11 + 11011	aaacagtgagacttcaactaa A/Δ tataatgcaatgtatttgc	2926
OATP2	112	intron12 + (1160-1169)	agcatgcatggttagaggtg (A)9-11 gcaatttlaacattgttaa	2927
OATP2	113	intron12 + (1310-1312)	tccatcttaataataaaagt TGT/Δ ctactcaaaaggagaggtct	2928
OATP2	114	intron13 + (9-34)	tacgagcactaggtatgatg (A)24-27 tataatataatataata	2929
OATP2	115	intron13 + (35-64)	aaaaaaaaaaaaaaaaaaaa (TA)10-21 cacacacacatacatatt	2930
OATP2	116	intron13 + (1379-1387)	aaatttttccaccacatac (A)8-10 caaagtaagttatgaacac	2931
OATP2	117	intron13 + (1916-1928)	aattctcttaaaataagtt (A)11-13 gtctgttttacagcaattg	2932
OATP2	118	intron14 + (588-596)	caattatactttacctcttt (A)8-10 caatttcaaatctcttat	2933
OATP8	1	5'flanking - 1413	aatagggttctaataactct G/C aaacttatgatttcalat	2934
OATP8	2	5'flanking - 1345	gaatttatactacagataig A/G ccacacagaaatgacatct	2935
OATP8	3	intron1 + 38962	atgaatttagtttaaaata G/A caaccttaactatactcttc	2936
OATP8	4	intron2 + 253	acagacttaccacaaagaa T/G tatcttcccaaatgtcta	2937
OATP8	5	intron2 + 329	actcatggtttgcaaatiaa C/G tttttaggaactttatctc	2938
OATP8	6	intron2 + 2568	ccattctgtgtctttcttc G/A tgaactattttccatcagl	2939
OATP8	7	intron2 + 2679	ctcttattgtctttcttcca T/C gttttatctaaataatla	2940
OATP8	8	intron2 + 2753	caggaaactttccaaagcc C/A ctatlaatttgaactccct	2941
OATP8	9	intron2 + 3132	tgttttaattgaggagagt T/C accttccagttlaaallaca	2942
OATP8	10	intron2 + 3193	aatgtcttggcatatttgc A/G ttcaatttgggcatcagtt	2943
OATP8	11	intron2 + 3207	atttgcattcatttgggca T/C tcaattctactagatacaaa	2944
OATP8	12	exon3 + 334	gaacttggagatttttgaac T/G ctttaccacattttctcag	2945
OATP8	13	intron3 + 76	agaattttattttatactt G/A taagtggcagttacattt	2946
OATP8	14	intron4 + 2443	tcaattttctgttctctta C/T agttataggtttcttaaga	2947
OATP8	15	intron4 + 67	taatacagctctataaagtt C/G tgatattcttlaacaaatt	2948
OATP8	16	intron4 + 91	tatttttaacaaattgat T/A taagaacaaatggagaac	2949
OATP8	17	intron4 + 197	ggtttgaactgcacattgtc G/A ctatattgcagctttgtcc	2950
OATP8	18	intron4 + 813	tttaacagataaaaaaaa T/A attttgtaacgacaaagaa	2951
OATP8	19	intron4 + 974	atatgcacattaaaaatac C/G tggatttttaaatatgtaet	2952
OATP8	20	intron4 + 1003	taaatatgtaattgatacaaa G/T gaattatagcatattttgt	2953
OATP8	21	intron6 + 155	catlaataacagaaataaaa A/G agaaatttagctctcttla	2954
OATP8	22	intron6 + 750	atccaactgggttttagatt T/G cctcttttgcctctctcc	2955
OATP8	23	intron6 + 780	gcctctctctcactctgcac C/T tctcttttctctagcaaca	2956
OATP8	24	intron6 + 1248	ctatgcctctgaatctcaca C/T ttccctttatttaaaattg	2957
OATP8	25	intron6 + 1500	tctgtctgttttagcalat A/G ataactctcaggttttgg	2958
OATP8	26	intron6 + 2008	ataacataatggttagaga A/G tatcaaggcaggaaattag	2959
OATP8	27	intron6 + 2087	actactctccccatcacac T/C aaactctatgtctccccag	2960
OATP8	28	intron6 + 12305	tcatctatgaggactgcaa T/C cattatcattatttccaga	2961
OATP8	29	intron7 + 363	taacaantgatccagccat C/G atactattctctgtaatag	2962
OATP8	30	intron7 + 411	ccittattttttgagaacct G/A gtggatgatattaaagcgt	2963
OATP8	31	intron7 + 428	cctgttggatgatatttga C/A gtatgatgatcaatgtaata	2964
OATP8	32	intron7 + 634	aaaattatataatatacat A/G taactttacctaagttatca	2965
OATP8	33	intron7 + 1791	tgttttttaaggtagtga T/C gtaatagtaaaagcgaatt	2966
OATP8	34	intron7 + 2000	agttggcaaatgtgtctca G/A gtatcataaagtcaacttga	2967
OATP8	35	intron7 + 2043	gtttattgtatcattttta A/G tggatcaactgttagtgag	2968
OATP8	36	intron7 + 2171	attttttttagcaaaaggtc G/A cgaactctttagaaagcctc	2969
OATP8	37	intron7 + 2173	tttttttagcaaaaggtcgc G/A actctcttagaaagcctcac	2970
OATP8	38	intron7 + 2179	teagcaaaaggtcgcactct C/T ttgaagagcctccaaatca	2971
OATP8	39	intron7 + 2219	atttgaacttttaagtttta T/G ataacttatatttacaatat	2972
OATP8	40	intron7 + 2261	cagatattaatatatttt A/T ttattgaatatgttatttt	2973
OATP8	41	intron8 + 150	acaaatatttccactttgt T/C atactctctgtttctgcat	2974
OATP8	42	intron8 + 154	aatttccactctgttaata A/T catctgtttgtctgatttga	2975
OATP8	43	intron8 + 1303	ttttttttagatgagttct C/T gctctgtttgccaggtctgg	2976
OATP8	44	intron8 + 1372	aagctcgcctccaggttc T/G ccaccttctcttaaaagaa	2977
OATP8	45	exon9 + 1272	tccttttttttcaactctt A/G tatttccctctaatctgcga	2978
OATP8	46	intron10 + 63	tcacagatttgatttaata A/T tacttatacaatcttctat	2979
OATP8	47	intron10 + 911	ctlgcccaatatctaccac G/T gtattattaaacggccttga	2980
OATP8	48	intron10 + 972	tcctagtcttcttgagata G/A gctacaacttttagtaactt	2981
OATP8	49	intron10 + 1101	tccttggttctgtgttctc A/T gtatgaaagacclgaagag	2982
OATP8	50	intron10 + 1103	cctgtctctgtgttctccag T/C agtgaagacctgaagagag	2983
OATP8	51	intron10 + 2027	ccccttttcatgattgctc A/G gttttgtcccttttcaact	2984

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
OATP8	52	intron10 + 2028	ccatttcatgagtgctaa G/A ttttgccttccaaacta	2985
OATP8	53	intron10 + 2148	gtatttggaaagaaagt A/G ggtggagagaaatattta	2986
OATP8	54	intron10 + 2214	atatacagaatttcataac T/G aatttctaaattccaaat	2987
OATP8	55	intron10 + 2316	taaatattttagtttgagac T/G tctttaaataatggaaig	2988
OATP8	56	intron10 + 2372	tgtatttggcaaatgttt G/T tteatttttcaaaactatt	2989
OATP8	57	exon11 + 1557	cagacagaaattactcagc A/G caatttgggtgaatgcccaag	2990
OATP8	58	intron11 + 147	ttcttgaattttttgat A/C ttcaataacatcataata	2991
OATP8	59	intron11 + 10339	aaaaaactgcatttttagt G/C ttacagaaagatttgc	2992
OATP8	60	intron11 + 10358	ggttagctagaaagattt G/C ctcatatacaaatataa	2993
OATP8	61	intron11 + 10538	caacagagatcaatgtaa T/G gaactctttaaattaaaca	2994
OATP8	62	intron12 + 55	ctaatattatgtttaa C/T taagactgaatgcaattaa	2995
OATP8	63	intron12 + 1802	taaaatgaatcgttaaa T/G tcatgtataatcactgtca	2996
OATP8	64	intron12 + 2612	ataggcatataactctt C/A ttccctctgtatataggag	2997
OATP8	65	exon13 + 1833	aacagctgtgggcacaagg G/A gctttaggtatataattc	2998
OATP8	66	5'flanking - (1590-1587)	ctatacatatataccta TATC/Δ tatgttatgtgtcttatt	2999
OATP8	67	5'untranslated - (11-28)	agcatcagcaacaaataa ATATTCATCT	3000
OATP8	68	5'untranslated - (4-7)	TGGTATCTG/Δ tagtttaataatggaccaac	3001
OATP8	69	intron4 + (213-214)	tattcaattgtatctgtag TTTA/Δ aataggaccaatcaaca	3002
OATP8	70	intron4 + (213-214)	cctgttcgttctatgcagc (T) ttgttccaacaaacagaa	3003
OATP8	71	intron4 + 505	cctgttcgttctatgcagc ttgttccaacaaacagaa	3004
OATP8	72	intron4 + 616	tataactttctctttataa G/Δ atgcaaatgtttatgcatt	3005
OATP8	73	intron4 + (804-812)	aaaaataaagtgaagtgagg A/Δ aaaaaatgtttcaagttt	3006
OATP8	74	intron4 + 855	acatcattgtttaacagaat (A)9-11 tattttgtaacgacaaga	3007
OATP8	75	intron7 + (619-628)	ggatgttttaaacaaatta G/Δ gaactctatttcaacacac	3008
OATP8	76	intron7 + (1773-1779)	tttttatetgaattaaat (AT)4-5 catataatcttcaactaag	3009
OATP8	77	intron7 + (1773-1779)	atttttatattatgaact (T)7-8 aaggtatgtatgtatag	3010
OATP8	78	intron8 + (1270-1290)	tagtgcgccaccctctctc (T)19-23 gagaatgagctctcgtct	3011
OATP8	79	intron10 + 665	tttttcttaactcaaaagg T/Δ tttttttccatgtgacac	3012
OATP8	80	intron11 + (247-250)	aaatatcttaaggcaccac TGAT/Δ tgacagttgacctgatga	3013
OATP8	81	intron12 + (1622-1630)	aaataaattgttgcacata (T)8-10 atttttcaaggctcgtct	3014
OATP8	82	3'untranslated + (2464-2465)	ggaaagcctgctgcttt A/Δ aaaaaaatgaacactttg	3015
OAT1	1	5'untranslated - 127	gcagctcagactcagctccc G/A gagcaaccagctcagagg	3016
OAT1	2	5'untranslated - 20	gaagccacagccccagcc A/G ctgagctggcctggcccaa	3017
OAT1	3	intron3 + 150	caatgaacaacattttctc G/A gctcagtcgcccctgaccc	3018
OAT1	4	intron4 + 211	ttctctgcttcccccactc A/C gttctcagctcgtctctc	3019
OAT1	5	intron5 + 33	gagacttccatgatgaact C/T ccaggcttcccccacaa	3020
OAT1	6	intron6 + 168	gaaccagatgccccagcct C/T gactcagtcacagctctcc	3021
OAT1	7	intron1 + (58-71)	ggagatgggggctttgtt (A)13-15 gtacatggagaattactg	3022
OAT1	8	intron3 + (1306-1319)	aataagttggagggagcag (A)12-15 tcaaggttggggggcca	3023
OAT2	1	intron4 + 842	ttgaactccaaagtgttg G/A attacaggcatggccattg	3024
OAT2	2	intron5 + 33	gtgtgtgtgagcatcat C/A tgtgtgtgtggaggtgg	3025
OAT2	3	intron5 + 183	ccacatccatctctggagc A/C aactcgtctcagctgccatg	3026
OAT2	4	intron5 + 184	caactccatctctggagc A/C actcgtctcagctgccatg	3027
OAT2	5	exon7 + 1269	actagctctagttctctc C/T ggtgagccagtcctcatagg	3028
OAT2	6	3'untranslated + 1792	ataaatgtgtacatgaggt A/G tgaacacaaatacaaggt	3029
OAT2	7	3'flanking + 1386	tgtagcagccacatgcaca G/A ttttcaacatgagagagag	3030
OAT3	1	5'flanking - 580	ctgtgtcagagacagagcca C/G ggaagctcgtgctgcccag	3031
OAT3	2	5'flanking - 463	ttcttgagaggaactccccc T/C tcccctctcggaggttcc	3032
OAT3	3	5'untranslated - 16	cctgccacagctctgctc G/A tcttgcgccagtgccatgac	3033
OAT3	4	exon2 + 153	cctgtccacccagctgcccc G/A ccccaaatgctccacagg	3034
OAT3	5	intron2 + 177	gcacaaagcccttggctc T/C tcccacagagtcacagca	3035
OAT3	6	intron2 + 6201	gtcatctctctgtctctt T/G tgcacacagaggttctc	3036
OAT3	7	intron3 + 79	tcgtctccacccgtgaccc G/C caaagggcaaaagagctgg	3037
OAT3	8	exon5 + 723	tggcgttggctgagttaac T/A gtgtccattcccttctctg	3038
OAT3	9	intron5 + 524	tggagttacaaaggaagt T/C aaaggaagcctgagcctgg	3039
OAT3	10	intron7 + 386	gacaaagggtttcagact G/A aagacaaaattatgttat	3040
OAT3	11	intron7 + 754	gcccacgtcagacatgacca G/A tcaatcacagcatttctcc	3041
OAT3	12	intron9 + 81	attgtctgtctcttacc G/A aagagcaatcctttatgac	3042
OAT3	13	5'flanking - (661-660)	tacatttggctccacgggg (G) agcggctgacagagagaa	3043
OAT3	14	5'flanking - (661-660)	tacatttggctccacgggg agcggctgacagagagaa	3043

Table 1

[illegible]

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ALDH1A2	59	intron4+7231	aalaggatcaaatcacaa A/T gtagtgattcagatctaa	3104
ALDH1A2	60	intron4+7958	taaaatcgtttttatgtta C/T taggtatataaaatttcta	3105
ALDH1A2	61	intron4+8090	tctgttttctcactgttta C/T agattgcttagctactca	3106
ALDH1A2	62	intron4+12823	tgttagcctgtagctaaatg C/T tttaaatatgtgaacgtt	3107
ALDH1A2	63	intron4+12939	atgaggtccgacttttaaga T/C tttgtctacattttctcc	3108
ALDH1A2	64	intron4+14935	tettgatggagtcttttta T/G aaatggactttaccttctt	3109
ALDH1A2	65	intron4+15321	gcatttgggtgtctggaga C/T atctccagaataatgctatg	3110
ALDH1A2	66	intron4+15412	tticaagttatttctgtt T/G tttttttttttttttt	3111
ALDH1A2	67	intron5+1888	aatccaaactctgtacttt G/T tagtggaacagattttgtc	3112
ALDH1A2	68	intron7+9166	gaasagclactttaticaaa G/A ataaagttattttaagaaaa	3113
ALDH1A2	69	intron7+9914	aagctggagaaactactgg C/T ttctccacacagtatttc	3114
ALDH1A2	70	intron7+18942	tttggaggggaactaatccc G/A tgaattctaggtttctctt	3115
ALDH1A2	71	intron7+19820	ttcaccctctattttaggtt A/G ggggggttgggttctacag	3116
ALDH1A2	72	intron7+19826	cctcattttaggttagggga G/A gtgcttgcacagttttag	3117
ALDH1A2	73	intron7+19913	cgtgaotcattcagttttt A/G tttaaaatccagtttgaa	3118
ALDH1A2	74	intron7+(20110-20111)	catgtttattctctaacta (ACTA) tgcatagtcaaatgttctgc	3119
ALDH1A2	74	intron7+(20110-20111)	catgtttattctctaacta tgcatagtcaaatgttctgc	3120
ALDH1A2	75	intron7+21857	acaatgaatataagaagg A/T gaaaggggaagaaagcaga	3121
ALDH1A2	76	intron7+21929	tacaagacacagggcatott A/G actagttactggatctct	3122
ALDH1A2	77	intron7+23308	ggctttgacttcgaaacct G/T tgggttatccaaagtctc	3123
ALDH1A2	78	intron7+23554	gacattgttgaaacacggg C/T ttttaggggtgtcgttcc	3124
ALDH1A2	79	intron7+(23701-23703)	catctgagatttacctgtg GTG/Δ ttaccogtttagtggctc	3125
ALDH1A2	80	intron7+26479	gatcatgtacaatttttt T/C atctcatgatattcttcaa	3126
ALDH1A2	81	intron7+26561	taagggccacaaatgcagta T/C tgaatctcagttacatt	3127
ALDH1A2	82	intron7+26662	tttcttagtcttccatca C/T gaactaaagctgtctcca	3128
ALDH1A2	83	intron8+78	tttatctctcactttttat G/A gacacatagcaaatatatt	3129
ALDH1A2	84	intron8+(700-711)	accatctcattcagtgattc (T)11-12 cctctcactgttggcaggc	3130
ALDH1A2	85	intron8+724	ttttttccctcactgtt T/C gccagggcagagctgtttcc	3131
ALDH1A2	86	intron8+800	cagattgttgtaatttcagc C/A ccagcttggaatttgcagag	3132
ALDH1A2	87	intron8+1251	gatttctgtgaatttga G/A gatctggcaacclggggctc	3133
ALDH1A2	88	intron8+1627	ggccctctccagcgaagc G/A gtgagaacatggctgtttcc	3134
ALDH1A2	89	exon9+141	tggagcgggccaagggcgg G/A tagtggaggtcccttggac	3135
ALDH1A2	90	intron9+778	aeccagctctgacagatccc T/C tgtagcttggaaagtgtg	3136
ALDH1A2	91	intron9+801	tagcttggaaagtgtaga A/G gtgaagggtggtcacttc	3137
ALDH1A2	92	intron9+868	tctgaaggctctgttactt T/C agtgggtggggggggccac	3138
ALDH1A2	93	intron9+1338	aatttttgccttttttact A/G tcaatcaaatgttctaagt	3139
ALDH1A2	94	intron10+(227-229)	ctatgtcttattgtattta TTA/Δ gccacagacaatcagaat	3140
ALDH1A2	95	intron10+316	ctaaatgtgggtcactggga T/C gtaaccaggagaggaatc	3141
ALDH1A2	96	intron10+368	ctttacattctgtgcaagga G/A ggcaagggcaaatcagcc	3142
ALDH1A2	97	intron10+660	gtaaacttgcatgaattgt G/A gaaagcaggtaaaggaatga	3143
ALDH1A2	98	intron11+104	tgggaataccaaagcaac C/T aagttcacccgaagagggg	3144
ALDH1A2	99	intron11+229	aaacttctaaagaantacc A/G tccagctcagattatgtct	3145
ALDH1A2	100	intron12+117	catcattcccaaacattt C/T gtggagcacatgctactata	3146
ALDH1A2	101	intron12+691	gatagggaagatcactgtga A/G ctggaanaatctgggaacc	3147
ALDH1A2	102	intron12+1934	catctgtctagattgatg T/C ttgtttgtttgtttctct	3148
ALDH1A2	103	intron12+1973	ctacttaccctcaaacatg T/A ttctctttcttaaatgacc	3149
ALDH1A2	104	intron12+2722	ccaggtgactccagatata C/A tcaatgccaggaccacag	3150
ALDH1A2	105	intron12+3855	cacttgaagcaaccataat T/C gtgagtttctgtatgtga	3151
ALDH1A2	106	intron12+4185	tigtcttaagcgaattgaac T/G atcggagcagaggaacgac	3152
ALDH1A2	107	intron12+4991	acaggaacactttagcatgc A/G acccactcccaacctcgtc	3153
ALDH1A2	108	intron12+(5018-5019)	cccacctcgtcttgggg (G) aggaagcacactactgtcc	3154
ALDH1A2	108	intron12+(5018-5019)	cccacctcgtcttgggg aggaagcacactactgtcc	3155
ALDH1A2	109	intron12+(5051-5052)	actgtcccaagaaactata (A) ctgaaccagtgctgcttgt	3156
ALDH1A2	109	intron12+(5051-5052)	actgtcccaagaaactata ctgaaccagtgctgcttgt	3157
ALDH1A2	110	intron12+(5300-5302)	ttaaagtttaaaaaactt CCG/Δ taaaactactcatgagtg	3158
ALDH1A2	111	intron12+5405	calccaggactgtctgttc G/C caggtgataaactgcacttc	3159
ALDH1A2	112	intron12+5435	aactgcacctcccaagact C/A cgcgtcactcacatgcagc	3160
ALDH1A2	113	3'flanking+449	tttggccggggaacaattt T/C caaggttgtaagccaatt	3161
ALDH1A2	114	3'flanking+597	acctgggatattcctgaccc A/C atctgttttttttaccac	3162
ALDH1A2	115	3'flanking+669	atagagactggaagtcatca T/C gtgcagttcacccgttctga	3163

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ALDH1A2	116	3'flanking+1122	cgctccactgagctctc T/G gtcacacccattctgccc	3164
ALDH1A2	117	3'flanking+2214	tcagctgtgaaagaaatc T/C gtaaatggtagccgtactac	3165
ALDH1A3	1	5'flanking-1425	cagtgtagccagccgatai C/T ggtcaaggctgcccgcctcg	3166
ALDH1A3	2	5'flanking-1379	ccattatcccccttccccg C/T ctacgtgtgacactcagge	3167
ALDH1A3	3	5'flanking-1270	aacttaccctctatccagc T/A ctatccagaaggacaccagg	3168
ALDH1A3	4	5'flanking-(1214-1213)	acggaggccctcaaacagga (GGA) aaataaggagacccctcccc	3169
ALDH1A3	4	5'flanking-(1214-1213)	acggaggccctcaaacagga aaataaggagacccctcccc	3170
ALDH1A3	5	5'flanking-1103	gcacagctttgtcaggagt C/T cgctccctcggctttgttc	3171
ALDH1A3	6	intron1+986	gccttaactttccccacctt T/G ggttctctgtgttttgc	3172
ALDH1A3	7	intron1+1462	glacaggatttcaaaactat G/A tatatagaaaccagacagta	3173
ALDH1A3	8	intron1+1661	ccgtgtgtctgtgtgtgtc G/A caacctttgccagtlaaagg	3174
ALDH1A3	9	intron1+2360	agggatagaagtcctctct A/G atttagagggcctcttctt	3175
ALDH1A3	10	intron1+2516	tgaaaacattctcttttga G/A tttagctgagtgccctgtg	3176
ALDH1A3	11	intron1+2624	cctgagacaccttaccagtc C/T gtcctgttccatgtctatc	3177
ALDH1A3	12	intron1+3255	tttctcttctcaaaatg G/C cccctcttccgtgtcact	3178
ALDH1A3	13	intron1+(3643-3656)	gcttcagagggtttttgtgg (T)12-14 acattctatcaactttaa	3179
ALDH1A3	14	intron1+4265	ccaaagccctctctttttaa T/C algacattaaagaacaatt	3180
ALDH1A3	15	intron1+5187	caagatggataagacgtcac C/T taaggtccttagcatgtga	3181
ALDH1A3	16	intron2+43	ctctaagttaattcaattatg G/T atgaccnaaggttaaggaa	3182
ALDH1A3	17	intron2+127	caggccctggctagctgcg T/C gaattggcatgtgttctca	3183
ALDH1A3	18	intron2+(285-300)	aggaaggggtttcttttct (T)16-17 atcaattattggacctga	3184
ALDH1A3	19	intron2+778	cggtgcagagtaggcttgg A/G ttattcttgcctatgagt	3185
ALDH1A3	20	intron2+1216	actcgttagagtcactctg A/C ctggtgtccacatccactc	3186
ALDH1A3	21	intron3+81	accatgggtgtgggaaaa A/C gatcacgttccgttttgt	3187
ALDH1A3	22	intron3+236	gctcagctcttgaccaggt T/G gtgtctataggcagttgag	3188
ALDH1A3	23	intron3+1467	ggccgggtgtgagggagg G/T atctcctttctgaccttga	3189
ALDH1A3	24	intron3+1725	ccacatgttccccggtag A/G gtatgctccctccagggtaa	3190
ALDH1A3	25	intron3+3777	gccegaagtagatgccccca A/G ttacgtgtctgaltactg	3191
ALDH1A3	26	intron3+3829	caagtcactgggcccgttgc G/C tccgtccctgcacctgaag	3192
ALDH1A3	27	intron3+4299	tcaatttccacagccacact G/A gccagcctggccgagaagg	3193
ALDH1A3	28	intron4+84	agggcccccctgactgttt G/G cctlaaggacacattccaac	3194
ALDH1A3	29	intron4+126	ccactccctctcacaatgtt G/G ctgcgaattcttctctaag	3195
ALDH1A3	30	intron6+(290-291)	tagagaatttccagggggg (G) tcaaccaagaggagccaaa	3196
ALDH1A3	30	intron6+(290-291)	tagagaatttccagggggg tcaaccaagaggagccaaa	3197
ALDH1A3	31	intron6+705	aacagctggtgatgagcaa T/G ttccactttcctttgtga	3198
ALDH1A3	32	intron7+56	ggggcgtgttatttgcacc C/T gtgagctttcctttgacg	3199
ALDH1A3	33	intron7+1107	gatgctgttaactctccttgg A/G gacagacactgacctgtga	3200
ALDH1A3	34	intron7+1610	aagagccacacagaaccacc C/G cctactggcctgttggat	3201
ALDH1A3	35	intron7+1820	cactctgaagtgagccgtt T/C agaccaaggtatccaggatg	3202
ALDH1A3	36	intron8+963	gagaaaggacagggaggga C/T acaggctctcaggaaggaaa	3203
ALDH1A3	37	intron8+1824	accattcttatccactaagc G/A tglcccccagatcttatic	3204
ALDH1A3	38	intron8+2384	cgctcctctgccccctccc C/A tccagtggacttgcagtg	3205
ALDH1A3	39	intron8+24	atccccctggtgtgtgaa A/G ccatgtgtctgtgtatggg	3206
ALDH1A3	40	intron8+91	gcctacagggtccctctccg T/C gaaaggaatgctgacctgtc	3207
ALDH1A3	41	intron8+219	actgaggcatgggggggg C/G gctattcccaggccagaagg	3208
ALDH1A3	42	intron9+435	ccagacagagagagcctggg G/A caggagaatgtatctcagg	3209
ALDH1A3	43	intron9+1472	ttgacttttgaggccagata C/T accgatttctccagagaa	3210
ALDH1A3	44	intron9+2038	taaacaaatgttccctacgg G/A ctctccaggaggtgtggagt	3211
ALDH1A3	45	intron9+2124	caaacagggtctccagatg G/A catatgccagccagccagg	3212
ALDH1A3	46	intron9+2154	agcagccaggagggacctgc G/C gttggcgagccccctgt	3213
ALDH1A3	47	intron9+2197	cttttggccctcaggagg G/A gaagagcagctcagcagcat	3214
ALDH1A3	48	intron9+2466	ttcttagttctcatgttcc C/T ctctagaatgtttctgtg	3215
ALDH1A3	49	intron9+3655	gatttgcaagtggcatgca C/T gtttatgcccctctctctg	3216
ALDH1A3	50	intron9+3954	gggtgcgttttgacaactg C/G tccgtagcgtgttcacagc	3217
ALDH1A3	51	exon10+88	tggatgcgggggtcagcc A/G tggagacaaaggggtcttc	3218
ALDH1A3	52	intron10+8	tgcanaagagggttacaag G/A gggctgtggcaaggctacga	3219
ALDH1A3	53	intron10+307	ctctctgattttctaacaca A/C ccgttccccagtcagtc	3220
ALDH1A3	54	intron10+378	gtgggttttgcaggaaatca G/A ttcaagaacctgtgattca	3221
ALDH1A3	55	intron10+975	aatattgtctacttctcc C/G ctgtagttattatgaaac	3222
ALDH1A3	56	intron10+1088	cagtgcaggagccaggagg C/T ctctccaggtgactctgag	3223

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ALDH1A3	57	intron11+105	ttgtttacattgtatattat A/G taccaagccctgtctcagtg	3224
ALDH1A3	58	intron11+274	egggctccagtagctgtgcc T/G gtggccctgtgtgtactg	3225
ALDH1A3	59	intron11+1088	cagtgccaggagccaggggg T/A ctctccagatgactctgag	3226
ALDH1A3	60	intron12+96	ctccatctgtgtacacccc G/A tccccccacacccgctc	3227
ALDH1A3	61	intron12+5642	ttctgtctaactgtctgttc T/C ctcatgccccctaggctggc	3228
ALDH1A3	62	exon13+104	ggctccttctcctaaccatc G/C gacggcgaatgtggcagct	3229
ALDH1A3	63	exon13+281	atagggttctgtgaactcg C/T agtctgcccgtggagggag	3230
ALDH1A3	64	3'flanking+743	gtggcaggaactglagga G/A aaggatattttccctcattt	3231
ALDH1A3	65	3'flanking+1145	gcctccagctacccccccc A/G cctcaggaggggtcattcca	3232
ALDH1A3	66	3'flanking+1185	aecctagggtgctgagaatc T/C gggtaggattaccagcaaa	3233
ALDH1A3	67	3'flanking+1600	acaccacgcccctgcaaatg T/C lgggaactgtcgtgtgcaa	3234
ALDH1A3	68	3'flanking+1847	caggagccctgcggctccc C/G ggttctgtgaatggcagtg	3235
ALDH1L1	1	intron1+252	cgacgcccaggactggccc G/C ccgagagatctggccggcc	3236
ALDH1L1	2	intron1+544	ctcaggggctgcctggagt G/T ccagctccagccactgcgt	3237
ALDH1L1	3	intron1-6596	cagatttttctaagggtga C/G tagccacigaggtattttt	3238
ALDH1L1	4	intron1-6513	caattatggttlatcttgg G/A acatgtttctagagtagta	3239
ALDH1L1	5	intron1-6478	atagtcttcttacttactt G/A cattctaattttgttccct	3240
ALDH1L1	6	intron2+240	gtggcattagggtcctggag A/G agggctctagaggaagccag	3241
ALDH1L1	7	intron2+1326	gaggagagaccggagggga G/C agccagtcacgtcagggccc	3242
ALDH1L1	8	intron3+386	gtcctactctaaactccact G/A ccgtctgtctgtggcagaca	3243
ALDH1L1	9	intron4+271	gggccccttcactagacag G/C aaggctaaagccaggactg	3244
ALDH1L1	10	intron4+356	taggtattctatttctctct C/T ttactctgttgattctctt	3245
ALDH1L1	11	intron4+608	gtctctgtagggctgtctc A/C gtcacatgcttctgtctgg	3246
ALDH1L1	12	intron4+664	gttcacatggcctgagccgc A/G gggcggtcagtcacccctgg	3247
ALDH1L1	13	intron4+785	gagggtctgtgcccctgcc C/G gaggacggctgacagggac	3248
ALDH1L1	14	intron4+874	ccctgggagccctgtctgt T/G tggcgacgcaggaagagca	3249
ALDH1L1	15	intron4+1349	tccttcaggctctgtctcac G/A tgggccagactccttggct	3250
ALDH1L1	16	intron4+1789	ctgggtctgggaaggaggca G/A ggtctattgtctggggtag	3251
ALDH1L1	17	intron4+1815	ggcagggtctcattgtctgg G/A atagcaaccactggatctc	3252
ALDH1L1	18	intron5+272	aaagcccccaggagagtag A/G gtggggttagaggagcaaa	3253
ALDH1L1	19	intron5+301	tgaggggcaaacagtcagcc G/A tagtgcagcagcttctcaag	3254
ALDH1L1	20	intron5+343	caagggtgaggagcagtg G/A ggtctctggagcaatagcca	3255
ALDH1L1	21	intron6+926	ctgcctgggctacttgctt C/T gggggtcttctctacccac	3256
ALDH1L1	22	exon7+41	aacgctgaacacttcaggcc T/C ggtgcccggaggagacgtt	3257
ALDH1L1	23	intron7+305	cctgaatcagagagaagcc C/T tcccaggagccctgggttca	3258
ALDH1L1	24	intron7+837	gtccggcacaaccccatggg C/T gtgtacccccagccgtgtt	3259
ALDH1L1	25	intron7+866	cccagccgtgttctgtgtc C/T ggcctaccagagtgaggcgt	3260
ALDH1L1	26	intron7+884	tccggcctaccagagtgagg C/T gtggcagtatggggcctgac	3261
ALDH1L1	27	intron7+1118	aatgtccaggaactatgc G/C aggcagtaaggcagagga	3262
ALDH1L1	28	intron7+1168	aaagtaaggctcaggagaa G/A tctagcctggggctgtccc	3263
ALDH1L1	29	intron7+1451	caggccaccacagcatctg T/C ccagagacctgcaagagacag	3264
ALDH1L1	30	intron7+1489	caggatgcanaagaggaac T/C taagtgtcttaaggaggaac	3265
ALDH1L1	31	intron7+1579	tcagggtgggggggagtag G/A gagagaccagctgagcacac	3266
ALDH1L1	32	intron7+1691	ctggctgggcttttagcttgc A/C gaagctccagaaactcttt	3267
ALDH1L1	33	intron8+2627	aaagaggagagccgggggtg C/T ttgtgccaggggttggggga	3268
ALDH1L1	34	intron8+2646	gcttgtagccaggggttggg G/A aactgtgtctgattggcct	3269
ALDH1L1	35	intron8+2925	ctgctgcccctcataggctcc C/G agactgaatccttcagagga	3270
ALDH1L1	36	exon9+4	caggtcttctgttgagagt G/T ttgtgacggatccctccoc	3271
ALDH1L1	37	exon10+109	cagctgttagtgaggaagct G/T cgaaggagcagtgaggggg	3272
ALDH1L1	38	intron10+(671-672)	tggcattttctctgtctga (AG) gtctcttagccccacctaa	3273
ALDH1L1	38	intron10+(671-672)	tggcattttctctgtctga gtctcttagccccacctaa	3274
ALDH1L1	39	intron11+8	caccgatggaagtgtagtg C/A agggccagcaccctctctcc	3275
ALDH1L1	40	intron11+447	atgagccaaagcagccctat G/A gtatgataccctgtacat	3276
ALDH1L1	41	intron11+601	ctcaaatgagtcatttag A/G ggaagtaatgaagactcct	3277
ALDH1L1	42	intron11+639	catctgcagaaggagggga G/A gggtagggacacagcagg	3278
ALDH1L1	43	intron12+684	tcctgggagagagaggggtg C/T gggcagatgagccgagaca	3279
ALDH1L1	44	intron12+767	ggtctaggggtgcgaagcca A/G gttatggcgtgtcccaacc	3280
ALDH1L1	45	intron12+1014	tcataggttccagctccctt C/T gcaagccctcaattctaga	3281
ALDH1L1	46	intron12+1359	ctggttctgctcagctcag C/T acagcagaggcgggtcttg	3282
ALDH1L1	47	intron12+1734	ggtggtccagctgctgttg G/T tcagtggggccggccagcc	3283

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ALDH1L1	48	intron12+1901	ttcgcgcgcctaactgaatt G/A acaatagaatagtcctgca	3284
ALDH1L1	49	intron12+470	gggatggggccacctctcca T/C ctctggagatgccaggctca	3285
ALDH1L1	50	intron12+334	aaeggcagcctcttgggcca T/C gaccccttgcgtctgcag	3286
ALDH1L1	51	intron12+325	ctcttggccatgacccctt T/C gctgtctgcagcaagggt	3287
ALDH1L1	52	intron12+221	gaaggaaagcagggagagat G/G aggaaggagagaggacag	3288
ALDH1L1	53	intron12+4	cccgttccctcaccctgg T/C caggttgcagatctcatgg	3289
ALDH1L1	54	intron13+34	tccaccccggtgagacaca T/C gcagactggcccagccat	3290
ALDH1L1	55	intron13+58	gactggccagccatatagg A/G gaactccaaggccagcacag	3291
ALDH1L1	56	intron13+125	ccacaacitgggcttggaa T/G gacacctgtttatgcttg	3292
ALDH1L1	57	intron13+126	cacaactgtgtgcttggaa G/A acacctgtttatgcttg	3293
ALDH1L1	58	intron13+281	acctgcatccagacgagtic T/G ggtgttgacaggttcagtt	3294
ALDH1L1	59	intron13+299	tcgggtgttgacagattca A/G ttcctgttgagtcagagct	3295
ALDH1L1	60	intron14+121	catttatcaaacagccatcc A/G tctgtcttggagccactgc	3296
ALDH1L1	61	intron14+167	gccagccattgtgttaagga C/T ttgaggaactgttttaa	3297
ALDH1L1	62	intron14+205	taatctccagtaacactgg A/C tcaatgaggttccaggtggg	3298
ALDH1L1	63	intron14+219	cactgcatcagtcaggtcca C/G ggtgggaacaaagagtaaac	3299
ALDH1L1	64	intron14+2275	ttctctctgtgtgctatccg T/C cagacctgtctccagcct	3300
ALDH1L1	65	intron14+2431	agaatgactgagtgatcaga G/G ctgagagagcccccagcccg	3301
ALDH1L1	66	intron14+2660	agccagcattcttgggga C/T accaagaaaccttgcctgt	3302
ALDH1L1	67	intron14+2740	aactcacccctcagctcca T/C gcagctcccccagagcgtca	3303
ALDH1L1	68	intron14+2756	tcctgcagctccccaggag T/C gtcagagggcagagggaggg	3304
ALDH1L1	69	intron14+2805	ccgcacagcagagaaatggc T/C ccaaggagggagggaggg	3305
ALDH1L1	70	intron14+(3636-3637)	ttctctgggtgtgttggg (G) tgtggggcagctccctatc	3306
ALDH1L1	70	intron14+(3636-3637)	ttctctgggtgtgttggg tgtggggcagctccctatc	3307
ALDH1L1	71	intron14+4347	ttcaggacagaaacagcagg C/T gtgagctgccttcagaggg	3308
ALDH1L1	72	intron15+380	atgcccttatgtggttcc A/G agaccagaggtcctggagag	3309
ALDH1L1	73	intron15+(1055-1056)	gcccaaatctcagctaatc (C) tccagctgtctgtgggt	3310
ALDH1L1	73	intron15+(1055-1056)	gcccaaatctcagctaatc tccagctgtctgtgtgggt	3311
ALDH1L1	74	intron17+15	gaaaggttccgtgctggg G/C tggagcagaggggggctgc	3312
ALDH1L1	75	intron17+44	aggggggctgctgtgggt G/C gctgggacatggcagtgct	3313
ALDH1L1	76	intron17+51	gctgtgtgagtgccctgg G/A acatggcagtgctgcacaa	3314
ALDH1L1	77	intron17-(2224-2223)	ctgtgtcatctcccagact CT/A gtaactaaaccacatsta	3315
ALDH1L1	78	intron18+140	agctcatcacaaagcatagc G/A tggcaggcagcaggttagg	3316
ALDH1L1	79	intron19+(51-52)	tgttccctgggagcagcgc GC/A ctgctggagggggttagg	3317
ALDH1L1	80	intron19+399	tcaggtcagcctggccctga C/A catggacaggggcccctggag	3318
ALDH1L1	81	intron19+1794	gtctgtcttggggtcttaa G/C ggaatcagagacttccaca	3319
ALDH1L1	82	intron19+1969	tgatcgggttgcgttggg G/T ccagagagcagggagcagaga	3320
ALDH1L1	83	intron19+1972	tcgggttgcgttggggc A/G caggacagggagcagagata	3321
ALDH1L1	84	intron19+2083	tgaagagcagaggggtgt G/T ccgggtcctcagtcacacc	3322
ALDH1L1	85	intron19+2119	acacctgtgtctgattagg G/T tgaatagggtgcagagttt	3323
ALDH1L1	86	intron20+1388	ttccctcttccacactccc C/T tggacttgagttccatgag	3324
ALDH1L1	87	intron20+1564	cccaggaaacaggaacagt G/A ggaagccatcccccgcctg	3325
ALDH1L1	88	intron20+1873	tcaggttaaaacatcatll G/A tgtgtgtatgaaaatattg	3326
ALDH1L1	89	intron20+2427	actaggattggtgacttg G/C gatcaggtctcagctctgtc	3327
ALDH1L1	90	intron20+2458	cagctctgtcaactgccaac C/T ggcggcccccatttccctcaa	3328
ALDH1L1	91	intron20+2544	ccgggtgggagagccatctg C/T agcgtgtgacacccatcac	3329
ALDH1L1	92	intron20+2573	gacpccatcacacgggtgc C/T gtagcccggtgcttatgctg	3330
ALDH1L1	93	intron20+2574	acacccatcacacgggtgc G/A tgaacccggtgcttatgctg	3331
ALDH1L1	94	exon21+33	agccaactgtttcacagac G/A tggagaccacatgttcata	3332
ALDH1L1	95	exon21+87	ccttcgggcctgtcatgac A/G tctctcggttgcgtatgg	3333
ALDH1L1	96	intron21+323	ccatgcattaaacaccccc C/G acactgagtgcttgaata	3334
ALDH1L1	97	intron21+361	ataatcagagattttttta C/G tcaagctctaggttcagta	3335
ALDH1L1	98	intron21+478	gtcttgcggaggttctctc G/A gcttggcagctcggggttg	3336
ALDH1L1	99	intron21+1086	caacccaactcttcccccg C/T gctgcagcccgacatttt	3337
ALDH1L1	100	intron22+235	gggctgtgagggagactcc A/C gccaggagggcactggggcc	3338
ALDH1L1	101	intron22+313	atagcagggaggggttggcc G/A tgaagaccagggagccgtg	3339
ALDH1L1	102	intron22+1214	tgggccaacttatgactct G/C cccgagttccctcagctccc	3340
ALDH1L1	103	intron22+1226	tgaatcctccccaggttccc T/G cagctcctcctaaccctag	3341
ALDH1L1	104	intron22+1623	ggggttcccatgctccaga C/G aaggcgggtggagctgggg	3342
ALDH1L1	105	intron22+1698	attctgggaggtcctggccc A/G ctatccactgcaggggata	3343

1 **Detection Using PCR**

The amplification can be performed using a polymerase chain reaction (PCR). The DNA polymerase can be LA Taq DNA polymerase (Takara), Ex Taq polymerase (Takara), AMPLITAQ Gold polymerase (Applied Biosystems), AMPLITAQ (Applied Biosystems) or Pfu DNA polymerase (Stratagene), as well as other polymerases.

An illustrative example of amplification conditions is provided below. The present invention is not limited to the conditions provided in this example. In preferred embodiments, each cycle in the transforming phase should last between 10 and 40 seconds at 85°C to 105°C and preferably 20 and 30 seconds at 94°C, each cycle in the annealing phase should last 30 seconds to 1 minute at 50°C to 72°C and preferably 20 seconds to 1 minute at 60°C, and each cycle in the elongation phase should last 1 minute to 4 minutes between 65°C and 75°C and preferably 2 minutes to 3 minutes at 72°C. There should be 30 to 40 cycles, although fewer or more cycles are contemplated. In order to completely transform the template DNA and the primer, each cycle in the transforming phase should last 1 minute to 5 minutes at 95°C before the amplifying cycle. If AMPLITAQ GOLD polymerase manufactured by Applied Biosystems is used, it should last from 8 minutes to 15 minutes and ideally from 10 minutes to 12 minutes. In order to completely elongate the amplified DNA, the elongation phase should last between 1 minute and 10 minutes at 72°C after the amplification cycle. If the amplified product is not immediately detected, it should be processed again at 4°C to make sure the amplification was not irregular. In this way, the gene encoding the drug metabolizing enzyme is amplified.

After amplification, gel electrophoresis is performed on the amplified product, the amplified product is stained using ethidium bromide or SYBR Green, and one, two or three bands are detected in the amplified product (DNA fragments) to determine the portion (DNA fragment) of the drug metabolizing enzyme containing the genetic polymorphism in the gene encoding the drug metabolizing enzyme. Polyacrylamide gel electrophoresis or capillary electrophoresis can be performed instead of aerogel electrophoresis. PCR can be performed using a primer tagged with a fluorescent dye to detect the amplified product. A detection method that does not require electrophoresis

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCA1	1	(5' flanking region -99)	acataaacagagggccgggaa G/C gggggcggggaggaggagag	3361
ABCA1	2	(intron 1 159)	gcgggtgttaaatggggagac G/T atgtcctagtacagctctg	3362
ABCA1	3	(intron 1 506)	gaattggctatatgtcccc G/C ggactggagcggcacagctcc	3363
ABCA1	4	(intron 1 5897)	gtcaaaaacccttttagcttt T/G gcaaaccctccttaagacc	3364
ABCA1	5	(intron 1 5929)	ttaagaccggatttaaatgc C/T tccctcctcatgaagctctt	3365
ABCA1	6	(intron 1 5962)	aagctctcttggtaccactc T/C tccccactcaagtgtgaa	3366
ABCA1	7	(intron 1 5985)	cccatcactaagtgtgaagt A/C agatcccccttctcttactt	3367
ABCA1	8	(intron 1 11416)	ttacagtgccttttatagga G/A agaaagaagaaatgtgtct	3368
ABCA1	9	(intron 1 11935)	ttctctgtggagcaaatagag G/A gctgtctgacacttggttcc	3369
ABCA1	10	(intron 1 12281)	gaatgtttgattgttgaaaa T/A cttaataacagtagtttttt	3370
ABCA1	11	(intron 1 12924)	gtctgacaaactttatactc T/C aggttgaaacctccggggaag	3371
ABCA1	12	(intron 1 13002)	gagcctcaatcacagattct C/G tctagctcacatgaagtaa	3372
ABCA1	13	(intron 1 17715)	ggagcatgactttgtggaag C/T ctctcctcttccaccagag	3373
ABCA1	14	(intron 1 17848)	gagggctgactgtcacccctt T/C gataggagcccagcactaaa	3374
ABCA1	15	(intron 1 21384)	gtgggtggggaggaattggag G/C aggaagcttgctcaagtgtg	3375
ABCA1	16	(intron 1 23063)	ggaggcacctgtgacaccca G/A cggagtggggggcggtgtg	3376
ABCA1	17	(intron 1 23131)	agtgtgcatatgtgtgtgacc G/A tgggagcttgtttgtcgtt	3377
ABCA1	18	(intron 2 2801)	aagaaaagtgtatttttca A/G gttgtgatgtcttagattgt	3378
ABCA1	19	(intron 2 2830)	tgttagattgttagattgt C/G aaagatctggcttgcatctt	3379
ABCA1	20	(intron 2 2856)	tctggcttgcatctgttaca A/G ctgacagaactggggtcag	3380
ABCA1	21	(intron 2 3187)	tgatagctgttgccctgacc A/G tacggagcttcattggcag	3381
ABCA1	22	(intron 2 3190)	tagctgttgctgctgacata C/T ggacgttcattggcagttc	3382
ABCA1	23	(intron 2 3194)	tgttgctgctgacatacggg C/T gttcattggcagttcctgt	3383
ABCA1	24	(intron 2 3204)	agcatcgggacgttcattgc G/A cagttcctgtctctctagat	3384
ABCA1	25	(intron 2 3401)	acataaagcctgtgtgtgc T/C gccaggaagactagaaacgc	3385
ABCA1	26	(intron 2 13927)	gtcaccacatacctggcact A/G tgctaaggctgggaatgcag	3386
ABCA1	27	(intron 3 4163)	ccagcccacttcatcttacc G/A tagttacctctcttagat	3387
ABCA1	28	(intron 3 4262)	tgtcaaaagaggaaactaagga T/C gccagggactttctgcttag	3388
ABCA1	29	(intron 3 4306)	ccctctcatcacttctccaa C/T gctggtatcatgaacccat	3389
ABCA1	30	(intron 5 490)	gatgggcatttgaacttgtt G/A tctttaaaagtgaatctt	3390
ABCA1	31	(intron 5 583)	tatctggggagtgggcattt T/G ctgactgaggcattggctgc	3391
ABCA1	32	(intron 5 1051)	ggctacaaaactgtgtttt C/T ttgggcagtaaaagaggcaa	3392
ABCA1	33	(intron 5 1051)	tagagaacaaagtctaatct G/A ttttcttgaatagtcgaa	3393
ABCA1	34	(intron 5 3127)	aagtcctgatttttttaggc A/G aaatggcctcttctctctt	3394
ABCA1	35	(intron 5 5924)	ctttctttcacaaaattgcc C/T cccagagctttctggaagg	3395
ABCA1	36	(intron 5 6831)	ccagtcctcagccttgcca T/C tgcttatgtgtgttgga	3396
ABCA1	37	(intron 5 12678)	gtcaccgctctgtctcacc G/C accctctggccatctctct	3397
ABCA1	38	(intron 5 14214)	cagcttggttccagaggcct G/A gacctgggtcccagaggtcc	3398
ABCA1	39	(intron 5 14257)	gctggttcccccgggtgttc C/T cagaggcctggatgtgtgc	3399
ABCA1	40	(intron 5 18078)	cctaccacacatgtcacgtg C/T acagccaagggtgtgtgact	3400
ABCA1	41	(intron 5 18795)	ctgggcttctcttgacact G/A ccagctaaaaggaaatctcc	3401
ABCA1	42	(intron 5 18948)	gcattgggtgactaagaac G/A catattccctatctctag	3402
ABCA1	43	(intron 5 19053)	ctcccccaacattaaagtg T/C aagggtgtcttattcaaatg	3403
ABCA1	44	(intron 5 19148)	ggcccaagaaactgcatttt C/A gcattgtctcctaaatgaagc	3404
ABCA1	45	(intron 5 19229)	atgctaacagtgttagagta C/T atgtgatgggaagcatcagg	3405
ABCA1	46	(intron 5 19405)	cttgctcaattttattctgtc T/C atataactcaattattactga	3406
ABCA1	47	(intron 5 19534)	catgtgacctcttagctcc G/A cggattaaactctgtctctca	3407
ABCA1	48	(coding region 474 (Leu 158 Leu))	gaaacctctctgtgggtctc G/A tatcacacctctctctccc	3408
ABCA1	49	(intron 6 210)	gcaacctggcgtcatgggcc A/C gctggttaaaataaaattga	3409
ABCA1	50	(intron 6 334)	acagttctgaggcaataacc G/A tgggttaagggttattgatct	3410
ABCA1	51	(intron 6 2288)	cttctttcaaagcttgggt C/T cactggaccagctatgaagt	3411
ABCA1	52	(intron 6 2322)	atgaagtgaatagtttagg T/C ccagaaaggcaattaagtaa	3412
ABCA1	53	(intron 6 2820)	gtgcttctgatacattctgag T/G ttcagttaaagagacctgatg	3413
ABCA1	54	(intron 7 416)	catcataaagatgacattgt G/A ggctgtcacagttggaaggc	3414
ABCA1	55	(intron 7 471)	agaccacactatttagctta C/T ttagtaataacattgcaag	3415
ABCA1	56	(intron 7 504)	ttgcaaaagaaaaattccgac G/A aagtttttccagcctaggaa	3416
ABCA1	57	(intron 7 679)	gctctggtgaaattctcttc G/C ctaccccaaacatcatcatt	3417
ABCA1	58	(intron 7 1740)	acaaatgctcaccctttcag C/T tgggaatgattgaaattttgg	3418
ABCA1	59	(intron 7 2122)	tgattaagggtgctactacc A/G ggtgctttctgcatatctcg	3419
ABCA1	60	(intron 7 7753)	taggaattccaagctgtgaa T/C tttttactgaagctctttgg	3420
ABCA1	61	(intron 7 8973)	atggaaattgttttatattg A/T ctacagattgccaatattat	3421
ABCA1	62	(intron 7 8976)	gaaattgttttatattgact A/G cagattgccaatattattag	3422
ABCA1	63	(intron 7 11327)	ctaacaattcttatttccatt G/C agtccttataaaagaagtgg	3423
ABCA1	64	(intron 7 11738)	ctgacgttttaaggagacgg C/T gtaggtccctttgaggactg	3424
ABCA1	65	(intron 7 12295)	agtctgtaaaattattgtct T/A ttttttcttttagcttatgt	3425
ABCA1	66	(intron 8 387)	tagcaaggccaatatttta C/G caacacacatgctgtcaac	3426
ABCA1	67	(intron 8 697)	ggaaactgtctggtgtcccc A/T gcatagggaagctgagccagg	3427
ABCA1	68	(intron 8 3036)	ctttatgtgggaagaatttt T/G tttttttgattggggagtg	3428
ABCA1	69	(intron 8 3176)	aaatggcctgtgtctctgtc C/A cctttctgtctgtatgctc	3429

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCA1	70	(intron 8 3364)	ggcagaaggcaaaagcttagg A/T cctagagagtgtctggaccac	3430
ABCA1	71	(intron 8 3373)	caaagcttaggacctagaga G/A tgctggaccacgccactcac	3431
ABCA1	72	(intron 8 3561)	cagggatttattaatgattt C/A ttgtgaaatgtttggaata	3432
ABCA1	73	(intron 8 3654)	agtgcggaatacatttgca T/C gtaagacagaacgctgctcg	3433
ABCA1	74	(intron 8 4715)	ggcagagggtctcagaatc C/T gcatttccacaatgtctcc	3434
ABCA1	75	(coding region 936 (Pro 312 Pro))	cgtattgtctgcggcatcc C/T gagggaggggggctgaagat	3435
ABCA1	76	(intron 9 2309)	ccctcaagagtcagtttaa A/G tgttggtcatgttagttgtc	3436
ABCA1	77	(intron 9 2392)	atgggagggtctgtgcttca T/C gaaacatttttccagatca	3437
ABCA1	78	(intron 10 228)	tggggatggggaggactggc A/G cagggctgtgtgtaggggt	3438
ABCA1	79	(intron 10 319)	ttctgcgttcctggctccc C/T acctgactccaggtgaacaa	3439
ABCA1	80	(intron 11 377)	gaaagaagtgtgggagcaa A/C gcattgtgttacatgtagac	3440
ABCA1	81	(intron 11 521)	agtgtcttagagacaattgg G/A ttcaaatgtggagcaggctg	3441
ABCA1	82	(intron 11 2850)	ctctatacaatcattatgct G/C ccattgaaataataatata	3442
ABCA1	83	(intron 11 2976)	ctccaattcggtagaaccag A/G gcttcctctctctgtcgaa	3443
ABCA1	84	(intron 11 3056)	gtttgcagctgtgtgttttc C/T ggcagcacatctgtgcaggc	3444
ABCA1	85	(intron 12 340)	ggcattattgtgaaactta T/C ctaaaaatgaattcgggtcc	3445
ABCA1	86	(intron 12 381)	aattaaattttgaaatttt A/G tattaaaaattatattagta	3446
ABCA1	87	(intron 14 1728)	caggctcagaggccttgcc C/T atcacccctggctcacgtgtg	3447
ABCA1	88	(coding region 2040 (Ile 680 Ile))	atggccctggacaaacagcat C/A ctctggttttagctggtcat	3448
ABCA1	89	(intron 15 1382)	cttttagacagaaaagttac G/A tgggatattatctcccacag	3449
ABCA1	90	(intron 15 1453)	tatataaggagaaaccagtt G/A aaattacctattgaagaac	3450
ABCA1	91	(intron 15 1567)	ttctgcgtagttttgggtaa G/A tcatttatcttcttttaggt	3451
ABCA1	92	(intron 15 1617)	cagttgcctcatcagaaaga T/A gaacagcattacgctctgc	3452
ABCA1	93	(intron 16 95)	agttgagaacagaagatgat T/A gtcttttccaatgggacatg	3453
ABCA1	94	(intron 16 452)	tggtgttttctgtgagtaat G/A ttttctgaactaagcacac	3454
ABCA1	95	(intron 16 657)	ctgttgctcagctctgggt T/C cataggcatcagcagccca	3455
ABCA1	96	(intron 18 1730)	tgaagttaacgctgagtc C/G ctgtgtccttacactccact	3456
ABCA1	97	(intron 19 426)	aggaccttacagtggttagt A/G tcaggagggtcaggggtg	3457
ABCA1	98	(intron 19 468)	aaagcaccagcgttagctc A/G gtggcttcacagcagattcc	3458
ABCA1	99	(intron 20 876)	ccctcctcatctaaagtga C/T acatgggggtcatgtgcagg	3459
ABCA1	100	(intron 22 118)	catgggatactcttctgtta T/G cacagaagagataaaggga	3460
ABCA1	101	(intron 22 560)	aaagctttgccattctaggg G/A tcatagccatacagggtgaa	3461
ABCA1	102	(intron 23 102)	accccttttgccatgttgaa A/G ccaccatctccctgctctgt	3462
ABCA1	103	(intron 23 287)	gtcaagaagaagagacttgt C/T aagaggttaagagccttggt	3463
ABCA1	104	(intron 23 1063)	acctttcacctcaggaagc G/A aggtgtttcacacggcacac	3464
ABCA1	105	(intron 25 321)	ctctttacttaagtacagtg T/G gaggaacagcggcatcaga	3465
ABCA1	106	(intron 25 376)	gttagaaattcagcaacttg G/C gccagctcagacctactga	3466
ABCA1	107	(intron 25 478)	catacataggaaatgacaaa C/T gtttatggatggatagtcta	3467
ABCA1	108	(intron 25 579)	tcatttaattctcaaaaaa G/T atgaaaaaatgaacactcag	3468
ABCA1	109	(intron 27 153)	aatggttaaaagccacttggt C/T tttagcagcatcgtgcattg	3469
ABCA1	110	(intron 28 1058)	actatcatgggagataatga C/T tatggtgtccatgatgtga	3470
ABCA1	111	(intron 28 1317)	caggaccagtggttctgagt C/T acctgaatgtgagacacta	3471
ABCA1	112	(intron 30 372)	tatatgtatttttaggttttg T/C ttatcagcttcttctgctttt	3472
ABCA1	113	(intron 30 506)	cccttttaaaagtaagcagt A/G gataaataaattcagtgaa	3473
ABCA1	114	(intron 30 1033)	ctggatttcatgggtgcctt G/C attttccacatgaaggttgt	3474
ABCA1	115	(coding region 4281 (Thr 1427 Thr))	tcttccctttgcagagacac G/A ccttgccaggcaggggagga	3475
ABCA1	116	(intron 33 626)	ggctccttgttactgatttc C/T gtcttttctctctgctttt	3476
ABCA1	117	(intron 33 719)	taatagccctcatgctagaa G/A ggagccggagcctgtgtata	3477
ABCA1	118	(intron 33 726)	cctcatgctagaaggagcc G/A gagcctgtgtataaggccag	3478
ABCA1	119	(intron 33 889)	ctttcctcaatgtctcagct A/G tctaactgtgtgtgtaatca	3479
ABCA1	120	(intron 33 1097)	ctgtgcacccactgtctgg G/C ttttaagtgcaggctgttct	3480
ABCA1	121	(intron 35 234)	aacctatctaaacctcagtt T/C cctcatctgtgaaatggaga	3481
ABCA1	122	(intron 37 411)	aaactctgtacattttatcag C/T agcttatccatccattgcaa	3482
ABCA1	123	(intron 37 1224)	caggcataggtgattcagag A/G tgaagggtcaagtcctgaa	3483
ABCA1	124	(intron 37 1720)	aaattaaaattactctgact G/T ggaatccactggtcagtaag	3484
ABCA1	125	(intron 40 251)	tgaaggtaaggaaaatagtg T/G tatttgcttgatccactgg	3485
ABCA1	126	(intron 40 252)	gaaggtaaggaaaatagtg T/C atttgcttgatccactggc	3486
ABCA1	127	(intron 40 319)	agcactggaaaagtcaaac A/G taactttgagaattaggtga	3487
ABCA1	128	(intron 40 957)	ctgttactcttttttctt G/C tcattgggtgatgccatttg	3488
ABCA1	129	(intron 41 146)	tgatgtgggcatcccgagc C/T cctccctgcccatcctgga	3489
ABCA1	130	(intron 42 239)	cattgggttttatgcttac A/C tttatgtgttagttattaaa	3490
ABCA1	131	(intron 42 321)	ataaatgggttgatttgag T/A ttgagtttcatagtcacaaa	3491
ABCA1	132	(intron 42 322)	ataaatgggttgatttgag T/C tgagtttcatagtcacaaa	3492
ABCA1	133	(intron 42 533)	agatgaaaaattatgtatag G/A ataataatgatcacggttct	3493
ABCA1	134	(intron 42 546)	tgtagatgataatgaatgat A/G cggttctaaaaagacaggtt	3494
ABCA1	135	(intron 43 739)	tacagccacacttaaaatgg T/A ccattatgaaatacatatt	3495
ABCA1	136	(intron 44 18)	taggtgagaaaagaagtggc T/C tgtattttgctgcaaaagact	3496

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCA1	137	(intron 44 264)	acaatataatttgccttgttt T/C ttaagagtataatttagtga	3497
ABCA1	138	(intron 44 279)	tgttttttaagagtataatt T/C agtgatttttggtaaattga	3498
ABCA1	139	(intron 44 508)	tttacatttgcacataaaat C/T cccctatgtacatgtaccta	3499
ABCA1	140	(intron 44 1477)	gatcctctctcctgtctctt A/T catttttgcagtagcaatgt	3500
ABCA1	141	(intron 44 1665)	tggttgtaagaactgatttg G/A ttggtatagctgtgagggcc	3501
ABCA1	142	(intron 44 1956)	gtgttgctcacactcaaaat T/G tctgggctctctcatttgggt	3502
ABCA1	143	(intron 45 68)	aatatataccttatggcttt T/C ccacacgcattgacttcagg	3503
ABCA1	144	(intron 46 608)	ttatactgacttcaatagag G/C ttccagacaaaaagttgttt	3504
ABCA1	145	(intron 47 336)	ttcacaaattgtaaacaccac T/C acactgaacagcatcatccc	3505
ABCA1	146	(3' untranslated region 7479)	aacaaaaatgtgggtgtctc C/T aggcacgggaaacttgggtc	3506
ABCA1	147	(3' untranslated region 8226)	aggagccctctgtaacaata C/T tgggcagccttttttttttt	3507
ABCA1	148	(3' untranslated region 8697)	ttccagaatttgaatattaa C/T gctaaaggtgtaagacttca	3508
ABCA1	149	(3' untranslated region 9097)	aactattttgaagaaaacac A/G acatttttaatacagattgaa	3509
ABCA1	150	(5' flanking region (-1033)-(-1032))	tgacttaaatatttagacat (AT) ggtgtgtaggcctgcattcc	3510
ABCA1	150	(5' flanking region (-1033)-(-1032))	tgacttaaatatttagacat ggtgtgtaggcctgcattcc	3511
ABCA1	151	(intron 5 6368)	ttctgtatgggggttgttgcgt C/Δ tgagaatcatgactgggtgg	3512
ABCA1	152	(intron 5 9709)	cattttctgtctgaaccccc T/Δ caccattcaggcagctgct	3513
ABCA1	153	(intron 5 13816)	tcctacttctctcttttttt T/Δ catttgctctctccaccac	3514
ABCA1	154	(intron 10 270-271)	cttttcaggaggagcccaaa (G) cgctcattgtctgtctct	3515
ABCA1	154	(intron 10 270-271)	cttttcaggaggagcccaaa cgctcattgtctgtctct	3516
ABCA1	155	(intron 20 611-612)	tttagcccatcctctccccc (C) gccaccctccttattgagge	3517
ABCA1	155	(intron 20 611-612)	tttagcccatcctctccccc gccaccctccttattgagge	3518
ABCA1	156	(intron 32 391-392)	gagtgccttgggtactctct (T) gatgggggactccatgataa	3519
ABCA1	156	(intron 32 391-392)	gagtgccttgggtactctct gatgggggactccatgataa	3520
ABCA1	157	(intron 37 847)	gctgtatattgtgaatgtcc C/Δ gttttcaaaagcaagccaa	3521
ABCA4	1	(5' flanking region -1005)	tgccatcataagcagaaact A/C tctctctcttcttgggaagct	3522
ABCA4	2	(5' flanking region -819)	gtctagagtctttcaaagag A/T acacattctgagatttgagg	3523
ABCA4	3	(5' flanking region -680)	agcaccaccccttgcaggg C/A tggaatgacagtaatgggccc	3524
ABCA4	4	(intron 1 208)	tgcccttcccaggagatgt G/A tttctctgtcctcagccaca	3525
ABCA4	5	(intron 1 234)	ctgtctctcagccacatgaaa A/G tcttttgctaccgtgcctg	3526
ABCA4	6	(intron 1 510)	agctcccgatcaagtcacag T/C ttaactggacacattatttt	3527
ABCA4	7	(intron 1 1527)	gcttaacaaccagcataaaa G/A agagcagcatgggacacgct	3528
ABCA4	8	(intron 1 2077)	caggactgtagctgtctggcc T/C aaaaatgagccattcctgtg	3529
ABCA4	9	(intron 1 2174)	ccctctcaatctggcctttc G/C ctggcatgggtgggagactc	3530
ABCA4	10	(intron 1 2246)	gtctccaggagatggagcc A/G ctctgggctgagggccttggc	3531
ABCA4	11	(intron 1 2364)	ttctgtctggcagcctctccc G/A atggctcccccactgctacc	3532
ABCA4	12	(intron 1 4243)	ctccctggggatgcctgtta C/G gcagtttaagcgtcaaggaca	3533
ABCA4	13	(intron 1 4287)	atgccgctctggggagggga A/C gctgagcatgattttggaag	3534
ABCA4	14	(intron 1 4309)	ctgagcatgattttggaagc C/T ggcagaagaggctattgtga	3535
ABCA4	15	(intron 1 4416)	tgacagcaaccgccccccccc C/T ccgcaaaaaacacacact	3536
ABCA4	16	(intron 1 4996)	tttaccctgggaacaggcag G/A ccaagctggc t/c ggtccctc	3537
ABCA4	17	(intron 1 5007)	aacaggcag g/a ccaagctggc T/C ggtccctcctctgatacaca	3538
ABCA4	18	(intron 1 5080)	gtgtgtggctgttttcttag C/G aagcaccatgtgttccaagtt	3539
ABCA4	19	(intron 1 5152)	gggagatgaacgttaagtga G/A ggcaggcctacaagggttga	3540
ABCA4	20	(intron 1 7110)	ccactggatctgcttttga A/G tcaagagtccttaagctcca	3541
ABCA4	21	(intron 1 7290)	gatttttgttggtttgcaa T/A ggtatcacagtcattattca	3542
ABCA4	22	(intron 1 7483)	tctgagcctctttccttaac T/C gcagagtgtgtgg c/t tacaga	3543
ABCA4	23	(intron 1 7497)	cttaac t/c gcagagtgtgtgg C/T tacagagaaatctttactac	3544
ABCA4	24	(intron 2 1067)	tcaagcagcagcagcaactg C/A gtggagtcttcttgaactaa	3545
ABCA4	25	(intron 2 1243)	caccagcagcagggaactggc A/T cacatgagatgctctgtct	3546
ABCA4	26	(intron 3 26)	tggtgagatccctaccatgc A/G ggggaggaagttgcacacc	3547
ABCA4	27	(intron 3 101)	agcatggagcactgagtgct C/T ttgtggcttctgtgagcccc	3548
ABCA4	28	(intron 3 330)	tgcttgggtggagtgaatca T/C tgtaggagaaaaactcagtt	3549
ABCA4	29	(intron 3 470)	tgaagtgcaggtttacaaagt C/G aagtttacttcttgggagaa	3550
ABCA4	30	(intron 3 634)	tgaaaaccaatgacccctct T/C ccaagaaaaatggccacata	3551
ABCA4	31	(intron 3 1016)	ccttgggggagctcagtatg A/G ttcttccaggagaaagcctgc	3552
ABCA4	32	(intron 3 1554)	gaaagtgtgggtttcatgttt T/C gcactcacattatgagtga	3553
ABCA4	33	(intron 3 1686)	ctagacattctcacagagcc A/G agggcagcaaggcggggctc	3554
ABCA4	34	(intron 3 1823)	ttcacctctctccatggacc A/G gtctccctgtctcctcaatg	3555
ABCA4	35	(intron 3 1938)	caaattcctgggaacaaatc G/A ggttgaccagc t/g ttattct	3556
ABCA4	36	(intron 3 1951)	acaaatc g/a ggttgaccagc T/G ttattctccctgtcccatca	3557

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCA4	37	(intron 3 2063)	ggctgtcagagcctacctgc G/T tgaatgggtggaagg g/a cagg	3558
ABCA4	38	(intron 3 2079)	ctgc t/g tgaatgggtggaagg G/A caggtctcagagaattgggt	3559
ABCA4	39	(intron 3 2186)	agacacacagagcatggggac C/T gagaggcgagcagaccctgc	3560
ABCA4	40	(intron 3 2214)	gagcagaccctgccaaaact G/A ggagactgaatagatcgctc	3561
ABCA4	41	(intron 4 3182)	ccccagagccacagcagcc C/G tgtctcctgggtggttctgt	3562
ABCA4	42	(intron 4 3515)	agtataataaaagcaggagc C/T atagcccccactctcaaga	3563
ABCA4	43	(intron 4 3952)	agagaagccactgtgccact G/C tgtggtcgaacttcaagacc	3564
ABCA4	44	(intron 4 4637)	aatcacttgccccaaggtca C/T cttaactgttaggtgttctt	3565
ABCA4	45	(intron 4 5319)	acctctagggggtccccagag A/G ccccaagaacagaaccttcc	3566
ABCA4	46	(intron 6 2266)	cacccttgacagacctcagac G/A ggtcctggggggttgccttc	3567
ABCA4	47	(intron 6 2857)	ccagaggagaaagctctgcc G/A tag t/c cggcctcagttaacca	3568
ABCA4	48	(intron 6 2861)	aggagaaagctctgcc g/a tag T/C cggcctcagttaaccacgga	3569
ABCA4	49	(intron 6 3078)	gcaggcattaaaaatgggact T/G tgcctttattgtcctctgggc	3570
ABCA4	50	(intron 6 3375)	ttaaattgccaaatgagttct C/G attacaagaagaaggga	3571
ABCA4	51	(intron 6 3412)	ggaaaatctcagtaaacacc C/T gtgacggcatctaccactt	3572
ABCA4	52	(intron 6 4635)	cttctgggtggatattgcta C/T gtcaagtgtctgggaagcc	3573
ABCA4	53	(intron 6 -264)	aaacagcaattagaatcact T/C tgaaatagttagatttta	3574
ABCA4	54	(intron 7 828)	gatgtgggaaggttagagaa G/C agcccatgttactaatgtct	3575
ABCA4	55	(intron 7 1019)	aggctctctgactgtctaga T/C agcaagtctaactattgtg	3576
ABCA4	56	(intron 8 374)	gtaaacacggctgtgggatg C/A ttttacaacacaatatcgt	3577
ABCA4	57	(intron 8 874)	tgatgagctgttatttggtg G/A ggtacagcctatttaatttag	3578
ABCA4	58	(intron 9 605)	tcgtgtctctgtctttagct C/T tgtctggttttagggccaact	3579
ABCA4	59	(coding region 1268 (Arg 423 His or His 423 His))	aacttttgaagaactggaac G/A c/t gtaggaagttggtcaaag	3580
ABCA4	60	(coding region 1269 (Arg 423 Arg or His 423 His))	actttttgaagaactggaac g/a C/T gtaggaagttggtcaaagc	3581
ABCA4	61	(intron 11 5687)	atcatgtaatgtacttttaga C/G tcagatatataaatatttgt	3582
ABCA4	62	(intron 11 7136)	gacttcccaacttaccttag T/C ggagctgtagtacacatagaa	3583
ABCA4	63	(intron 11 7180)	acgctcataaatgtcttctct G/A ggctgtaaagggtgaatttt	3584
ABCA4	64	(intron 11 7701)	gttagacgcaggcattacct C/T gtggctttgccccagtgta	3585
ABCA4	65	(intron 11 8073)	gggatgtttgcccacatcca T/C tggcattttctcaaaaggaac	3586
ABCA4	66	(intron 11 8586)	cagctgcctgcgctggagag G/A gctcaaacctcttccgccag	3587
ABCA4	67	(intron 11 11234)	cccaataattttgttttttc G/A ttttaggaattaaatttcag	3588
ABCA4	68	(intron 11 11641)	aagaacaacaactttattga C/G aacttttggtgtgtgacctg	3589
ABCA4	69	(intron 11 11808)	tggattttcttaaagaata C/T caattccattttccttttaac	3590
ABCA4	70	(intron 11 11923)	aagatcattattaatatctc A/G tcagcgtggtgtcacttaag	3591
ABCA4	71	(intron 12 305)	tcaccctgtgtgtcgaggag G/A tgagtgtgctatccaagccc	3592
ABCA4	72	(intron 13 1461)	ttgggtttcagtgctcagcat G/A tagctgtctactcagatccc	3593
ABCA4	73	(intron 14 1268)	ggagctgtgagcccttctct T/C atctaggtttcccttgttct	3594
ABCA4	74	(intron 17 23)	gagtccttttaaacacacaaat C/G ttaatgtttgaaatcaactc	3595
ABCA4	75	(intron 17 715)	gggactcccctagagctgaa G/A tactctcccactctgtttgtt	3596
ABCA4	76	(intron 18 1282)	ggaagatgaagaacctaaag C/T gcttcagaaattcatgagg	3597
ABCA4	77	(intron 20 -195)	acagattattccattgtatg C/A atgaactatgttaagccatcc	3598
ABCA4	78	(intron 23 755)	ctggctgcccgtgggttttc C/T tatgtccatccacggggagg	3599
ABCA4	79	(intron 26 702)	tatcaatacaactcagacg T/G cagtcctctggcccttttga	3600
ABCA4	80	(intron 27 156)	cctgctttccaaacccttat C/T ttgattotttgtaacatgaa	3601
ABCA4	81	(intron 27 385)	tttaagaacagtgagtac G/A tgacttgcctttgaaatgc	3602
ABCA4	82	(intron 28 299)	gacatgccatcagaccactg C/T gagtgttcaggcagcctacc	3603
ABCA4	83	(intron 29 168)	ctccttccacacttgtgtgc A/G gggacattcactactccta	3604
ABCA4	84	(intron 29 497)	gctgtcaataaggaccacaaa C/T agactaatttcaaatctctc	3605
ABCA4	85	(intron 29 567)	agctgtcagggaataaaaagg G/A agacaaaac g/a atccacaagc	3606
ABCA4	86	(intron 29 577)	aataaaaagg g/a agacaaaac G/A atccacaagctagagatggt	3607
ABCA4	87	(intron 30 -2494)	aatcacagctcatctgtgc A/G tcatagggatcccaaaagaa	3608
ABCA4	88	(intron 30 -2169)	aatgtaacagccaaagtctt A/G gaaaaaggcaagccagttcc	3609
ABCA4	89	(intron 31 535)	ctaactgtgaattatcatct T/G tgatcactgcccctttgagat	3610
ABCA4	90	(intron 35 209)	ctccccacatttatgtgg C/A aagtaagttacatttggtt	3611
ABCA4	91	(intron 37 525)	ttaatttgatgagtaattc A/G tccatctcggcctcagtttc	3612
ABCA4	92	(intron 37 766)	tgttgcaggctggagaaccc T/G cctatgaattgtacagggtc	3613
ABCA4	93	(intron 37 856)	aaaaccccatgaagtggta A/G ggcaggcatcattatctcca	3614
ABCA4	94	(intron 38 62)	tagtagagtatgtgtgttc G/A agcagagccaggggcaagca	3615
ABCA4	95	(intron 38 761)	tccttgggcaagttaattct G/A atgaagagactgggtgttct	3616
ABCA4	96	(intron 38 1315)	cagagtcagactctggaag G/T c/a ggggggataagaacacagc	3617
ABCA4	97	(intron 38 1316)	agagtcagactctggaag g/t C/A ggggggataagaacacagcc	3618
ABCA4	98	(intron 38 1561)	gtattttcatgtaaattatc C/A g/a atacacagctgctatggaa	3619
ABCA4	99	(intron 38 1562)	tattttcatgtaaattatc c/a G/A atacacagctgctatggaaa	3620
ABCA4	100	(intron 38 2874)	ctagacaaaagggg a/c agctcc C/T gccactagaaacttcagg	3621
ABCA4	101	(intron 40 1904)	gacactgtacagccagccca A/C tctgtaccccttttcttcat	3622

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCA4	102	(coding region 5814 (Leu 1938 Leu))	ggaataaaaactgacatctt A/G aggtcatatgaactaaccaa	3623
ABCA4	103	(intron 41 122)	atttgggtcccagttttatg T/G aggggtcatcatccctgtgtt	3624
ABCA4	104	(intron 41 411)	cctcttcccctcctgtctct C/A accctgtctcagttctcagtt	3625
ABCA4	105	(intron 41 443)	gttctcagtcgggtttcttc G/A tatcttgagatttatcc a/g g	3626
ABCA4	106	(coding region 5844 (Pro 1948 Pro))	c g/a tatcttgagatttatcc A/G ggcacctccagcccagcagt	3627
ABCA4	107	(intron 43 328)	ttttagcctattcctataa A/G aatgcaccattgcttc c/g cat	3628
ABCA4	108	(intron 43 345)	taa a/g aatgcaccattgcttc C/G cattacctccctccacacat	3629
ABCA4	109	(intron 43 370)	acctccctccacacattttt A/G caaaa c/t gtttcaggaggattt	3630
ABCA4	110	(intron 43 376)	ctccacacattttt a/g caaaa C/T gtttcaggaggatttactgag	3631
ABCA4	111	(intron 43 670)	ttaaacagactggtccctta T/C gggcaggacagagaggatga	3632
ABCA4	112	(intron 43 822)	gttaggtgctgctgacatct G/A tccagcatctgcttgactgg	3633
ABCA4	113	(intron 43 915)	ggcaggacagagtcctgagca C/T gcttcactggctcagacagg	3634
ABCA4	114	(intron 43 1242)	actgagctggagcctagaaa G/T aaactatagcttgaagacac	3635
ABCA4	115	(intron 43 1671)	tagagaaagtttacttccatc G/A ggacacatgcattcttttca	3636
ABCA4	116	(intron 43 2036)	ttgaaggatactcagtaatt G/A ctttttttcttgagcattttt	3637
ABCA4	117	(intron 45 176)	gtgtttggttcacacagctc C/T ggagaaaaaacaagtc c/t ggc	3638
ABCA4	118	(intron 45 193)	ctc c/t ggagaaaaaacaagtc C/T ggcacagccttgactggga	3639
ABCA4	119	(intron 47 238)	cccaagtctctggtggggc A/G tctgacagagatgcagtcag	3640
ABCA4	120	(intron 47 269)	atgcatgacagagcctggct G/A gatgagggagggtgcttacc	3641
ABCA4	121	(intron 47 326)	accacttatctcaacagatc C/G gggacctgtggcctatttac	3642
ABCA4	122	(intron 47 715)	aagtcactaagctggttgg G/A ggaggaacagcacataac c/t c	3643
ABCA4	123	(intron 47 734)	t g/a ggaggaacagcacataac C/T caccttatctatgctgaggt	3644
ABCA4	124	(intron 47 931)	ggacactgcatagatatac T/C agaaatagcagcatgtcagg	3645
ABCA4	125	(intron 47 1260)	acactctctggtggaccatc A/C ctcatccaagagagggtaac	3646
ABCA4	126	(intron 48 1663)	tctcgtctctctcttaccctc T/C aggtgttttgaattttgct	3647
ABCA4	127	(intron 49 127)	agagagccccaccacacca C/T ggtccctaccaagtcaccac	3648
ABCA4	128	(5' flanking region (-1441)~(-1400))	gtaaatctcagttgaatcag (TCA)14-16 atttttcagctgtggttct	3649
ABCA4	129	(intron 1 4712-4720)	gaggggccccgactatagcc (A)8-10 cagcctaattcaaggatgag	3650
ABCA4	130	(intron 1 7295-7304)	ttgttggcttttgcaa t/a gcat CACAGTCAT/Δ ttatttcaactatt	3651
ABCA4	131	(intron 2 951-952)	cctgtccatcagactctctt TT/Δ acctctccccgaggagccca	3652
ABCA4	132	(intron 3 2642-2653)	cctgggtgacagagcgagat (A)10-12 tagcatgagattattact	3653
ABCA4	133	(intron 4 5202)	cacaagacatctgacacccc C/Δ atccagccctggcttaacttt	3654
ABCA4	134	(intron 6 3029-3044)	cactaaaaacaaaaatttac (A)16-18 cctgaagaattgcaggca	3655
ABCA4	135	(intron 6 5138-5139)	ttcatgacagatcagatgtt (G) cttttatggtatttacaaga	3656
ABCA4	135	(intron 6 5138-5139)	ttcatgacagatcagatgtt cttttatggtatttacaaga	3657
ABCA4	136	(intron 6 5985)	tttctctcttcaaaccccc C/Δ agactaggagaaggtctgtc	3658
ABCA4	137	(intron 6 6094)	gggacggacagaaaaagacc T/Δ agttttctgttgagccaaaga	3659
ABCA4	138	(intron 6 -161)	tattttttcaattaaataaa A/Δ gagttttttgtttctaaag	3660
ABCA4	139	(intron 7 809-810)	gggccgagtagtcacactga (TG) tgtgggaagttagagaa g/c a	3661
ABCA4	139	(intron 7 809-810)	gggccgagtagtcacactga tgtgggaagttagagaa g/	3662
ABCA4	140	(intron 8 472-484)	atcttccccacctttcacta (T)10-13 ggtctctctatggggtaaagg	3663
ABCA4	141	(intron 9 48-71)	gtaccctggacccctccagaa (GT)11-13 gagagagatgtgcttctctg	3664
ABCA4	142	(intron 9 554)	ataggggacagaaaagacaca A/Δ ccaaaagtctctctcactt	3665
ABCA4	143	(intron 10 11)	catgatcagagtaagggggg G/Δ ttggaggatggggggggag	3666
ABCA4	144	(intron 11 4242)	ggagaggaatgatgttagt G/Δ cctcctgttaaataggcccag	3667
ABCA4	145	(intron 11 13743-13753)	tgctcttttgtgggtaatgg (T)9-11 cctcttcacaggagaagaaaa	3668
ABCA4	146	(intron 13 636-637)	cgggggtggaggggtgggagg (G) ctcatctgtcattatagatg	3669
ABCA4	146	(intron 13 636-637)	cgggggtggaggggtgggagg ctcatctgtcattatagatg	3670
ABCA4	147	(intron 18 569-570)	tgctgccctcatctctctc TT/Δ aaactagttctgtatttctc	3671
ABCA4	148	(intron 20 (-304)~(-297))	tataacctgactttttttt (A)7-9 ggattgcttttttaaacata	3672
ABCA4	149	(intron 22 1236-1246)	gctgaattagttccctggg (T)9-11 agttaactcctgatttttgc	3673
ABCA4	150	(intron 26 4626-4635)	gataatcaatgctgtgaagg (A)9-10 tggcattagagatccagacc	3674
ABCA4	151	(intron 33 115-116)	taaaacgctctgtttgttt GT/Δ ttacatgggtttttaggccc	3675
ABCA4	152	(intron 36 1078)	taagcagctatcacttaaca A/Δ taaaaaacagagattatca	3676
ABCA4	153	(intron 37 290-291)	ccttgaccaaagcctggggg (T) cagccattcccca a/g cccctc	3677
ABCA4	153	(intron 37 290-291)	ccttgaccaaagcctggggg cagccattcccca a/g cccctc	3678
ABCA4	154	(intron 38 896)	ataaaaagaggggaaaaaa A/Δ gaaggcagtcgctgcagggc	3679
ABCA4	155	(intron 38 1209-1210)	gtggacccctgagactgact CT/Δ ttccagatctttaggggtt	3680
ABCA4	156	(intron 38 1322)	agactctggaag g/t c/a ggggg G/Δ ataagaacacagccccag	3681
ABCA4	157	(intron 38 3107)	gggccccacctgctgaagag A/Δ ggggggggtggggtttgcccc	3682
ABCA4	158	(intron 40 152)	tttttccaataatacaagt A/Δ gaggatcgggttaaaatagg	3683
ABCA4	159	(intron 43 330)	tgtagcctattcctataa a/g a A/Δ tgcaccattgcttc c/g ca	3684
ABCA4	160	(intron 43 1354)	tttaattggcccagccatgc C/Δ ttgtgtgctttttgtcattg	3685
ABCA4	161	(intron 47 1305-1308)	catcctgctgaaggagaag AAAG/Δ caccatggcccaagcccta	3686
ABCA7	1	(5' flanking region -1596)	agaatgttggccccctcccc C/T t c/t ctgcattcctctgcagaag	3687
ABCA7	2	(5' flanking region -1594)	aatgttggccccctcccc c/t t C/T ctgcattcctctgcagaagcc	3688
ABCA7	3	(5' flanking region -1180)	ggccagtgagtgacgggcag G/A tcgcccaaatagcagcgtgc	3689

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCA7	4	(5' flanking region -460)	agagctggggctcgtgcctcc A/G gctgggcaactgcctgtctc	3690
ABCA7	5	(5' untranslated region -	ctctgtcccgctccctgccc A/G gtctcaccatggcctctg	3691
ABCA7	6	(intron 5 91)	ccccgggccaaggacctccc G/A ttcaggcatccaggctgtc	3692
ABCA7	7	(coding region 563 (Glu 188 Gly))	cagcttgttgaggccgctg A/G ggacctggcccaggaggtac	3693
ABCA7	8	(intron 8 103)	gcggagggtcacggaaact A/G tttgaagaagtaggagttag	3694
ABCA7	9	(intron 8 166)	tgcgaggatcagaggcaca C/T gcaggagcaaggcagagg	3695
ABCA7	10	(coding region 955 (Thr 319 Ala))	accggaccttcgaggagctc A/G cctctgctgaggatgtccgg	3696
ABCA7	11	(intron 9 421)	tttttttttttttttttttt T/A taagagatggagctcactc	3697
ABCA7	12	(intron 9 463)	gtgtccaggctggactgca G/A tgg c/t gagatcttggctcact	3698
ABCA7	13	(intron 9 467)	cccaggctggactgca g/a tgg C/T gagatcttggctcactgcaa	3699
ABCA7	14	(intron 9 488)	gagatcttggctcactgcaa C/T ctccgctcctggattcaag	3700
ABCA7	15	(coding region 1184 (His 395 Arg))	cgcacacgctgatgtggggc A/G cctggtgggacgctgggccc	3701
ABCA7	16	(intron 10 10)	gagtgacggaggtgagggcc T/C gtccacctgcggggtctgtt	3702
ABCA7	17	(coding region 1388 (Arg 463 His))	cctgggccccggccacgtgc G/A catcaaaatccgcatggaca	3703
ABCA7	18	(intron 12 115)	caggctgcgaactttgcacc T/G ttaccacctccacgtgacc	3704
ABCA7	19	(coding region 1824 (Ala 608 Ala))	cccttcctgctcagcgccgc A/G ctgctggttctgtgtgctcaa	3705
ABCA7	20	(intron 13 55)	ggtgcgctggagggtgacag A/G cagggcgggccccacgtggg	3706
ABCA7	21	(intron 13 78)	ggggcgggccccacgtgggtg C/A gcgccccaggccaatccag	3707
ABCA7	22	(coding region 1851 (Gly 617 Gly))	cgttgcctctcacagctggg A/G gacatcctcccctacagcca	3708
ABCA7	23	(coding region 2153 (Asn 718 Thr))	cgagggcgcgagtgccaca A/C cgtgggcacccggcctacgg	3709
ABCA7	24	(intron 15 34)	ggcggggctccgggcccgggt C/G gcacctgctttcgggaggcc	3710
ABCA7	25	(intron 16 8)	ctggaccacaagggtgagggc A/C ctacgaggcttaatagctgg	3711
ABCA7	26	(intron 16 161)	tcccgcagcttttataggcc C/T cggccacgacggtcccggt	3712
ABCA7	27	(coding region 2385 (Leu 795 Leu))	caccccatctctgcagtgct G/A gtagaaggagccacggccgg	3713
ABCA7	28	(coding region 2421 (Val 807 Val))	cccggcctgagtcctggcgt C/A tccgttcgcagcctggagaa	3714
ABCA7	29	(intron 20 166)	cgagacagtaagagttgggg A/G tagacagaggttcccctgga	3715
ABCA7	30	(coding region 3027 (Ala 1009 Ala))	ctgctgggagaccgtgtggc C/T gtggtggcaggtggccgctt	3716
ABCA7	31	(intron 22 1386)	gggtggggcggtgagccgggg C/T tccctgaagcacccctttgt	3717
ABCA7	32	(coding region 3417 (Leu 1139 Leu))	gggatctccgacaccagcct C/G gaggaggtgtgaggcctggg	3718
ABCA7	33	(intron 23 147)	ggagctctggtggtcagat G/A tcccttgggaaggcctgggg	3719
ABCA7	34	(coding region 3528 (Leu 1176 Leu))	gctggcctagacgtaacct A/G cggtcaagatgccgccaca	3720
ABCA7	35	(coding region 4046 (Arg 1349 Gln))	cccagcctgccagtgtagcc G/A gcccggtgcccgccgctgc	3721
ABCA7	36	(intron 30 81)	ccccctgggagctctcccg C/A cccccggccctcagctccc	3722
ABCA7	37	(intron 32 1)	caaggagcagctgtctgagg G/C tgcaactgtgagtcctccac	3723
ABCA7	38	(intron 33 54)	ccactgcttgcactgccct G/A tctggcccttgttaggcagg	3724
ABCA7	39	(intron 34 245)	cagtacttgggagggccgag G/A caggaggactgcttgtggcc	3725
ABCA7	40	(coding region 5057 (Gln 1686 Arg))	ggtgagccggatcttgaac A/G ggtcttcttattcttccccc	3726
ABCA7	41	(intron 38 65)	ggcccaactcaactttctgaa A/G gacctgcaactctccaggta	3727
ABCA7	42	(intron 40 154)	ctctacctccacacgcggga C/G caggccctgagacacccctg	3728
ABCA7	43	(intron 40 277)	ctgagcccccgccgccccca T/C cccagcgtggcccggaac	3729
ABCA7	44	(coding region 5592 (Ala 1864 Ala))	gtggcccggaaccagtgcc T/C gcgcacctcagcatgggata	3730
ABCA7	45	(intron 41 286)	ctccttgactctgccttctg T/C ggccctgcccacttgcctct	3731
ABCA7	46	(intron 41 389)	tggccgttcccagtttgcag C/T cgtttcaactgcctcttccat	3732
ABCA7	47	(intron 41 991)	cacactatggccctgccccca C/T ac c/t cat c/g cc a/g gctc	3733
ABCA7	48	(intron 41 994)	actatggccctgccccca c/t ac C/T cat c/g cc a/g gctccac	3734
ABCA7	49	(intron 41 998)	tggccctgccccca c/t ac c/t cat C/G cc a/g gctccacccac	3735
ABCA7	50	(intron 41 1001)	cctgccccca c/t ac c/t cat c/g cc A/G gctccacccacac	3736
ABCA7	51	(intron 41 1051)	actcatgtggctccaccaca C/T accatggccccgccccatac	3737
ABCA7	52	(intron 41 1131)	tgccttgcctcatgccatt A/G tgccttgcctccactcaa	3738
ABCA7	53	(coding region 5985 (Leu 1995 Leu))	gaagcgctctgtcgcgcct G/A gccatcatgtgtaatgggag	3739
ABCA7	54	(intron 44 201)	ggcgaggaccaggagcggt G/C agccggggctctggttgga	3740
ABCA7	55	(intron 44 233)	ctgggtgatttagaagaca C/T aatcaggtgtgcgttggagt	3741
ABCA7	56	(intron 44 313)	agttaggggaggcctggtt A/G gtggcggggcataggaaa	3742

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCA7	57	(coding region 6133 (Ala 2045 Ser))	tggcggccgagttccctggg G/T cggagctgcgcgaggcacat	3743
ABCA7	58	(coding region 6159 (Gly 2053 Gly))	ctgcgcgaggcacatggagg C/T cgctgcgcttccagctgcc	3744
ABCA7	59	(intron 45 27)	acggcgccggggtcggtcg G/C gggaggcaggctgggggcca	3745
ABCA7	60	(3' flanking region 108)	caagctgagtggtgcacatac G/A ggccaagtggcgattcatag	3746
ABCA7	61	(3' flanking region 376)	cttacaggagccgggtgtcc C/T ggagcacaggccaggggccg	3747
ABCA7	62	(3' flanking region 687)	cagcaggagagacttggggag G/A g/a gggagagagttcacactgc	3748
ABCA7	63	(3' flanking region 688)	agcaggagagacttggggag g/a G/A gggagagagttcacactgcg	3749
ABCA7	64	(3' flanking region 1169)	cctcgacctgaccttca C/T ggggctgcaggcggtgat	3750
ABCA7	65	(intron 9 398-422)	cgtgaactaccagctctgc (T) 22-26 aagagatggagttcactct	3751
ABCA7	66	(intron 12 175-184)	ggggactctgagggtctggt (G) 8-10 actctgagggtctggggcc	3752
ABCA7	67	(intron 30 81-87)	ccccctgggagctctcccg (C) 6-7 ggccctcagctcccttccc	3753
ABCA7	68	(intron 34 349-361)	agaaaagagaaagagaaaag (A) 12-14 cagaaatgtgctttgggtga	3754
ABCA8	1	(intron 1 204)	ctggttaattaatattagata A/G ataaaaacattgagttagaa	3755
ABCA8	2	(intron 1 266)	aacattatgtgttttaaac A/G taactgagtgtagaataag	3756
ABCA8	3	(intron 1 733)	ttgccatagtataataaag T/A attcatgtttttgctagcct	3757
ABCA8	4	(intron 1 861)	agactggagtttgcagtgta C/T ctaagactgtagctgattcc	3758
ABCA8	5	(intron 1 907)	gaggagatcatctctctggc C/T aatgtctattaacttcgcca	3759
ABCA8	6	(intron 1 1262)	cagaaacttttgcctctct G/A taggctagctcactgtgaaa	3760
ABCA8	7	(intron 1 1537)	agctctctttaaagatcca T/C gctgaattttctgcacctta	3761
ABCA8	8	(intron 1 7622)	tcgttaacagcaatgataat T/C tagcccatcttattcc c/t a	3762
ABCA8	9	(intron 1 7639)	t t/c tagcccatcttattcc C/T agaaacaacaggctcacaag	3763
ABCA8	10	(intron 1 7720)	tcctagtgtttacaaactgcc C/T tggagaacagaaaaagagaa	3764
ABCA8	11	(intron 1 9397)	cataatatatatacatatgc G/A cacacacacacatacacaca	3765
ABCA8	12	(intron 1 9519)	agtagtctcatgttggaacaa T/C atgcttgagaaatgcagaaa	3766
ABCA8	13	(intron 1 12973)	ttgataacaggcacaggcca T/C cacaataaatgatggaaca	3767
ABCA8	14	(intron 1 13100)	cattggagttattaggctacg T/C tttttgtgttttcaggat	3768
ABCA8	15	(intron 1 13128)	ttgtttgcaggatatttctt T/C ttcttaagaacttcatatta	3769
ABCA8	16	(intron 2 420)	caattagttttcttcaaaaa A/G gtagaaaagtgggaattgta	3770
ABCA8	17	(intron 2 505)	catataaaaaatcttgatta A/T actttggtatatttttaaaaa	3771
ABCA8	18	(intron 2 819)	gcaatgccttggaaactatct C/T ttaaacacattgactttca	3772
ABCA8	19	(intron 3 915)	ttgtgttcgtagatcagta G/A ggtgactagttaacaatgat	3773
ABCA8	20	(intron 3 1539)	aaagggaaatctgtgtgat C/T gccctgtcattcattcatag	3774
ABCA8	21	(intron 3 2341)	ttccttctcttgcacttc C/T gtccaaattccactcaagct	3775
ABCA8	22	(intron 3 2882)	tattctatattctgtactct A/G ttaattattctataataataa	3776
ABCA8	23	(intron 3 3314)	atttaaatatctatctctct A/G tatttaccatttcaaattta	3777
ABCA8	24	(intron 4 89)	gagggttagtatgccaaatta G/A agcatcactatctgtcataa	3778
ABCA8	25	(intron 4 3264)	ttccattggcctattatgcc C/T gtgttatatccagtggttaga	3779
ABCA8	26	(intron 4 3403)	aagagaccaaaaaattctt C/G atcagcagaaaagcacagga	3780
ABCA8	27	(intron 5 389)	gcttactgaatatataaatt G/C agaaaagccatgcacagcaa	3781
ABCA8	28	(intron 5 479)	tgagagtggtgagtaactca A/G aatgcctggactcc g/a aggtc	3782
ABCA8	29	(intron 5 494)	actca a/g aatgcctggactcc G/A aggtcccagcaggtaaatga	3783
ABCA8	30	(coding region 792 (Ala 264 Ala))	atgggtctctcgggattcagc G/A ttctggtgagtcaaacgcag	3784
ABCA8	31	(intron 6 200)	cctcccaagtagctgggact G/A caggtgccg a/g ccaccatgcc	3785
ABCA8	32	(intron 6 210)	agctgggact g/a caggtgccg A/G ccaccatgcctggataattt	3786
ABCA8	33	(intron 6 1751)	gtgagttattattgtgttg C/T ttgacagctgtttgttttt	3787
ABCA8	34	(intron 6 1808)	atttcattatagttttcaaa G/T aatattgttaaaccaaaagaa	3788
ABCA8	35	(intron 6 2412)	tattcctaattctaaagaat T/C ctgccccaaacttttacctt	3789
ABCA8	36	(intron 6 2506)	tggatgaataagtgaaatga G/A agttatcttaga a/g tccattt	3790
ABCA8	37	(intron 6 2519)	gaatgaa g/a agttatcttaga A/G tccatttcagggtcttcttt	3791
ABCA8	38	(intron 7 28)	agtgaattaaatcttttcc A/G tccacctatagcctaaaaat	3792
ABCA8	39	(coding region 991 (Gly 331 Ser))	taaagaaatctttctcacc G/A gccctggtgttctctctc	3793
ABCA8	40	(intron 8 74)	tggaatccataggctgtaat C/T atttacaactcagcattgt	3794
ABCA8	41	(intron 9 1417)	acacatacttaaatatattt T/C ctctgttctacttttgtttt	3795
ABCA8	42	(intron 9 2504)	agagggaaattatggtttgg G/A aatgaataaagcagaaata	3796
ABCA8	43	(intron 10 2013)	tggccaaagatctttccaac C/T tgtgccagtggttcacagga	3797
ABCA8	44	(intron 10 2378)	ctgaagaaaattgtcacttt G/A aagtatcttttctttttttc	3798
ABCA8	45	(intron 11 -697)	aaaaaaaaaaaaaagagag A/G gagaagaaaaatatttgtta	3799
ABCA8	46	(intron 11 -528)	tataaaagttagaaaaaat G/T a a/g tatgttttagaaaatagat	3800
ABCA8	47	(intron 11 -526)	taaaagttagaaaaaat g/t a A/G tatgttttagaaaatagatgt	3801
ABCA8	48	(intron 11 -342)	ctcaaaggagtttagccat G/A taataacttactattaatct	3802
ABCA8	49	(coding region 1632 (Asn 544 Asn))	ggttcagtcaccatctataa C/T aataagctttcagaaatggc	3803
ABCA8	50	(intron 14 252)	cttatttgcaaaaagtga G/A ttgagtttctaaagagatcaa	3804
ABCA8	51	(intron 15 130)	ttttgtttttgagacggagt A/C tcgatcatctcgggtcactg	3805
ABCA8	52	(intron 16 534)	acatatcattcattcaaat A/G cacattttatggtgacaaca	3806
ABCA8	53	(intron 16 588)	gaatcatcaggaaagtgtta C/T gcaattctgattagtactt	3807

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCA8	54	(intron 16 645)	atttaagaaaaattttaga C/T gtttttagtggaatgaagaa	3808
ABCA8	55	(intron 17 431)	tgtaggttttttcttttttt T/A ttctttatgttagaattgg	3809
ABCA8	56	(intron 17 1390)	gctgtaaaactcgtttttgtga C/A tttagtaccatgatttcta	3810
ABCA8	57	(intron 17 2452)	cacgtttatacctatagtaac G/A cggaaga g/c tctaatacatgag	3811
ABCA8	58	(intron 17 2460)	acotatagtaac g/a oggaaga G/C tctaatacatgagat g/c ctt	3812
ABCA8	59	(intron 17 2475)	gaaga g/c tctaatacatgagat G/C cttagcagagccaatctcta	3813
ABCA8	60	(intron 18 152)	gaagaagcacaggagagagg C/T agaactctgacatccaaagg	3814
ABCA8	61	(intron 19 7477)	aaaatctattttgaaagaca C/T ttggaaactaaaaaatcttt	3815
ABCA8	62	(intron 21 196)	ttgttttaagtaaaaaaaa T/C g/c acaaaaacatttttcaaag	3816
ABCA8	63	(intron 21 197)	tgtttaagtaaaaaaaa t/c G/C acaaaaacatttttcaaaga	3817
ABCA8	64	(intron 21 287)	actgtggtgggtggggggg G/T gggggagggtatgacattggg	3818
ABCA8	65	(intron 21 403)	cctgcacaatgtgcacatgt A/G ccctaaaacctaagataaa	3819
ABCA8	66	(intron 21 1207)	cccagcc g/a gagtgcagtggc A/G ggatcatagctcactgtaac	3820
ABCA8	67	(intron 24 692)	ctcctagatatagacaaaaa A/C caaggtgcacaatggccatg	3821
ABCA8	68	(intron 25 212)	cctgattataataggggaag G/A aagggttaaggggtagtgagg	3822
ABCA8	69	(intron 26 67)	aataatttttcagtctctgtac A/G cactgtgaacctcttttat	3823
ABCA8	70	(intron 27 515)	gtgtctcccaaacacatca G/T ttctatcttttgcatttaca	3824
ABCA8	71	(intron 27 661)	cctggatattatcagactta G/A aatggagagaaaagtccaat	3825
ABCA8	72	(intron 30 1967)	caaaaattagatacaagggg G/C tgaattgacttttaattgta	3826
ABCA8	73	(intron 31 112)	ctctaaatgctgacccagggt C/G acactgggtagatttacaac	3827
ABCA8	74	(intron 33 401)	cttctcactaggtgtgtgaga C/T gctgtgtttaaattttatgt	3828
ABCA8	75	(intron 35 484)	taacagcatcatcctg a/t tgt A/G tttattttcatagacagaaa	3829
ABCA8	76	(intron 36 258)	tttgcattgtatgttggtaaa A/G cctaagtcaaaactcagtta	3830
ABCA8	77	(intron 36 375)	atattttttactgtcttag C/G ctgtatattaaagaaactgac	3831
ABCA8	78	(3' flanking region 674)	gcggtggacatagaaagccc G/A gaagcttcttgatgtgctta	3832
ABCA8	79	(intron 1 56-57)	ttttgcttttgtgtgtgagt TT/Δ gtttcagagggttttgccttt	3833
ABCA8	80	(intron 1 1180-1191)	taaagtataataataaaacg (A)9-11 gaaattctctctgtacagag	3834
ABCA8	81	(intron 1 9877-9885)	ctcctgcaaataggtatgac (A)8-12 tcaactgagtacaaaagct	3835
ABCA8	82	(intron 1 12588)	gtactagagtgcactccttt T/Δ gcaacaggacggccaaagga	3836
ABCA8	83	(intron 6 78)	tcaatgcactcttttttttt T/Δ gaaatggagctctgctctgt	3837
ABCA8	84	(intron 9 265)	gtatatgggtatttttttttt T/Δ agacctcttagaaagctagt	3838
ABCA8	85	(intron 9 2666)	attttttttaaagggtatcca A/Δ tagtctattctcaatttcttc	3839
ABCA8	86	(intron 11 -447)	ggatattctgggttttttttt T/Δ ctacaaactcaagttttttg	3840
ABCA8	87	(intron 15 8407)	gtggaataatttttgactta T/Δ gcatttgggtcaataaaatt	3841
ABCA8	88	(intron 15 9458-9470)	tatgtcgagtaacatagtc (T)11-15 ctgaatgccagctgtcagtt	3842
ABCA8	89	(intron 16 54-56)	tgaataatagtcacatcat CAT/Δ aattattatcattacaacta	3843
ABCA8	90	(intron 17 433)	tcagggtttttcttttttt t/a t T/Δ ctttatgttagaaattggac	3844
ABCA8	91	(intron 24 1462)	actccatctcaaaaaaaa A/Δ gagagaaaaaaattctgcat	3845
ABCA8	92	(intron 33 155)	caatactttgcaaaaaaaa A/Δ gatctttccctgtagatatt	3846
ABCA8	93	(intron 34 184)	atactgaatgggttttttttt T/Δ ctcttttctcatatgacctc	3847
ABCA8	94	(3' flanking region 1240)	atccttggacccccaaaaaaa A/Δ ctttatctgtgctttgcgtg	3848
ABCB1	1	5' flanking - 196	gctttggagccatagtcctg T/C actcaaatttattttatct	3849
ABCB1	2	5' flanking - 16	tactctttacctgtgaagag T/C agaactgaagaaatctact	3850
ABCB1	3	intron 1 + 71660	cttgctggagggaaggggtgt A/C gaaatataccaatccaag	3851
ABCB1	4	intron 1 + 80091	gaaataattatcaggttctg A/C aataatcatgacacatag	3852
ABCB1	5	intron 1 + 103126	gatatgaatcagaattcatc T/C gtgtctcaagaaagggtcat	3853
ABCB1	6	intron 1 + 103148	tgcttcaagaaagggtcatg C/T gataaattaaagttctgtag	3854
ABCB1	7	intron 1 + 108428	aattaatattatcatcatctg A/G tcaccatttcacacaaactca	3855
ABCB1	8	intron 1 + 112042	cataagttgaatgtcccca A/G tgattcagctgtagcggtt	3856
ABCB1	9	intron 2 + 491	gctctctggcttcgacgggg G/Δ actagagggttagtctcacct	3857
ABCB1	10	intron 4 + 36	attaactattcaaaatactt C/T ggaaatttgacatctcttta	3858
ABCB1	11	intron 5 + 1596	ttagctctcttactgcttca T/C agtggagaatcaaaacttt	3859
ABCB1	12	intron 8 + 1789	aaacactctgaaatattaaac C/T gctcctggaaccacagctca	3860
ABCB1	13	intron 14 + 24	agttgtccttgccctttggc T/C ttctagagggtgcaaaaaata	3861
ABCB1	14	intron 14 + 81	tgcagggaagttaggaaacta C/T tataaatcggaagaaaggaa	3862
ABCB1	15	intron 15 + 38	caaaccaacctgattataaa A/G cataagaaccttctactact	3863
ABCB1	16	intron 17 + 73	gtttgggtgggctagggctac A/G gtaggagtggaacaagaga	3864
ABCB1	17	intron 18 + 564	caacagtaaaagttaaatct G/A aaaggaatgctctctgttta	3865
ABCB1	18	intron 18 + 2062	tttccctgagggaatggttat C/T ctctgtgttcccttgagtcca	3866
ABCB1	19	intron 18 + 2293	ccacatcaggtttttccccc A/G caccttgggacagtttgaag	3867
ABCB1	20	intron 20 + 557	aaaaccctaaccattgacac G/A tgtgaatgttttctctgggga	3868
ABCB1	21	intron 21 + 24	cgtgctctcttctactgggt G/A ttgtcttaattggccattt	3869
ABCB1	22	intron 21 + 2725	ctgacctgttttttggtgac A/G ggttttagttctctccctca	3870
ABCB1	23	intron 21 + 4725	tctttggtattaaaagatcca A/G agagataggaatatgtaat	3871
ABCB1	24	intron 22 + 8507	tgcacttaggaaaaaaacaa T/C atggaaatgtgtaaaatata	3872
ABCB1	25	intron 22 + 8537	tgtaaaatatacttttttt T/A aaaaaaaggacacattttat	3873
ABCB1	26	intron 22 + 8565	aggacacattttatcagcat T/C atgatcagactattacattt	3874
ABCB1	27	intron 22 + 8952	caccttgggtttctatggttg G/A caaagtactggcctgtacca	3875
ABCB1	28	intron 22 + 9520	caccaacaaatattttttt A/G cagttgggtgggcatctggt	3876
ABCB1	29	intron 22 + 9836	agactctgacttagacatga C/T ggcagggggaagagagactt	3877

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCB1	30	intron 24 + 377	taaaatcacagatgtgttga C/A taagttctgcaagcctttgg	3878
ABCB1	31	intron 24 + 1493	ggggagggtgtccaggcacga A/Δ catggagagctggacttgat	3879
ABCB1	32	intron 24 + 1495	ggagggtgtccaggcacgaac A/T tggagagctggacttgatac	3880
ABCB1	33	intron 25 + 342	tgcagccttgatcttctggg C/T tcaagcgatcctcctgcctc	3881
ABCB1	34	intron 26 + 134	cttgataaaagtctgagagc C/G taaatatggcttccaagtgg	3882
ABCB1	35	intron 26 + 1272	gtccttcaattttgtgtga A/G cttaaaaaacaggactctaaa	3883
ABCB1	36	intron 26 + 1394	tattaagtggtgtgtttaaag A/G ttgtgctataatgaattgta	3884
ABCB1	37	intron 26 + (1987-1988)	aagggtgtggaagagtgaag (AAAG) gaggctatttgctcccagac	3885
ABCB1	37	intron 26 + (1987-1988)	aagggtgtggaagagtgaag gaggctatttgctcccagac	3886
ABCB1	38	intron 27 + 59	gcagcctctctggcctatag G/T ttgatttataagggctggt	3887
ABCB1	39	intron 27 + 80	ttgatttataagggctggt T/C tcccagaagtgaagagaaat	3888
ABCB4	1	exon 3 + 3	aacaccccttatttatagat C/T caatgactgagctcaagaatt	3889
ABCB4	2	intron 3 + 45	cagcatctctacttatacca T/C gctctgctttaaggttctct	3890
ABCB4	3	intron 3 + 498	actcaaatagggtggttaggag C/T agagacaattcaatacagac	3891
ABCB4	4	intron 3 + 515	gagcagagacaattcaatac A/G gacagaagcttagatgaga	3892
ABCB4	5	intron 6 + 1030	tagttttgccatgtagaatt G/C aaaaagtgtagatggtgtt	3893
ABCB4	6	intron 6 + 1437	gttaagcctgtctcaatcaa G/A ttagtattatcttctgttcta	3894
ABCB4	7	intron 6 + 2449	ttgacttagcgacactgtta G/A catacttatcttctctgtgt	3895
ABCB4	8	intron 7 + 451	ccttgctgcacctgtgctgt A/C taagtttgctttattatagt	3896
ABCB4	9	intron 7 + 530	agtagagacaggtggtgat C/G acaccggacagagctaactg	3897
ABCB4	10	intron 7 - 152	aacagaatcatgaattaaag T/C tgttaagtattgaaggcct	3898
ABCB4	11	exon 8 + 40	aggataaattgtttatgtcg C/T ctgggtaccatcatggccat	3899
ABCB4	12	intron 8 + 130	ctggttgactccagatatca T/C agaaggagtgtgtaaaattct	3900
ABCB4	13	intron 8 + 248	aatacacaggaagcttctaa A/G taaagtaagggaagctactct	3901
ABCB4	14	intron 8 + 531	ctaaagagtgaattgattca A/G tacgtcccttggaactcacc	3902
ABCB4	15	intron 8 + 4240	ctgaggttccagcttatctc T/A tagagatgtttacttagtct	3903
ABCB4	16	intron 8 + 4343	tgttagaagaaaaaagggtt C/T atattacaagagggtctgac	3904
ABCB4	17	intron 8 + 4677	cccaagatatcttcataact G/C tccatagtgcctagggtgcc	3905
ABCB4	18	intron 9 + 113	tttaccagagattcactatt A/G ttatcatttttgcctccaaa	3906
ABCB4	19	intron 9 + 982	tgctctatacagtttttgtt T/A taagtttagtaaatgtatta	3907
ABCB4	20	intron 11 + 241	gcactttgggaggccaaggt A/G cataaatcacttgaggtcag	3908
ABCB4	21	intron 11 + 457	tccagcttgggtgacagagt A/G agacttcatctcaaaaaaaa	3909
ABCB4	22	intron 11 + 1337	tactcttggggagcctatca C/G cagggtgggtcagatatagc	3910
ABCB4	23	exon 12 + 3	tgttttttttctgtccagat A/T ctctcgccatttagtgacaa	3911
ABCB4	24	intron 12 + 1288	cagaccacactaacctcag T/C tggacctcaggatgtcagtg	3912
ABCB4	25	intron 13 + 206	tgtggataagaaaaatagcat G/A tggttagaccatttgtgaaa	3913
ABCB4	26	intron 13 + 988	cagtcggttttgggaagcttgc T/C accctttcttctacttctca	3914
ABCB4	27	intron 13 + (1413-1414)	tttatcttcaacttatgtttt (T) ctacagtttaagttatgtaat	3915
ABCB4	27	intron 13 + (1413-1414)	tttatcttcaacttatgtttt ctacagtttaagttatgtaat	3916
ABCB4	28	intron 13 + 1931	cttgcaaatgttgctcttcc A/G caaaaaaaaaggaaaggat	3917
ABCB4	29	intron 22 + 767	acagttgggtctgacataga A/Δ cctgtagcaatccaccagca	3918
ABCB4	30	intron 23 + 784	agtatctctcaactcttgc T/C atgcaggaaaaattatttta	3919
ABCB4	31	intron 25 + 158	gaaatattttactgtattaa T/C gtctagaacttaaatagaag	3920
ABCB4	32	intron 25 + 2920	ctgagttctctatatactct T/A ttccattctcctggatgctgt	3921
ABCB4	33	intron 29 + 411	cttctcttaccctgaattct A/C ggctctcgaactttgacttt	3922
ABCB4	34	3' flanking + 458	agaaaatgaaattgccttac T/C gagctaactctgaaagcaca	3923
ABCB7	1	intron 1 + 220	acggggcaggaggttctggg C/A agaggacacctggagcgctg	3924
ABCB7	2	intron 1 + 480	agtttaactcccttgcgtgaca G/A gcgtgctcttgcagtgcca	3925
ABCB7	3	intron 1 + (512-513)	gataggccaaaaccgttaact AT/Δ ctttccaaaacatagaccgc	3926
ABCB7	4	intron 1 + 1690	agtttcccaataaggcagat G/A aagtttaagataaaatttgta	3927
ABCB7	5	intron 1 + 5309	aattaatatcatttattgct G/A tattgttgcagtgttatct	3928
ABCB7	6	intron 1 - 11274	tgcttcttttcaagccagcc A/G gctttaaaaaaaagttagct	3929
ABCB7	7	intron 1 - 11085	cagggtttcagggtctcatgt A/G gacctgaagaaaaatgagag	3930
ABCB7	8	intron 1 - 10037	attctactttctcaacttct T/C ttattacattatctcatcat	3931
ABCB7	9	intron 1 - 21	ccactctgaacttccccct G/A cttttttctctgtgcagcag	3932
ABCB7	10	intron 3 + (135-136)	ttctctaatagaaaaaaa (A) catattaattgaccatagtt	3933
ABCB7	10	intron 3 + (135-136)	ttctctaatagaaaaaaa catattaattgaccatagtt	3934
ABCB7	11	intron 3 + 333	aaaacaatttgtgtgtgtgc G/A tgtgcttcaaggttaattgtt	3935
ABCB7	12	intron 12 + 524	taaccactctgccctcagta C/T gaaacacagtgccgaaccca	3936
ABCB7	13	intron 13 + 1543	atcctgtgaggtggggaagc G/A tatggctagcataaataataa	3937
ABCB7	14	intron 13 + 2400	tgttaccttactgcctcatt C/G tcattcttccccacctgctat	3938
ABCB7	15	intron 15 + 2201	ctccttctcaaccttagcaa G/C agtctggagatttactatc	3939
ABCB8	1	5' flanking - 2272	ggcttaggcctaagggtga T/C gttggggccagtaccctga	3940
ABCB8	2	5' flanking - 2070	agctatgaaaaacagacct G/A tccttctagaggtagcaaaa	3941
ABCB8	3	intron 1 + 25	aaacggaaaaacctactcag A/C gcggggccattgaccgccgg	3942
ABCB8	4	exon 2 + 308	tgctggtcctgggggtagcc G/A tcgtggtgaggttttcccca	3943
ABCB8	5	intron 2 + 334	ccccacttaaaacatttgt C/G ccctctgtctccccattcca	3944
ABCB8	6	intron 4 + 12	cctgctcgggtactgccagc C/T gcagggtgcagagttggggt	3945
ABCB8	7	intron 5 + 547	agttcatagcattctcgtc G/A gccctctcaggcctgctgct	3946
ABCB8	8	exon 7 + 57	ggcaatgtgcggactgtgag A/T gccttgcctatggagcaacg	3947

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCB8	9	intron 9 + 1231	tttccgcagctgcatggaca C/T cctcgcgtgccccgtttctg	3948
ABCB8	10	intron 9 + 2164	cctcttgagggtccttctag C/T gctgcctatgtggagattct	3949
ABCB8	11	intron 9 + 2645	ttcctgccttggtgctctccc C/Δ ggtcgtcttagcaagtgtct	3950
ABCB8	12	intron 9 + 2646	tcctgccttggtgctctccc G/A gctgccttagcaagtgtctg	3951
ABCB8	13	intron 9 + 3229	cagggccgagcaggaggtcc G/A tgggtcagctgggtccctt	3952
ABCB8	14	intron 12 + (113-114)	tcctccactgccacaagggg (GG) cctctttctctgggacaatc	3953
ABCB8	14	intron 12 + (113-114)	tcctccactgccacaagggg cctctttctctgggacaatc	3954
ABCB8	15	intron 13 + 128	tgctctcgggagaccctggc C/T gtcttcacatgtctctcagct	3955
ABCB8	16	intron 13 + 305	atccaggtctagagaagcct A/G tagtggaggtgctgagctgc	3956
ABCB8	17	intron 14 + 135	acagttgtgtcagggaagac C/G agaaccacagccaaagggga	3957
ABCB8	18	intron 14 + 159	accacagccaaaggggacag A/T gtcgttggtggggacaggg	3958
ABCB8	19	intron15+747	gttgagccttggtctgt A/G agggggacagaggaatcat	3959
ABCB8	20	3'flanking + 333	cctatcccttggtcaccccc G/A ggaccacagctccccatctt	3960
ABCB8	21	3'flanking + 1168	ccctctttcaggggtgtgat G/A cagtgcattgatggagcagc	3961
ABCB8	22	3'flanking + (1719-1721)	tagaccgcaggagcccgccc GTC/Δ ttcctaacctcgctcggcc	3962
ABCB9	1	intron 1 + 69	aggggtgccaggccaggcag G/C gttggggggcgtctgggcac	3963
ABCB9	2	intron 1 + 8873	tggggcccagcagctggggcc T/C ggaactacctcaaggcttc	3964
ABCB9	3	intron 1 + 8940	accagctcagcctgccacc G/A tgcacacggcaccagctgg	3965
ABCB9	4	intron 1 + 11410	agatccaagggatccagagg T/C tggaaatgtgacctcctgtgc	3966
ABCB9	5	intron 1 + 12863	gggaagccagatgcccaaa G/A gctctgtgacttcaacttcca	3967
ABCB9	6	intron 1 + 19731	gccaaagtgtcaagatcgagc G/A aggggagggcctgacaggg	3968
ABCB9	7	intron 1 + 29649	cagaatccagatgcccgtaa T/C gttgttaagaagcctgcaca	3969
ABCB9	8	intron 1 + 31793	ggccaggcggggagggtac C/T ggccagaccggtgggcaaaa	3970
ABCB9	9	intron 1 + 37537	agagtcaacaggggtgggtg C/A ccccggaaggtggcatcta	3971
ABCB9	10	intron 1 + 38293	taccagccctgtgctttcag G/A gacctgtgacctgtcaact	3972
ABCB9	11	intron 1 + 44661	cccaggtgcttggtttcac A/G gcaggattgccgtcctgcag	3973
ABCB9	12	intron 1 + 49576	aaagtggcccggtgcttgt C/T cctgaagccctaagcacc	3974
ABCB9	13	intron 1 + 64669	ccacagacaagccggtagc C/A cactctgcagctcaaacacac	3975
ABCB9	14	exon 2 + 448	cctggttttggccctgttc G/A tgtggacgtacatttctac	3976
ABCB9	15	intron 7 + 3364	ggtaccaggagtcgggtatc A/G gtgggacaggaacgcgtgtc	3977
ABCB9	16	intron 11 + 113	gggcccagagagctctccca G/T actatcagcctcctgggctg	3978
ABCB9	17	exon 12 + 370	cccaggtcctgcagcactgaa A/G gacgacctgccatgtcccat	3979
ABCB10	1	5'flanking - 424	tcgctgtctgcgcctccgcc C/T ggtctgcggcggtgagaaag	3980
ABCB10	2	exon 1 + 491	acaagggggcgttgcgcccc G/T cagcgcccgactcccggag	3981
ABCB10	3	intron 1 + 37	ccacttccctcccgccggcc T/G ctcccttctccacacgcgggg	3982
ABCB10	4	intron 1 + 217	actcgtttgcagattttaca C/T ttgttttcttggtagacac	3983
ABCB10	5	intron 1 + 405	gctgtttatcttttttttt T/Δ aacccaaacacattatttg	3984
ABCB10	6	exon 3 + 185	agggccggggcccgaggttc C/T gtaggcatcagtatgatgtg	3985
ABCB10	7	intron 6 + 1269	caaatccacaactgtgcctt C/G cacagaatgggttggaanaac	3986
ABCB10	8	intron 9 + 632	cccactccacttgggtgag G/A gcaggtggatgggtgatgggt	3987
ABCB10	9	intron 10 + 2373	tacctcagggcactcagaca G/C cctcaccatcagaggtcca	3988
ABCB10	10	intron 11 + 108	tccttttctgtttttttgt T/G ttttttttcttggagtgg	3989
ABCB10	11	intron 11 + 2379	cattgggttttagtgtatc T/A gtgtgtgtcatccatcatca	3990
ABCB11	1	5'flanking - (2596-2595)	tgtgttttagagctttctct (TT) gagacattttgtctaaggtt	3991
ABCB11	1	5'flanking - (2596-2595)	tgtgttttagagctttctct gagacattttgtctaaggtt	3992
ABCB11	2	5'flanking - 1746	agctgaagtgaattagcac G/A atcaactcagttactcacact	3993
ABCB11	3	5'flanking - (326-314)	agggggaaagttttaaggta (T)9-12 gctctgttatgttttaagt	3994
ABCB11	4	5'flanking - 135	agagggtttcccaagcacac T/C ctgtgtttgggttattgct	3995
ABCB11	5	intron 1 + 511	aaatatagatgcacacacac A/Δ tgagctgtggatgcattgtt	3996
ABCB11	6	intron 1 + 581	aatttcagtttttaggtcac C/T caagccagtgaggatcacat	3997
ABCB11	7	intron 1 + (1938-1951)	aaagacgtttttaaggcttt (A)10-13 gaaagaaaagaaactgtag	3998
ABCB11	8	intron 1 + 4517	ggtttcccaacatctcatct G/A ataaaaaaataatttgcca	3999
ABCB11	9	intron 1 + 5651	aaagagaataggtttagtga T/C tagtattcctgtgcttaag	4000
ABCB11	10	intron 1 + (12200-12201)	aagagatggtctctagcccc CT/Δ gtttgatttggggcacttac	4001
ABCB11	11	intron 1 + 13023	gtttggctactttgattaaa G/A aagaagaagagataataat	4002
ABCB11	12	intron 2 + 739	cctgcactctattctgacct C/T actggggaaaaacagtatgtg	4003
ABCB11	13	intron 2 + (921-922)	tattttgtagttcaaaaagt (CAGATCTTCTTACGCTAATTAGAAATGT) tgctgtccatttgatattca	4004
ABCB11	13	intron 2 + (921-922)	tattttgtagttcaaaaagt tgctgtccatttgatattca	4005
ABCB11	14	intron 3 + 644	agccacacgtttcttattgc G/A tgggaagtttaaaaaatggg	4006
ABCB11	15	intron 3 + 2231	agtgaacctgagattgagct A/G tactgaaatctctagaagag	4007
ABCB11	16	intron 3 + 2406	aaaggggtggtcttttaaatcc T/C tatgtttttctcatcaggtt	4008
ABCB11	17	exon 4 + 10	tttctcatcaggttacaaga T/C gagaagaaaggtgagtcgt	4009
ABCB11	18	intron 4 + 434	acaatttatagttatttctca A/G tgccccacacagtttatcta	4010
ABCB11	19	intron 4 + 518	gtagatgagtagctaaaaac G/T aaagtgcagctcctgaaataa	4011
ABCB11	20	exon 5 + 120	ggcacaatgacagatgtttt T/C attgactacagcttgagtt	4012
ABCB11	21	intron 5 + 320	gggaggtgacccatgaattt T/C acttgagtatcatctccaag	4013
ABCB11	22	intron 5 + 16076	agaagaggttaacagtaagcc T/G cctgatttacagcacatcc	4014

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCB11	23	intron 6 + 303	atttgcaggtgtgtttgttag G/C gggcagttgagtagcttgaa	4015
ABCB11	24	intron 7 + 1141	aaaggattcagcagggcatga A/G gaaagaaaagcttttgaaga	4016
ABCB11	25	intron 8 + 2463	ccattggcctaataagcaatga A/C ctatgacatggtcttaactta	4017
ABCB11	26	intron 8 + 2677	tcaatgatgtttacagtgaga A/C tctaataattgtattaaaccc	4018
ABCB11	27	intron 8 + 2699	ctaataattgtattaaaccca T/A gccacatgttaaatgaatct	4019
ABCB11	28	exon 9 + 24	gtgtcccaagtttacggacta T/C gagctgaagcctatgcca	4020
ABCB11	29	intron 9 + 108	caccttggtctgtggcctcc A/G gaggaagtacttgttcaaga	4021
ABCB11	30	intron 10 + 2475	taatcattccaaaccacgga C/A tttatttcaattaagaacatg	4022
ABCB11	31	intron 10 + 2478	tcattccaaaccacggactt T/A atttcatttaagaacatgata	4023
ABCB11	32	intron 10 + 2711	tttcagattggaaaagcca C/T tgaagtattgcaggtccaga	4024
ABCB11	33	intron 10 + 3539	agtgaactgttaattagatca C/G ttgtgcacagagaaaaatg	4025
ABCB11	34	intron 10 + 3623	tgcagaaggtgtgtcttttca T/C gaccttcctgagtttcagaa	4026
ABCB11	35	intron 10 + 3661	gaattcattataaaaaataa A/T cacataatggagcgtgacat	4027
ABCB11	36	intron 10 + 5100	gggccactcttctgtcttggc A/G atagactgtggccaatgaaa	4028
ABCB11	37	intron 10 + 5292	gctatttggtaggaacatct G/A ggcctgatcaggtagccttc	4029
ABCB11	38	intron 10 + 5912	gagtaaatatcagtaaaaaa A/Δ taaagtgggtatttttaata	4030
ABCB11	39	intron 12 + 116	tggttccagtaaatagggaa G/A gaggtgtctttctctgaaag	4031
ABCB11	40	intron 12 + 326	gataaatgacaaaggcaatta G/C aacaatcaggagacaggt	4032
ABCB11	41	intron 12 + 335	caaggcaattacaacaatca A/G gaagcacaggttcttcccaa	4033
ABCB11	42	intron 12 + 2572	cctcatccttgccaatgttt C/T cttttactggtttttgatgg	4034
ABCB11	43	exon 13 + 23	tctaataatgacctcaacatgg T/C cattaaaccaggggaaatga	4035
ABCB11	44	intron 13 + 70	atggcagtatattgatcaaa C/T agaaaggtgtagcatacatt	4036
ABCB11	45	intron 13 + (1578-1579)	ttattggcctctattttttc (C) tgcccatttggtcaagtatga	4037
ABCB11	45	intron 13 + (1578-1579)	ttattggcctctattttttc tgcccatttggtcaagtatga	4038
ABCB11	46	intron 14 + 32	catcacattcctgggagaaac C/T aagaggtcatagaaggaaaa	4039
ABCB11	47	intron 14 + 80	cacaattatacacatttctt C/T tctgtatgattcccaagtcac	4040
ABCB11	48	intron 14 + 439	tattgtgtcaaaaacaattc A/G ttgtatatctccattctaa	4041
ABCB11	49	intron 14 + (1262-1263)	cagcctttgcatatatttt (T) gctgtgtgtgttaacaggag	4042
ABCB11	49	intron 14 + (1262-1263)	cagcctttgcatatatttt gctgtgtgtgttaacaggag	4043
ABCB11	50	intron 14 + 1283	gctgtgtgtgttaacaggag A/C aaagacacaggtatttgctc	4044
ABCB11	51	intron 14 + 1339	tgagatagatatttaggacc G/A tgaccaatttttattttggt	4045
ABCB11	52	intron 14 + 1359	gtgaccaatttttatttttg T/C tgaataattcttatttgaagt	4046
ABCB11	53	intron 14 + 1480	tattgattagacaataaccc G/A tctggggaagggaattttct	4047
ABCB11	54	intron 15 + 370	ccttttctaaagtctgcaca G/A cctatttaagaatatttccca	4048
ABCB11	55	intron 16 + (550-559)	aaagtttagtgtttctatca (T) 9-12 gctacttctgaggtctct	4049
ABCB11	56	intron 17 + 188	tttctctcccaattctatgg T/G tttttggttagcttctctc	4050
ABCB11	57	intron 17 + 194	tccccaattcatgggttttt T/G gtttagcttctctctctctt	4051
ABCB11	58	intron 17 + (197-198)	caattcatgggttttttggt (T) agcttctctctctctctggg	4052
ABCB11	58	intron 17 + (197-198)	caattcatgggttttttggt agcttctctctctctctggg	4053
ABCB11	59	intron 17 + (289-296)	ggggactcttttaaaaaaa G/A(A) 4 tctgtgttagtgttctct	4054
ABCB11	60	intron 17 + 1070	tcagacttgggttttctctat C/T tttcttcttgagaaacaggt	4055
ABCB11	61	intron 17 + 1651	tgtaaaatatctctattgta T/C atgctgacggatttttcttg	4056
ABCB11	62	intron 17 + 2226	ccttaagtctctctctatca T/A gcaccttgttctcaccagct	4057
ABCB11	63	intron 17 + 2979	ctctctctctctctctcagc T/Δ ctactatttcaactgttggt	4058
ABCB11	64	intron 17 + 3288	aatccccatatctctaccta T/G ccactctcctcctgaatctt	4059
ABCB11	65	intron 17 + 3289	atccccatatctcacttag C/T catctctcctcctgaatctt	4060
ABCB11	66	intron 18 + 97	aatatgagttttctaggtat A/G tatctagcagtggttcaagt	4061
ABCB11	67	intron 18 + 98	atatgagttttctaggtata T/C atctagcagtggttcaagtc	4062
ABCB11	68	intron 18 + 892	ctctgaaagttagtgataca C/T cttatttgtgtttgaatcaa	4063
ABCB11	69	intron 18 + 2681	atgtatgagatcaagtcagg A/G tcaaatattagacaccata	4064
ABCB11	70	intron 18 + 3780	ggaccatcctgtggggcaat C/G gttccagaaaatgctggtat	4065
ABCB11	71	intron 18 + 5741	ctcaccgggtataatacaac C/T gtacgaaagggttttctttt	4066
ABCB11	72	intron 18 + (5882-5883)	tgcgtattccctcagttcag (C) tttttattcaagccacagca	4067
ABCB11	72	intron 18 + (5882-5883)	tgcgtattccctcagttcag tttttattcaagccacagca	4068
ABCB11	73	intron 19 + 10022	tggctaagttaaaaaaaa A/Δ gagattcaactataatttgct	4069
ABCB11	74	intron 21 + 322	caagattcaatactgcccc C/Δ agggggtgggtgaacagggc	4070
ABCB11	75	intron 22 + 257	ctgttcaatttctctctcga T/C agtgattcattccacattcc	4071
ABCB11	76	intron 22 + 552	taattaatatcttctcttg G/C ggggtaaatgaggatggta	4072
ABCB11	77	intron 22 + 569	ttggggggttaaatgaggat G/A gtacataaacacttctcaa	4073
ABCB11	78	3' flanking + 243	aaacaccacagaatgacata G/A aactaaaggcggcagggaatc	4074
ABCC1	1	5' flanking - 1661	cattcacccttgggggaccc A/G ggccaataaaaaaatcacag	4075
ABCC1	2	intron 2 + 635	gatgtgcccctacctgacct T/C ggctcggggcagacttgggg	4076
ABCC1	3	intron 2 + 4769	gggcaggagtgagctcagg G/Δ ttcttggtcccaatgggttc	4077
ABCC1	4	intron 2 + 10069	tatggaggtttttctcttct T/C tctgtgagttttctctctga	4078
ABCC1	5	intron 2 + (11965-11984)	taaaagccaatacaataaac (T) 18-20 aaacaagccacgcatgtgc	4079
ABCC1	6	intron 4 + 4302	cacctgtaatccagcacct T/G gggaggccaaggcgaagtga	4080
ABCC1	7	intron 4 + 4394	gtctttactaaaaatacaaa A/C attagctaggcatggtggcg	4081
ABCC1	8	intron 4 + 4524	ccactgcctccagcctggg T/C gacaagagtgaacactctgtc	4082
ABCC1	9	intron 6 + 9045	aggtccttaaaactaccctgc G/A ctccaagaatcagtgcttg	4083
ABCC1	10	intron 7 + (3059-3071)	agtcctttgtatgcaccact (A) 11-13 gccatttttctgcatgacc	4084

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCC1	11	intron 8 + (886-889)	ttctatgtaacagtaagaaa GAAA/ Δ agcagctgccaatataacaa	4085
ABCC1	12	intron 11 + 198	tgaattgtcaggttgatgtt C/A tccttggtggcagtgccgttt	4086
ABCC1	13	intron 11 + 784	tgtggattgatccaggagat C/G aagcaatgttgcagtactc	4087
ABCC1	14	intron 12 + 122	agccttgctgccagttgga C/G tcaacttggggagccttaaca	4088
ABCC1	15	intron 12 + (3138-3148)	accccatctctattgaaaag (A)10-12 tcaatataaaaaacatttac	4089
ABCC1	16	intron 12 + 3227	tggatgatgttgatgatggg C/T tgatcccagggtgcgccag	4090
ABCC1	17	intron 13 + 2060	tgtcattacaactattctct T/C cttggtcaggttgggcaatt	4091
ABCC1	18	intron 13 + (2061-2062)	ctcattacaactattctctc (C) ttggtcaggttgggcaatta	4092
ABCC1	18	intron 13 + (2061-2062)	ctcattacaactattctctc ttggtcaggttgggcaatta	4093
ABCC1	19	intron 13 + 11776	gccacctggggaggggcccaa G/A cgcgtctccagggtcgtga	4094
ABCC1	20	intron 14 + 179	aaagaagaacacacatttg A/T cttcttgacagagaactgc	4095
ABCC1	21	intron 16 + 219	ctagcacagaggggtccctg G/T gattgtaagttacagcagcc	4096
ABCC1	22	intron 16 + 310	ggaagtcttactttcaggtg C/T ggtgtgatccagggtactctg	4097
ABCC1	23	intron 16 + 890	ctctccagagaaaacaatct G/T tagaaggcctgcattgaaaa	4098
ABCC1	24	intron 17 + 1171	aaacccagggtcacaagaagc G/A tgggaaataatgcatactcc	4099
ABCC1	25	intron 17 + 1332	caactctttagtgtctgtgc A/G actgcacatttgtctcttgg	4100
ABCC1	26	exon 18 + 53	gattcagaatgattctctcc G/A agaaaacatccttttggat	4101
ABCC1	27	intron 19 + (3373-3379)	ccaagctaggcagttctaca CA/ Δ tgtgcaactcagtgccggg	4102
ABCC1	28	intron 20 + 2730	gcgtgaggtctgtctctcta C/T ccttcggtccaggtgagcaa	4103
ABCC1	29	intron 20 + 2789	cttggcccccagataggttcc G/C caccceccgttttcttccc	4104
ABCC1	30	intron 20 + 2919	gatgcaaatgcgcccaccca C/T cctggcacctcgtgcgttca	4105
ABCC1	31	intron 20 + 3024	cttacaataaactggggcac C/T cccctctctcaccaccacc	4106
ABCC1	32	intron 20 + 9718	gtggctgcgctcagtgacga A/C caggagaagtgaaggctgag	4107
ABCC1	33	intron 20 + 9733	gacgaacaggagaagtgaag G/C ctgaggcttataggaggtg	4108
ABCC1	34	intron 20 + (9895-9896)	gctgggtcccaagtgacacac AT/ Δ gtgtgtgaggacagctgca	4109
ABCC1	35	intron 20 + 9952	ggtatcattcttctctctct G/A gtgatgtggctatttgtgtt	4110
ABCC1	36	intron 20 + 11120	gcggagtggtgggagtgatc A/G tcatcatcactgagttattg	4111
ABCC1	37	intron 20 + 11147	tcaactgagttattgtgaacc G/A ggaagagatgatgtctgtg	4112
ABCC1	38	intron 20 + (11629-11631)	tattttgaatatcacttctt CTT/ Δ tcaatgcttgggaatcacgg	4113
ABCC1	39	intron 20 + 11864	gagctccagataaccactgc C/T ccacaaccagacagcctgtt	4114
ABCC1	40	intron 21 + 3860	tggagagtgacatggtgggg G/A tgtggtgcatatattcatat	4115
ABCC1	41	intron 22 + 878	ttaaagatcgtctatttttg G/A caagtgttaataattctcca	4116
ABCC1	42	intron 22 + (4445-4446)	gtggggctggggctggggct (GGGGCT) ggggtcgtgcatgtgctaag	4117
ABCC1	42	intron 22 + (4445-4446)	gtggggctggggctggggct ggggtcgtgcatgtgctaag	4118
ABCC1	43	intron 23 + 62	gttgtggtttgttctaatta T/C agaaatggatccttagatc	4119
ABCC1	44	intron 24 + 3171	aaccatgaggctcaccatat C/T tcaaacacagctgcacagct	4120
ABCC1	45	intron 24 + (3349-3368)	ctcttgaattggtgccagc (T)19-22 ccttgcatttaccaaatag	4121
ABCC1	46	intron 24 + 3369	tttttttttttttttttttt T/C ccttgcatttaccaaatag	4122
ABCC1	47	intron 24 + 3584	ccaaggattttttattttca A/G caacaaaggaaatgatttta	4123
ABCC1	48	exon 25 + 60	gagtggtgcagccgctcccc G/A gtctattcccatttcaacga	4124
ABCC1	49	intron 27 + 4539	tcttttttactcactgcagt G/A tgaggacaacatcacattta	4125
ABCC1	50	intron 30 + (1708-1714)	gaccaaacactatctcctgg (T)6-7 cttccggtcaagtgctgggc	4126
ABCC1	51	exon 32 + 652	tggagaaaaatcattttctcc C/T cttggcagtgctccaggcc	4127
ABCC1	52	3' flanking + 158	ctgatgtctctccaggacac G/A aaaagaaccatctttgaat	4128
ABCC1	53	3' flanking + (187-199)	ccatctttgaatatcaatga (T)11-13 aagtactgttccggggagaa	4129
ABCC1	54	3' flanking + 2227	cattagaataggtagtatca G/A ccagccgggcatggtggctc	4130
ABCC2	1	exon1+77	catattaatagaagagtctt C/T gttccagacgcagctccagga	4131
ABCC2	2	intron1+413	gataagttctagaactggca A/C ctaatgatattggactagaag	4132
ABCC2	3	intron2+192	atcaaatggcctttgatttt T/G gcataagaatgggtactctt	4133
ABCC2	4	intron2+1020	agtgtgcgattacaagcct G/C agccacctgcacagcctctg	4134
ABCC2	5	intron2+3639	gtcatatccccaccccaaat C/A gacccaataggtacaaatga	4135
ABCC2	6	intron2+3930	aaaactggcaggagaatttc A/G ctggagctgcattgcaggact	4136
ABCC2	7	intron2+3989	agttatgaaccgatttttc C/T gggactgggtgttctagtct	4137
ABCC2	8	intron2+4078	aggtttccagatgtgttccc T/C aggcattcctggtgttagga	4138
ABCC2	9	intron2+4171	cttatctcttgggtcagttgg C/T tttctaccacctcttagctt	4139
ABCC2	10	intron2+4257	gggtattggaagtctctgc G/A gctgctggaggctgctgtgt	4140
ABCC2	11	intron2+4436	ggactagtggagaattaga C/G ctttcttgataaataatagac	4141
ABCC2	12	intron2+5227	taccataatttatgtgtct A/G tatgacatgaatttcatttgg	4142
ABCC2	13	intron2+5373	gttaaggatattgtgaactca A/G gtgtgtctataggataaatt	4143
ABCC2	14	intron2+5538	ttaatgaggttaagcacatg G/T tcatatgtttaaaagccttt	4144
ABCC2	15	intron3+772	ggtataaggcaagatttttt A/T aaaaatttaattgtcttaac	4145
ABCC2	16	intron3+1145	acatccttctccctcagtc C/T tcggttagtgccagttattct	4146
ABCC2	17	intron7+1658	ggactcttaccagcttagtt G/T cctggttttctaatctaaaa	4147
ABCC2	18	exon10+40	tggccagggaaggatcaccc G/A ttggagaaacagtgaaacctg	4148
ABCC2	19	intron11+1672	aaactttttaagtcttaagac T/A ggaaggcctgtgtccttaggc	4149
ABCC2	20	intron12+148	ccctctcaccgcccattgcc A/G ctttctctcctttgtaccat	4150
ABCC2	21	intron13+180	catgagttttctgagcccca G/C tttatctaaactataaatga	4151
ABCC2	22	intron13+1497	gtgcagggtcccccgtatgc T/C atagccagttcctctttaga	4152
ABCC2	23	intron15+169	atgagctgaaagcaaggtt T/C tcagccctctccctgtataa	4153
ABCC2	24	intron15+949	ttccagggtgacacatttagt A/G cctaatttgggaaatgttaa	4154

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCC4	101	intron 19 + 7445	ttttggcataatttttaac T/C actagaatgttctgattcat	4295
ABCC4	102	intron 19 + 9018	tacgtgatggcctgaagaga A/G aaaccgtacattggttcttt	4296
ABCC4	103	intron 19 + 11388	aagagttcagagattttggg A/G gttggaggaaaaaatagcat	4297
ABCC4	104	intron 19 + 11646	cattatttttaatttttttt T/Δ cctcctgttgggtgcagaat	4298
ABCC4	105	intron 19 + 13517	gagaaacttacattattttt A/T aaaaatgctataactagtcc	4299
ABCC4	106	intron 19 + 21033	tgggagtgccctgggctagc G/A ctgaaacttcagggttttcag	4300
ABCC4	107	intron 19 + 21095	agacttttggaagaagcaga A/T ctgaaggtaagactgagtaa	4301
ABCC4	108	intron 19 + 21634	gtgctatttctgagcactca C/T ggccccattgggcatgggct	4302
ABCC4	109	intron 19 + 21715	tgttttgctcaccctcaca C/T agcttgccctcactgctctc	4303
ABCC4	110	intron 19 + 23090	agcaacagacttgagactt G/A agcttctaaaagtctcata	4304
ABCC4	111	intron 19 + 24297	cgaatgtgatgaatgtggga A/G cctttttgagatagcagcac	4305
ABCC4	112	intron 19 + 25947	gagttctaaattaatatgag C/A aaaactagaaccattttaa	4306
ABCC4	113	intron 19 + 30193	acagatttgcaagagctctac A/C aaagtataatattctgtca	4307
ABCC4	114	intron 19 + 36938	aagccgagtgcaatctcttgg C/G tatcttctgtggactacttt	4308
ABCC4	115	intron 19 + 37322	gttccctagagggtgagccc C/T gcttcaccctggttaacccgc	4309
ABCC4	116	intron 19 + (38361-38362)	cgggggttagcttccctagct (T) gcggagggtttctgagaaaa	4310
ABCC4	116	intron 19 + (38361-38362)	cgggggttagcttccctagct gcggagggtttctgagaaaa	4311
ABCC4	117	intron 19 + 38746	taaaagacatgctggtaatta T/C gtaaaaataagataagtaaa	4312
ABCC4	118	intron 19 + 42343	tgtaagggcagaatcagcag C/T aacgattggatgttcccgga	4313
ABCC4	119	intron 19 + 44733	agcaggctgggggaaaaaaa A/Δ tacagagggttatcattatgt	4314
ABCC4	120	intron 20 + (405-419)	aaggggcaaaacttaggcac (T)13-15 gtagaaccagggttggtt	4315
ABCC4	121	intron 20 + (637-648)	ctaagctcttaagctgtcttt (A)12-13 ccaacaatcctacagaaata	4316
ABCC4	122	intron 20 + 842	caagctggggcacttttttt T/Δ tcccaagtgtttatttttgga	4317
ABCC4	123	intron 20 + 843	aagctggggcacttttttt T/C cccaagtgtttatttttgga	4318
ABCC4	124	intron 20 + 1347	ggacctctgatttttttttt T/Δ cttttgcaaacattttttaa	4319
ABCC4	125	intron 20 + (14553-14567)	tccctacacacccctcatct (A)13-15 tcagcagcttgactgagctt	4320
ABCC4	126	intron 20 + 15487	ggttttttccagtgtagtag C/T acatgtagaagcagtagctg	4321
ABCC4	127	intron 20 + 16161	gcgttgagtcagtaagccga T/C agtgccgcttgtagcagcga	4322
ABCC4	128	intron 20 + 30891	acgtcccccactgttctatc C/T ttctcaagaagcaagcgttg	4323
ABCC4	129	intron 20 + 31180	ccttgcaagtgctcctacat G/A tcatttgctattgttatcat	4324
ABCC4	130	intron 20 + 31283	gtgttaagctaaaaaaa A/Δ cctgttagacatttttgact	4325
ABCC4	131	intron 21 + 4204	ttgacccctgccctgaaaccc A/T gttggagataaaacagtggc	4326
ABCC4	132	intron 22 + 1026	gtgcccactactccagtaaaa A/C tcttctgtagctcaactgag	4327
ABCC4	133	intron 23 + 377	gcctgggtcatgaggttgag A/G aaaattctcagcaggagagt	4328
ABCC4	134	intron 25 + 4122	cccttttgattaaaattgca C/G/T tgggacaagaaccaccccca	4329
ABCC4	135	intron 25 + 6418	ttgcaactgaggaatggctg C/A agaaattaaagtgggttat	4330
ABCC4	136	intron 25 + (8765-8775)	tgcactctgtgatttttttc (T)5-11 aatcctgccgctggatctc	4331
ABCC4	137	intron 26 + 67	tattgttaattgctttttact G/C ttattgttttttttaattgg	4332
ABCC4	138	intron 26 + (101-109)	taattggatgaaggatgtgt (T)8-9 caccacatagacatgtttt	4333
ABCC4	139	intron 28 + 391	tagatatgatcttttttttt T/Δ aaatctctattgtgaagtag	4334
ABCC4	140	intron 29 + 2569	atctcttttttttctaatac G/C accactatctccacattaaa	4335
ABCC4	141	intron 29 + 7820	gaaaaacaacccgtgtctctg C/T ttggagggttcagcatattct	4336
ABCC4	142	intron 30 + 6269	tagatgtttctttgggcattg A/G aaagtgtgttatctgttt	4337
ABCC4	143	intron 30 + 6320	gtttaataagggttaattag C/T tctactttgttaattacatt	4338
ABCC4	144	intron 30 + 6474	ctttgatgctatgtgttttca A/G tccacagatgttcataactt	4339
ABCC4	145	intron 30 + 6519	ttccactatgaattataatt C/T ctgccattttaacacacctt	4340
ABCC4	146	intron 30 + 6574	aatgggttttggctcctaaac C/T acactgggttcaaaactagac	4341
ABCC4	147	intron 30 + 6680	aggtgtgtctcctgttatatg A/G cgtgggttaggttttactctg	4342
ABCC4	148	intron 30 - 704	acgtttatcagaaaacctgt A/C tctcttctagtctcagtaga	4343
ABCC4	149	intron 30 - 228	atctatgaatcagagtgtac A/G gaactaaaatggatctacag	4344
ABCC4	150	intron 30 - (14-5)	acattctttttatgcttaac (T)9-10 ctaggataacttcaaaagaa	4345
ABCC4	151	exon 31 + 146	agtccgttccgaaggcattt G/T ccactagtttttggacatg	4346
ABCC4	152	3'flanking + 173	atttttaaggagtaggaca A/G agttgtccacagggtttttgtt	4347
ABCC4	153	3'flanking + (430-440)	tgtacccttactccctatc (A)10-11 tggatacatgggttaaggat	4348
ABCC4	154	3'flanking + 556	aaaggtgctttgatactgaa G/A gacacaaatgtgaccgtcca	4349
ABCC4	155	3'flanking + 1144	cctccctgaaattgcataata T/C gtatatagacatgcacacgt	4350
ABCC4	156	3'flanking + 1426	tttaggtgactgaaattgca A/T cagtgtatcataatgaggttt	4351
ABCC5	1	intron 1 + 628	ttctgccacagagcccg G/C gtggctttgtgtttatcaca	4352
ABCC5	2	intron 1 + 1834	tgagttccagtgacctctc C/T gtttcaactgctcacgcc	4353
ABCC5	3	intron 1 + 3055	agaaagctctttaaaaaaaa A/Δ ccaacctttctattgtatc	4354
ABCC5	4	intron 2 - 20280	gaatgcacgctactaagta T/C ttttgaagttcagacacca	4355
ABCC5	5	intron 2 - 20260	tttttgaagttcagacacc A/T tctagaatctgctgacctg	4356
ABCC5	6	intron 2 - 19204	tgaataaagcattgcgaca C/T ctaccacctttcttcgggac	4357
ABCC5	7	intron 2 - 19043	ttggctggcattaggctggc G/A ttacttcagctaactgaag	4358
ABCC5	8	intron 2 - 18824	ttgaacactcttcaagatgc A/G tgcacagcactgaaccgagt	4359
ABCC5	9	intron 2 - 18807	tgcacgtcacagcactgaacc G/A agtggctggtgcagataaa	4360
ABCC5	10	intron 2 - (18735-18734)	atagaagcttaaaactcaca (A) cagctactctacatagatga	4361
ABCC5	10	intron 2 - (18735-18734)	atagaagcttaaaactcaca cagctactctacatagatga	4362
ABCC5	11	intron 2 - 15903	taccaaagcctgctcatgga G/A gtgaaagcaagactgacat	4363
ABCC5	12	intron 2 - 15901	ccaaagcctgctcatggag C/T agaaagcaagactgacatgt	4364

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCC5	13	intron 2 - 15847	tggatggaacctcaaaggcc G/A tcttgcccagtcgccattta	4365
ABCC5	14	intron 2 - 15605	aggagacgcacgacactga C/T agctgtacctgacctgagg	4366
ABCC5	15	intron 2 - 13571	ccgattgtgccccagatacc G/A ctttatttgaggggtgtgcc	4367
ABCC5	16	intron 2 - 13402	taccctgtctgtttcccgcc G/T ccaggaagggattggattgt	4368
ABCC5	17	intron 2 - 13325	cccagaggcctccgtgcagg G/C gaaaagcccttggtgccct	4369
ABCC5	18	intron 2 - 7293	tttgtaggataaaaatgca C/T ttagtgccctgttctaacc	4370
ABCC5	19	intron 5 + 374	ccgggctggtgagccagcac C/T ggggaacataccaagtgcctg	4371
ABCC5	20	intron 5 + (2212-2213)	cgccctctgcagtgctctct CT/Δ tgggtaagtctaactctgct	4372
ABCC5	21	intron 5 + 3283	accagagagagtgctgggtt C/T tgggaattcagcgtagctacc	4373
ABCC5	22	intron 5 + 3469	ttggctttcttttgggtgg C/T tttttgtttttttttgtca	4374
ABCC5	23	intron 7 + 443	cacttttattaaagacagta C/T gattacataacatttggccc	4375
ABCC5	24	intron 7 + 458	cagtcgattacataacatt T/G ggcccatcctagcaagcagg	4376
ABCC5	25	intron 9 + 176	caaaacaaaacaaaacaa A/G acaaaaaaaataccacat	4377
ABCC5	26	intron 9 + 214	catatggagatgatgctgtg G/T tctctctctactggacctg	4378
ABCC5	27	intron 10 + 703	tgtgggctggaattccctga T/C gttgccactgcatagattag	4379
ABCC5	28	intron 10 + 3580	catggggctggagctgtgaa A/G accagtaggtactggcatgt	4380
ABCC5	29	intron 10 + 3655	atcctttgaataactcttta G/A gggagagaaatgatggaaat	4381
ABCC5	30	intron 10 + 3854	gaagtttagaatcatgacac T/C tcggggaagatagattcagg	4382
ABCC5	31	intron 10 + 5040	ctttgaagacatgagagttt C/T ttggcaagaagatgttctct	4383
ABCC5	32	intron 10 + 5316	cagtttaaatgtcattaggtc C/T gcttttagctggctgagggg	4384
ABCC5	33	intron 12 + 234	tgactgttgtcccagctgga G/A ccatttggctcatgccttc	4385
ABCC5	34	intron 12 + 300	tgccacaggtatgcccggtg A/G ttgaaatgtcagagataag	4386
ABCC5	35	intron 12 + 318	gtattgaaaaatgtcagagat A/G agagatgacgacaccccta	4387
ABCC5	36	intron 12 + 1545	gtagcatccctaaaccaaga C/T aaatgtctactatcagtcctc	4388
ABCC5	37	intron 13 + 20	ggcaaggaaatgtttggcttc T/C gtcatgtcttccatcttggc	4389
ABCC5	38	intron 14 + 278	ttctatccagatatttttaa A/G actacaagtaagcgtgtgca	4390
ABCC5	39	intron 16 + 1663	tgactggagacttttttttt T/Δ aaatattattagatcaattc	4391
ABCC5	40	intron 16 + 1664	gactggagactttttttttt A/T aatattattagatcaattca	4392
ABCC5	41	intron 17 + 20	ggtaatggccttttttgaaa T/G ttttagatttgtcatcaaa	4393
ABCC5	42	intron 18 + 232	ggacacctgcaggctatctg C/T tctcatcctgtgtgtattag	4394
ABCC5	43	intron 19 + 249	ggaccagtaggaacagagcc G/A tccctgggcccgtgaccactc	4395
ABCC5	44	intron 20 + 846	ttaacccagaagaaaaaggc G/A gtggggtggggagacagcca	4396
ABCC5	45	intron 20 + 1154	tcttgagacgaaaaaaaaa A/Δ tcagagcatccagggtttcta	4397
ABCC5	46	intron 22 + (1424-1425)	gaggaaatgcagcggaatat (AT) caactctgggttttaacaggg	4398
ABCC5	46	intron 22 + (1424-1425)	gaggaaatgcagcggaatat caactctgggttttaacaggg	4399
ABCC5	47	intron 24 + 132	atcccacagaatctccagca A/G tctctcaacccgtgtgtgaa	4400
ABCC5	48	intron 24 - 874	gtgctggagaggttaggatt A/G cggtcagtggtgtgacaaag	4401
ABCC5	49	intron 24 - 630	tgatgataaaaattaccocaa G/A cagttatatcacagcatttt	4402
ABCC5	50	intron 24 - 102	acaggggtggcagctacctct G/C tgtggctactatggtgtgcc	4403
ABCC5	51	exon 25 + 120	taccgagaaaaacotccctct C/T gtccctaaagaagtatcctt	4404
ABCC5	52	intron 26 + 263	ctgggcccagggctctgctc C/T gtgacttcggacaagttatt	4405
ABCC5	53	intron 26 - 3257	ccgaggggtgaattgctgtgt T/C gtctcacactttgggagata	4406
ABCC5	54	intron 27 + 873	gtttttctctctgctctatc G/A ggattctctctcatttgaaga	4407
ABCC5	55	intron 29 + (2733-2734)	gtgtccaaaaggaaggacacg (TGTCCAAAGGAAGGACAG)	4408
ABCC5	55	intron 29 + (2733-2734)	gtgtccaaaaggaaggacacg	4409
ABCC5	56	intron 29 + 2959	acatgattttccacggctac A/G tagaagtcacatcataggaat	4410
ABCC5	57	intron 29 + 4020	aataaaaaataagggggga G/A gtgcacgcagggttagttga	4411
ABCC5	58	exon 30 + 684	ccctctgcgcctcctccac G/A gccgctccaggggtggctgg	4412
ABCC5	59	exon 30 + 947	agtctatccacagagagtc C/T actgctcaggttctctatgg	4413
ABCC5	60	exon 30 + (1145-1160)	tcaccgcagtcgtcgcagag (TC) 6-8 ccctcaaatctgcaacttt	4414
ABCC5	61	3'flanking + 4	attattttggattttgtaaa A/C ctcttcgtgtatcaaaacat	4415
ABCC5	62	3'flanking + 2008	ccgcagacctggcacagcc C/Δ tgttctcaaggaggactcc	4416
ABCC5	63	3'flanking + 2052	cccagctagagacaggccagc A/G ccaggcagttagaccgtgg	4417
ABCC7	1	5'flanking - 834	gctaaaaactccaaagcct T/G ccttaaaaaatgcgcactggg	4418
ABCC7	2	5'flanking - 729	cctccttgagatttttttt T/Δ ctctttcagtcagtgctcta	4419
ABCC7	3	exon 1 + 125	tagcagggacccacgcgccc G/C agagaccatgcagaggtgcg	4420
ABCC7	4	intron 1 + 6200	ctatgtgagagcttaagaag G/A tagaggtggccaagaaggaa	4421
ABCC7	5	intron 1 + 7538	agttctctttcttagcatgg C/A ctacagaggtgcaactacct	4422
ABCC7	6	intron 1 + 13519	gaaacttaaatcttgagta T/C acaattgtgtctacatactg	4423
ABCC7	7	intron 1 + 14110	attacacagttatttttttt T/Δ aattttggggaaagtgcatt	4424
ABCC7	8	intron 1 + 14293	gccaggcagattcctgactc C/Δ tataaccagagcttatcag	4425
ABCC7	9	intron 1 + 14316	taaccagagcttatcagag C/G atttatgtccccaaagagaa	4426
ABCC7	10	intron 1 + 14433	cagaataacaatgatggctc G/A gaaaaataggggtatttctg	4427
ABCC7	11	intron 1 + 14824	acgttttgacagttgcacaa G/C tttctttctttaagctttaa	4428
ABCC7	12	intron 1 + 23401	aatattttgaaaaatcacta C/G ggtatcctgcatagtgattt	4429
ABCC7	13	intron 3 + 879	gaaaaatttcagttcataca C/A ccccatgaaaaatacattta	4430
ABCC7	14	intron 3 + 922	acttatcttaacaaagatga G/C taccctaggccagaaatgt	4431
ABCC7	15	intron 3 + 933	caaagatgagtacacttagg C/T ccagaatgttctctaagtct	4432

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCC7	16	intron 3 + 13704	tttttccaaataaaaaaaaa A/Δ tcagggtgatctctgtaaatg	4433
ABCC7	17	intron 3 + 13758	tattaaagaacatgatgctt A/G aaacagattagggaaaacta	4434
ABCC7	18	intron 4 + 240	ctctgtgttagtttttttt T/Δ ctccaatcatgttatcatt	4435
ABCC7	19	intron 4 + 376	ttatgttcagcaagaagagt A/G taatatatgattgttaata	4436
ABCC7	20	intron 4 + 586	tgccagacaaagagaccaa T/C tgccgaggcatcatttaggt	4437
ABCC7	21	intron 4 + 1089	ttcaaatctgaacattttac G/A taagtgaagactttgttaga	4438
ABCC7	22	intron 4 + 1615	aaagttagggtggtattgtat C/T tgtcttcttcttctcaatgtt	4439
ABCC7	23	intron 4 + 1946	aatacaaaacaaacttgagct T/C tgccataacttttcaagaat	4440
ABCC7	24	intron 6 + 783	tatctaagttttggagctaa A/G tagcactttgtttgaatccc	4441
ABCC7	25	intron 6 + (1104-1131)	gattgattgattgattgatt (GATT) 6-7 tacagagatcagagagctgc	4442
ABCC7	26	intron 7 + (731-732)	gtagcaatgagaccattttt (T) cttcagttgagctccatgtt	4443
ABCC7	26	intron 7 + (731-732)	gtagcaatgagaccattttt cttcagttgagctccatgtt	4444
ABCC7	27	intron 7 + 1434	gaatgtttggtgttaacctg T/C ataactctggcatgaaattgt	4445
ABCC7	28	intron 8 + 752	catgctctctctcagtcctc A/G ttcttctcattatcaccta	4446
ABCC7	29	intron 8 + 1109	tatggccaagacttcagtat G/A cgtggacttaattcttctct	4447
ABCC7	30	intron 8 + 1312	atgaagacattcattttttt T/Δ ctccgtccaatgtgtgatta	4448
ABCC7	31	intron 9 + (6521-6522)	gtgtgtgtgtgtgtgtgtgt (GT) ttttttaacagggtattggg	4449
ABCC7	31	intron 9 + (6521-6522)	gtgtgtgtgtgtgtgtgtgt ttttttaacagggtattggg	4450
ABCC7	32	intron 10 + 2119	gaacactttatagttttttt T/G ggacaaaagatctagctaaa	4451
ABCC7	33	intron 11 + 3867	tttttcttcaagaatttaga A/Δ gaggggagaaattgttttaa	4452
ABCC7	34	intron 11 + 11844	tgaatcaaaatcattctaaa A/Δ gctttcagaaccagacttt	4453
ABCC7	35	intron 11 + 12144	atattaaacagagttacata T/C acttacaacttcacacatat	4454
ABCC7	36	intron 11 + 20975	gtgtgtagtagtaaatgccag G/A gtaaatcacatagcatctaa	4455
ABCC7	37	intron 11 + 27057	atggaagagaagtttttagta G/A aggggaggaaggaggaggtg	4456
ABCC7	38	intron 11 + 27131	gagagagacttttttttttt T/Δ aaggcgagagtttactacct	4457
ABCC7	39	intron 13 + 152	gtattaaactcaaatctgac T/A gccctactggggccaggattc	4458
ABCC7	40	intron 13 + 287	tttgtagtatacttgccttg T/C gatataattacttttaatta	4459
ABCC7	41	intron 15 + (85-86)	atacatatataatgcacacac AT/Δ aaatagtatatatacacat	4460
ABCC7	42	intron 15 + 106	taaatatgtatatatacac T/A gtatacatgtataagtatgc	4461
ABCC7	43	intron 15 + 3341	ggaagtataaatttgttaaat A/C actgagaccacaaacttaca	4462
ABCC7	44	intron 15 + 5556	tgctattgactaataagtaat A/T attttaggcgagctttatga	4463
ABCC7	45	intron 15 + 5919	tggtagttctatgttggaac C/A gtgaggaaataattttatat	4464
ABCC7	46	intron 17 + 2479	caaaaaggtaggaagtcag A/C ggagaaggagaccctatgt	4465
ABCC7	47	intron 18 - 81	aagtagtcaaaaaaataaaa A/Δ gaaataaactcactgcacac	4466
ABCC7	48	intron 19 + 751	cattataaaaaaacaatc A/G tatctattcaagaatggca	4467
ABCC7	49	intron 19 + 820	tgacatttgtgatattgatta T/C tctaatttagtctttttcag	4468
ABCC7	50	intron 21 + 1532	ttactcttaacttttttttt T/Δ agtttgatcagctctcttta	4469
ABCC7	51	intron 21 + 1607	atgcttttggagttgggtct C/T ataaatgtatagaatgttt	4470
ABCC7	52	intron 21 + 11260	atgtggaacaatcatgacta T/C atgccttttactttctctat	4471
ABCC7	53	intron 22 + (130-131)	agaatcaatattaaacacac AT/Δ gttttattatattggagtcac	4472
ABCC7	54	intron 23 + 1837	ctgtctcaaaagtttaaaaag A/Δ aaaaaaaaggaagaggaa	4473
ABCC7	55	intron 24 + (7100-7112)	ccctttacaaactcttagaca (T) 12-14 agtttaacatgtttacaaaac	4474
ABCC7	56	intron 25 + 237	actcttcccccttgtcaaca C/T atgatgaagcttttaatac	4475
ABCC7	57	exon 27 + 115	gggtgaagctctttcccccac C/T ggaactcaagcaagtgcaag	4476
ABCC7	58	exon 27 + 334	ggatgaattaaagtttttttt T/Δ aaaaaagaaacatttggtaa	4477
ABCC8	1	5' flanking - 1099	aaaggggctgaaggggtctt T/C cttttgtgttccctgactg	4478
ABCC8	2	5' flanking - (424-422)	caccccaccaccaccaccac CAC/Δ aaggtaacgttctgccccac	4479
ABCC8	3	intron 1 + 1212	agcctgggcaacatagtgag A/G cccccccgcccctttctaca	4480
ABCC8	4	intron 2 + 1003	aggaggactgtgaatcccag C/A ctgcatgtttgggtcgatt	4481
ABCC8	5	intron 2 + 1253	catctcactaaggaagaatc C/T agtaaccagcaaggatgaga	4482
ABCC8	6	intron 2 + 1382	cccagactgcactcctgcag T/C gctgctggctcctcttagtt	4483
ABCC8	7	intron 2 + 2371	tttcagagctgtctggaaat T/A tagggggcaggtgggagggg	4484
ABCC8	8	intron 3 + 1957	ccctaccccctagcccaggg C/T ccccatatgagtatgaatgg	4485
ABCC8	9	intron 3 + (2088-2089)	agagaacccttcattaacca (CCA) gggcggtggctgaccagtgtc	4486
ABCC8	9	intron 3 + (2088-2089)	agagaacccttcattaacca gggcggtggctgaccagtgtc	4487
ABCC8	10	intron 3 + 2204	taaaagcacaagttatcaccc G/A tggatggattgtccttttc	4488
ABCC8	11	intron 3 + 2286	ttatctcccccttgaaggac A/G ctccacagagccagaaattc	4489
ABCC8	12	intron 3 + 2312	cagagccagaaattcttagaa C/G agggaaaagtggaggggagg	4490
ABCC8	13	intron 3 + 2356	ctgtgaactgcagggacaga A/G ggaatgggtatttgggagaa	4491
ABCC8	14	intron 3 + 2359	tgaactgcagggacagaagg A/C aatgggtatttgggagaatgg	4492
ABCC8	15	intron 3 + 2370	gacagaaggaaatgggtatt G/A ggagaatggccagccctcca	4493
ABCC8	16	intron 3 + 2382	tgggtatttgggagaattggc A/G gccctccaagggcgtaggt	4494
ABCC8	17	intron 3 + 4910	ggggacagccttcagctgtg G/A aattcctccagctcctagaga	4495
ABCC8	18	intron 3 + 4969	cattattccagctcctgaggg A/G tgagagcagaaggccagatgc	4496
ABCC8	19	intron 3 + 5003	cogatgtcttctgcccctcat C/G ctaatgtctcctcctgagga	4497
ABCC8	20	intron 3 + 5019	ccatctc.aatgtctcctgc A/C gggaccacaaggtggatggca	4498
ABCC8	21	intron 4 + 14	ggtaggggttaagcagggcac C/T tgggccaaggttggggtggga	4499
ABCC8	22	intron 4 + 187	agacactgcacatggccac G/A tgtgtctcaccacgggtcc	4500
ABCC8	23	intron 4 + 204	cacgtgtgtctcaccacagg G/C tcccagaggagaggggggt	4501
ABCC8	24	intron 4 + 254	gttcgctgaggttggcggat G/A actttccgtagaagggaag	4502

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCC8	25	intron 4 + 357	tgtattcatatcgtcacgct G/C gtaaatgaatgagtaagtgt	4503
ABCC8	26	intron 5 + 92	ggcattaggtcaaaatcctg G/A tgggacaaaaggggaaactg	4504
ABCC8	27	intron 6 + 4205	tctgtagaagaatcacatgggg G/A catgaagatcattggccttga	4505
ABCC8	28	intron 6 + 5519	gattccccaggggaatgtttaa A/C aggaccgggtcttccctaaac	4506
ABCC8	29	intron 6 + 5575	tctgaccagtgaccagccag G/C ggggcaagtttccatccccc	4507
ABCC8	30	intron 6 + 6587	gttgccatctgagatcttgc C/T ggaagtacacaagagaccct	4508
ABCC8	31	intron 6 + 6747	ttccactggcctttttctgct C/T agtaattgctacattacagg	4509
ABCC8	32	intron 9 + 191	gaggaagctgctcccggtg A/G ggacaggaagcgggcatggc	4510
ABCC8	33	intron 10 + 1963	cccaggagtcacaacctccct T/G tgtccagctagaccatgggt	4511
ABCC8	34	intron 10 + 2724	cctgggacatgttttcttat A/G taaacagcatcaaaagatgt	4512
ABCC8	35	intron 10 + 2938	gcccgcccaggactcctcac G/C tgtccaaagtcacctaggagg	4513
ABCC8	36	intron 10 + 3094	tcggaggtgtgtttttttt T/Δ cctccggttagtcagcagtg	4514
ABCC8	37	intron 10 + 3368	tcctgtcatatgcgggcacc A/G tcagacttctggcgaggcaa	4515
ABCC8	38	intron 10 + 8897	ggtattgtattaaaagcctca C/T gggcagagaaaatcgccatc	4516
ABCC8	39	intron 11 + 308	tgtgtattgtagaagtgtg G/A gaaatccgaacagaaagct	4517
ABCC8	40	intron 11 + 1171	gccctctcatttcccttcca G/A tgctgagcgtttccagtgtg	4518
ABCC8	41	exon 12 + 7	gcctctgtccacagacttcc G/A tgggcccagctcagcttcttc	4519
ABCC8	42	intron 12 + 356	accaagaatgagggccatccc G/T tccccacgtggctgccccat	4520
ABCC8	43	intron 12 + 934	tggtgtcacaagatggaatgg G/T gcataactcagcaaaattat	4521
ABCC8	44	intron 12 + 1370	gggagggaggctggacagg G/G atgaaggcagagcctgggtgg	4522
ABCC8	45	intron 15 + 412	ggaggtgggagccaggatgg C/T gtttcttgggaccacaagga	4523
ABCC8	46	intron 15 + 688	actccccgggcccactcac A/G tctgccaccttccctccctg	4524
ABCC8	47	intron 16 + 4464	actcattccaagtattgtatc G/A agaagagaggttaggtactgg	4525
ABCC8	48	intron 16 + 4574	ttgaagatcttaagtgtttt T/C tgggtcactcatttcgcaaa	4526
ABCC8	49	intron 16 + 5011	agctaaaaagcaaaacagcct C/T tgacctggcaagcattccca	4527
ABCC8	50	intron 16 + 7608	tgtcctacttttctttttgac C/G cttataacttctgacttctg	4528
ABCC8	51	intron 16 + 7730	ccagctcctagtgggctgga G/A ggaaggacatcgsgttgggg	4529
ABCC8	52	intron 16 + 8369	ttgcaaaactgagttagggcc T/C ggagagcttactgtgtgctg	4530
ABCC8	53	intron 16 + 9708	tgcaacttggccctacttat T/G ccagacccaatgattgggtc	4531
ABCC8	54	intron 17 + 651	tatagattaatgaggtctctg A/G gtcctcctcaaaaccttccctc	4532
ABCC8	55	intron 17 + 692	cccttacctctccaaaaaac A/G cttgagataacctagaggtg	4533
ABCC8	56	intron 17 + 1541	ctcaggatcttctctggagga C/T atggttcaactcccatgagag	4534
ABCC8	57	intron 18 + 580	actaagcagatttctaccaa C/T tgcacctcctccatccctctg	4535
ABCC8	58	intron 18 + 658	gaacaagccctcgagaatgc C/T ttccgcacccctactcccg	4536
ABCC8	59	intron 18 + 660	acaagccctcgagaatgcct T/C ccgcacccctactcccgcc	4537
ABCC8	60	intron 19 + 93	gcccttccatcgatcaccga T/C acccagccatctcactcccc	4538
ABCC8	61	intron 19 + 123	tctcactccccagggtctta T/C ctgcactccagcctctccat	4539
ABCC8	62	intron 19 + 219	cataggggagagggcaggaa C/T ggagggagggagagagccc	4540
ABCC8	63	intron 19 + 845	tagtatttaacctgcccaaa C/T gctgtgtgaagtgtgctgacct	4541
ABCC8	64	intron 20 + 338	ttccctccacaagcttagac A/G aacaggattctcctgtgact	4542
ABCC8	65	exon 21 + 10	tttgggtgacagggcatcaac C/T tgtctggttggtcaacgccag	4543
ABCC8	66	intron 21 + 192	caaggatagcacaaatgacc C/Δ attgcagacttcagatggag	4544
ABCC8	67	intron 23 + 17	gaagggtgggtatatccagg G/A tggccaagcagccaccctctg	4545
ABCC8	68	intron 23 + 67	gttctgtctagaacctgaact C/T ataaaggcttctcctgtcctt	4546
ABCC8	69	intron 26 + 268	gtgagcgtctgcacatccaa G/C taaagattgttttctctcc	4547
ABCC8	70	intron 26 + 308	cgataagtgggtgtaatttg C/T ccatccccaccctagagttc	4548
ABCC8	71	intron 26 + 348	cagctcctgcccctcccctc A/G ctctctctcctcagccagc	4549
ABCC8	72	intron 26 + 807	gacagctgtgtgagtcaggcc G/A agccggcagctgagaaagcc	4550
ABCC8	73	intron 26 + 834	cagctgagaaaggcggcag G/C gtcagatgggcttgagaaac	4551
ABCC8	74	intron 28 + (118-121)	cctccaaaaataaaaacaa AAAA/Δ cagaatgaaaggaaatagaa	4552
ABCC8	75	intron 28 + 1348	tggggtaagcggaagacggg G/A tgaacgctttgagtttgggt	4553
ABCC8	76	intron 29 + 1253	ctcttagggatcttctctaa G/T taaagaagagcagagcaaaag	4554
ABCC8	77	intron 29 + 1589	cagatcccagcttctctgtaa A/G cagcctcagatcaggccaaa	4555
ABCC8	78	intron 29 + 2322	gcgcctcacactcctataac G/A cgcacatgccttgatgcaca	4556
ABCC8	79	intron 29 + 2348	atgccttgatgcacacacat T/C ttcaacagcacttactcta	4557
ABCC8	80	intron 29 + 2418	agacacgtcacccctccaca C/T gtctccacctgggggtgtg	4558
ABCC8	81	intron 29 + 2494	tcagtcctccctcagacacatg C/A cctctctccacgcagagaca	4559
ABCC8	82	intron 29 + 2735	gcggccaaggagagtgtatga C/T ggcagccaggttgatcaga	4560
ABCC8	83	intron 30 + 386	gtccttggggctccagcctt C/T gcagcccttggtgtgtgtctg	4561
ABCC8	84	intron 33 + 93	ggcttcgcagtcacctctgtg G/T ccctccaggccgagggcctc	4562
ABCC8	85	intron 33 + 358	agggacctggggggcagacag C/T gaggccaccttgatttgag	4563
ABCC8	86	intron 38 + 54	cccgggacaggaactggcct G/C ttgtggcgtcatcagtgca	4564
ABCC8	87	intron 38 + 466	aggacattcttgccacatgc C/Δ tcactctcctcctccaagcc	4565
ABCC8	88	intron 38 + 529	tggccccccacgggggtggt A/G ttcccccatctctgaccgc	4566
ABCC9	1	intron 3 + 38	tgtgttttctctttaaagag C/A tatttgtttttcccccaaa	4567
ABCC9	2	intron 3 + 305	gctggccttctgtggttcag T/A agttgtattttaagaatcag	4568
ABCC9	3	intron 3 + 320	tgcagaagtgtattttaag A/G atcagagctcttgtgaggag	4569
ABCC9	4	intron 3 + 631	ttctgtggaaatcagaggct G/C tctaaaaattctctaatttt	4570
ABCC9	5	intron 3 + 8644	tggacgcactcaacatttcc A/G agttattactccttcaactc	4571
ABCC9	6	intron 4 + 757	aggatatcatgaaacactga A/C tcttagtaaaaactatcttt	4572

One example of information generated using SEQ ID Nos. 1-3360 and 3361-7669 and information in publicly available databases is provided in Figure 143. The first column in this figure shows that 3360 entries are made, corresponding to the first 3360 entries found in Table 1. The second column, entitled "GENE" provides a gene name abbreviation, while the next column provides a long gene name. The next columns show the chromosome (CHROM), a reference mRNA accession number (REF. MRNA), a locus link database accession number (L-LINK), an OMIM database accession number (OMIM_ID) which allows disease association information to be readily obtained, the exon count for the gene (EXONS), and the number of polymorphisms in the gene (NO GENE).

Creating an Oligonucleotide Probe or Oligonucleotide Primer

In some embodiments, an oligonucleotide used as a primer and/or probe in the detection method of the present invention serves as the template of the base sequences (Sequence No. 1 through 3360 and 3361 through 7669) shown in Table 1 if, for example, a SNP is to be detected. The primer/probe can be designed so it is synthesized as the base sequence itself or as a portion of the base sequence. In preferred embodiments, the SNP is included in the base sequence of the primer/probe (and denoted in capital letters in the base sequence column of Table 1). The primers/probes may also be complementary to the non-mutant sequence.

The SNP in the following example is designed so it is on the 3' or 5' end of the base sequence. It is designed to be within four bases of the 3' or 5' end, and ideally within two bases of the end. The SNP can also be in the center of the oligonucleotide base sequence. Here, "center" means the number of the bases from the SNP base to the 5' end is substantially equal to the number of bases from the SNP base to the 3' end. If there is an odd number of bases in the oligonucleotide, the central region should be essentially five bases in length, preferably three bases in length, and ideally one base in length. In a base sequence with 41 bases, for example, the central region should be bases 19 through 23, preferably bases 20 through 22, and ideally base 21. If there is an even number of bases, the central region should be four bases and ideally two bases. In a base sequence

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCD3	16	(intron 9 1493)	tcacctcttccataggctt A/G ggtgtggagaggagatagaa	4643
ABCD3	17	(intron 13 1534)	tctgttgagttggggatcct A/G tggaaacctcttctctcatc	4644
ABCD3	18	(intron 16 4310)	gaaaagtgaatgctgagtag G/T tttagccaggcttgatttaga	4645
ABCD3	19	(intron 20 273)	ttctaaaagttcagagaaac T/A ctgtagctcattattctctgg	4646
ABCD3	20	(intron 20 1664)	ctcaaaagaaaaaa A/C aaaaaacacatgatccataa	4647
ABCD3	21	(intron 20 6693)	cttaaggtttgtgttttact C/T tgagcaattagtatttccca	4648
ABCD3	22	(intron 21 7171)	atcataaacagagaaataat A/G tcttaaatgagctctgaaaa	4649
ABCD3	23	(intron 22 1220)	ctagaaatcaaaggcattta A/G aatatagccaagcctttatg	4650
ABCD3	24	(intron 22 1358)	agtagcaaaataatcatcac G/A ccagtgatcatgtgaaggag	4651
ABCD3	25	(intron 4 4448-4461)	taactttctgttagtttagc (T) 11-14 aactgttttacttttttaggg	4652
ABCD3	26	(intron 5 268)	gttttttggcattttttttt T/Δ aaccttcagtcagggttttc	4653
ABCD3	27	(intron 5 891-902)	ttggtgtaaaacctgtagtg (T) 10-13 aacaaatgcaaatatagtg	4654
ABCD3	28	(intron 7 1226-1227)	gggaatgggggtgtatcta (T) tacaactttccatgtaattt	4655
ABCD3	28	(intron 7 1226-1227)	gggaatgggggtgtatcta tacaactttccatgtaattt	4656
ABCD3	29	(intron 8 1129)	cagatttactttttttttt T/Δ aatcttgaatacttactagc	4657
ABCD3	30	(intron 13 1595-1596)	tgaacataataaagcacac (TA) gttatcattaatactttatg	4658
ABCD3	30	(intron 13 1595-1596)	tgaacataataaagcacac gttatcattaatactttatg	4659
ABCD3	31	(intron 16 7337-7351)	ttaattacttcacagactga (T) 13-15 caggttcgatctggggctaa	4660
ABCD3	32	(intron 18 12)	gttcctcaggtgaagcctag C/Δ ttgagtattctttgatctaa	4661
ABCD3	33	(intron 20 1652-1670)	gcaagactctgtctcaaaag (A) 17-20 cacatgatccataatagagg	4662
ABCD3	34	(intron 20 2262-2273)	ttaatccattttgttaaatc (T) 11-13 accttaaatagcaactatc	4663
ABCD3	35	(3' untranslated region 2072-2079)	taaaataaagttgagcttag (T) 8-9 aaaaaaaacaaagcaaca	4664
ABCD3	36	(3' untranslated region 2080-2091)	gttgagcttagttttttttt (A) 10-11 caagcaacaaattaactag	4665
ABCD3	37	(3' untranslated region 3349-3368)	acttattttctgttcagatt (A) 16-19 ctcatatctctatacaacc	4666
ABCD4	1	(intron 1 276)	tggcattctttttttgaaaa G/A aagaacctcaggtgcacaaa	4667
ABCD4	2	(intron 1 329)	cttctcagttcttgacaccc T/C gtgggcccaatgcaaggctcc	4668
ABCD4	3	(intron 3 171)	ttaagcacgttgatcttgct A/G ttggcccaactgggactgat	4669
ABCD4	4	(intron 3 449)	ctacccctcattcagtagg G/A gggctaccacctgctcactc	4670
ABCD4	5	(intron 5 273)	gacaggggtacacctgagagg G/T aacaggagtcagggtcagg	4671
ABCD4	6	(intron 7 240)	tagtcttagtggttagcgt G/A gggcctgaattgtcaaatg	4672
ABCD4	7	(intron 7 267)	gaattgtcaaatgaatgaa T/C gcctcatcctcttgctggtg	4673
ABCD4	8	(coding region 910 (Ala 304 Thr))	tctatggagacctgagctccc G/A cagagcttagcacctggtc	4674
ABCD4	9	(coding region 981 (Leu 327 Leu))	atcagctgcttcaccagct C/A atcgacctgtccacgacgct	4675
ABCD4	10	(coding region 1102 (Glu 367 Lys))	gcgagatcctggggcgagagc G/A agtggggcttgacacgtga	4676
ABCD4	11	(intron 13 191)	tggattggggccactactca T/C agcagctcctgaggcaggta	4677
ABCD4	12	(intron 13 262)	acgcgtatgtcaaacaccca A/G ggtcggattctggggccctc	4678
ABCD4	13	(intron 17 848)	cctctgctcctctggcccat C/G cttctccttgaggcagggtc	4679
ABCD4	14	(intron 17 946)	gtgggaggagaagcagcggc G/A gcagaggcagggcctttgat	4680
ABCD4	15	(intron 18 41)	ggcctgaggaggagaagaa C/T ccaaaggctcagcctggcca	4681
ABCD4	16	(3' untranslated region 2)	gccacaggtctaggtttctgt G/A ggggacactgaatctccag	4682
ABCG1	1	(5' flanking region -386)	gcaataatcattggctagag G/A tattgtgatatgatgtcatt	4683
ABCG1	2	(intron 1 199)	caccaaatattggtgagctg C/T ctggatttgggagatgcagt	4684
ABCG1	3	(intron 1 291)	acttgggtccgggtgtgagg A/C tctctgactcgggtttctgtg	4685
ABCG1	4	(intron 1 318)	actcggtttctgtgatgggtg T/A gtgcaggaggagtcacaaagt	4686
ABCG1	5	(intron 1 468)	ggcccccaacgggtttctaga T/C cctccagagaagcctttgg	4687
ABCG1	6	(intron 2 434)	ctgggtacaggtttttgtcc G/A gttgtctgtctattgagtat	4688
ABCG1	7	(intron 3 1839)	ttaaaatgagttgtttttct C/G ctaaaccttttagggagttg	4689
ABCG1	8	(intron 3 3076)	tttgtcacttctctctgtctc C/T ggctctacttccctgggggt	4690
ABCG1	9	(intron 3 3352)	gttctctggaggaaacgtgg G/A gtacacagtggttccagtta	4691
ABCG1	10	(intron 3 8030)	acagtgagcacaaaggcagc C/T gaagacacagcaggcaggtc	4692
ABCG1	11	(intron 3 8066)	aggtcaggtctgtgtgcaca T/C ttggcaggctgc a/g tgcagacc	4693
ABCG1	12	(intron 3 8092)	ggctgc a/g tgcagaccagct C/T ggcccagggtggaagcaga	4694
ABCG1	13	(intron 3 8285)	ctggacatgtgactcccctg C/T acccaccctcacaagcaca	4695
ABCG1	14	(intron 3 8860)	cagggtgataggaggtccaa T/C ttggacacaggttcagtttgc	4696
ABCG1	15	(intron 4 2319)	gggggtgaacagaggcaga G/A gcctgggcatcttctactcag	4697
ABCG1	16	(intron 4 2557)	gaaggggaagaagcagcagca A/G gaaagaagccccctggccct	4698
ABCG1	17	(intron 5 139)	tgaccacgggcacccctagag T/A ggcgcgcggctccgatcgt	4699
ABCG1	18	(intron 5 177)	gctgccccctgccctccgcc A/C gggccacctggagcctcggg	4700
ABCG1	19	(intron 6 13)	cagttactgttaagtctgtt T/C ccaggggtgtgca g/a gaatct	4701
ABCG1	20	(intron 6 27)	gctgtt t/c ccaggggtgtgca G/A gaatctccctttctgtttt	4702
ABCG1	21	(intron 6 1191)	gctaagcagagttaggcccc G/A gctagtccttgaatgagaga	4703
ABCG1	22	(intron 6 1449)	atgctggagccctgagttc G/A gtgggcatacaaggggtggc	4704
ABCG1	23	(intron 6 2282)	ctcgcatcagcagttttca C/T gatcctattaattgggtgag	4705
ABCG1	24	(intron 6 3853)	cctgggcttcagcaggggcc T/C cacacctgcaatgggtg c/t ct	4706

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCG1	25	(intron 6 3871)	cc t/c cacacctgcaatgggtg C/T ctggggagaggggtgcagatg	4707
ABCG1	26	(intron 6 4175)	tccaaagcccagatttggtg T/C ttttggggctcttttggaaat	4708
ABCG1	27	(intron 7 4)	ctggtggaggaagaagagta G/A ggagggcggctgctttgtgt	4709
ABCG1	28	(intron 7 576)	agctcaggaggtgtctggaa C/T gccacacagtgccaggagttt	4710
ABCG1	29	(intron 7 1426)	aattctccttctcaacttaa A/G gaaatattttatagaaaaat	4711
ABCG1	30	(intron 7 2342)	agagcctgcaatggggccgc G/A agggacctgcccagactca	4712
ABCG1	31	(intron 7 2399)	gaggggttgacagacaggat A/G tgtctg c/g tgtgttccagctg	4713
ABCG1	32	(intron 7 2406)	tgacagacaggat a/g tgtctg C/G tgtgttccagctgctggttt	4714
ABCG1	33	(intron 7 2911)	ccctctctgtgcccactgtt G/C tcccaacaccagcctgttct	4715
ABCG1	34	(intron 7 4363)	tataatagattcctagcaga A/G aacataattgtgagaggaac	4716
ABCG1	35	(intron 7 4752)	gctttcagagcccatttcaca C/T aagggctctcattttattagg	4717
ABCG1	36	(intron 7 5026)	ccagggtctgtgggatttcag G/A ccaaaaagagcgtagcaag	4718
ABCG1	37	(intron 7 5532)	gggttaaatattccgggcag C/T gccaaagtcagattatctgta	4719
ABCG1	38	(intron 7 5681)	gctaaagtgcattggaaggca T/C catgaataaatcctttcagg	4720
ABCG1	39	(intron 7 9243)	gcctgagagcgctggcagta G/A gaagggtccgagctgtggag	4721
ABCG1	40	(intron 7 11371)	gggtctcttggagcccttt T/G tctctcccagcctgcgtct	4722
ABCG1	41	(intron 7 12420)	gggatttcgaatctcaacac T/C ctgagctctgtgctttcccc	4723
ABCG1	42	(intron 7 12985)	ctattggcagggtcgtgaaca T/C tgttcttggatttgcaaat	4724
ABCG1	43	(intron 7 20041)	acatggccggtctccctctt T/C cctc g/a gaatggcttgggaatt	4725
ABCG1	44	(intron 7 20046)	gccggcttccctctt t/c cctc G/A gaatggccttgggaattcgatc	4726
ABCG1	45	(intron 7 21058)	acaagacttagaatttgacc G/A tgattttaaaaactattttaa	4727
ABCG1	46	(intron 7 26189)	ttcttggatgtggccatgca C/T gggggcaagggtttgatgag	4728
ABCG1	47	(intron 7 27453)	atcatgtgtgttgggggaaa G/C ctgggaccccaattggtaca	4729
ABCG1	48	(intron 7 29810)	attgtttctcctgtgtttgt T/C tgtgttgactttccctttaa	4730
ABCG1	49	(intron 10 2116)	aaacagggcttgagctctcc G/A taaggacagagagaccttcc	4731
ABCG1	50	(intron 13 1196)	tgaaaagaaaatggatgagt G/A gaa a/c ccaaaagagagaaaaat	4732
ABCG1	51	(intron 13 1200)	aagaaaaatggatgagt g/a gaa A/C ccaaaagagagaaaaatgtgg	4733
ABCG1	52	(intron 13 2041)	aagcagaggcttttccaccc G/A gagactcaagaagctgtctcc	4734
ABCG1	53	(intron 13 2490)	gtggtgaagttagagctgagc A/T caccggggagccctccatcc	4735
ABCG1	54	(intron 13 2822)	cagcaggctccgtgtgtaag T/C cacagcaagccaggcccttg	4736
ABCG1	55	(intron 13 2850)	agccaggcccttggcctgcc G/A gagctggaagaccagaca	4737
ABCG1	56	(intron 13 2919)	gcctcccaggagtagctaca C/T gggaccgaaggcagatggc	4738
ABCG1	57	(intron 13 3506)	ggcagcctgggtgcccaga T/C cctccctggagcgcgcgcgc	4739
ABCG1	58	(intron 13 3538)	cgcccgccgggaagcccccag G/A ggggctggagctaca a/g gtgg	4740
ABCG1	59	(intron 13 3554)	ccag g/a ggggctggagctaca A/G gtggccttgacaggtttttg	4741
ABCG1	60	(intron 13 3721)	ccagctcatgggagggtg C/T ggagggaaggcaccacag	4742
ABCG1	61	(intron 13 3921)	gaagaccagcagtcgatgcc A/G gctgggaaggaggtctctgcc	4743
ABCG1	62	(intron 13 3979)	accacaccagcctttccaga C/T agccttccagaagctgtttc	4744
ABCG1	63	(intron 13 4291)	gagccgctggagtaggggtcc G/A cttgctatggctcccagggg	4745
ABCG1	64	(intron 13 4968)	tattgactggacacettctc C/T gtatggggcactgggctagg	4746
ABCG1	65	(intron 16 672)	atcagtaacgggtcactaac G/A gatgctgctgagtggggca	4747
ABCG1	66	(intron 16 891)	tggcccaactgttgagggtgt G/A ggtgaccagaggggcttga	4748
ABCG1	67	(intron 18 1616)	ctggaggagaagacaggata A/C agtctaagacgtg c/t tgtcac	4749
ABCG1	68	(intron 18 1630)	aggata a/c agtctaagacgtg C/T tgctacagagttcagggtcc	4750
ABCG1	69	(intron 18 1674)	gcttccaaaggccgcatccg G/T gttgttctctgagc c/t gagga	4751
ABCG1	70	(intron 18 1689)	atccg g/t gttgttctctgagc C/T gaggacggccttgccaacgc	4752
ABCG1	71	(intron 19 446)	tgggtgacagtgaacacagc G/A gctgcttctccagaacttta	4753
ABCG1	72	(intron 22 243)	accgggagagccatggcagg A/C ccaagtgttctggagcttgc	4754
ABCG1	73	(3' flanking region 1257)	atggggcccccagccctgcc T/C cagaagcagctttgtgtctg	4755
ABCG1	74	(3' flanking region 1438)	gggggaagagcttgggaacc A/G tgagggtgttaggctgcaa	4756
ABCG1	75	(3' flanking region 1518)	tgaagggtgaactggagtag G/C tgaggattctgcagttgacg	4757
ABCG1	76	(intron 3 3754-3755)	ctccaccctgcacctccctg (G) cctccttgatttccctcatc	4758
ABCG1	77	(intron 3 7848-7854)	cagtttccagaatttggggg (A)6-7 tccataagctgtcatactt	4760
ABCG1	78	(intron 4 190-191)	tgctgagagctccccctgcc (C) tgggtgacctcagggttct	4761
ABCG1	78	(intron 4 190-191)	tgctgagagctccccctgcc tgggtgacctcagggttct	4762
ABCG1	79	(intron 4 198-206)	agctcccttgctgctggttga TCCTCAGGG/Δ ttctacttagaatgcoct	4763
ABCG1	80	(5' untranslated region (-713) - (-741))	cgcagctcaagcctgttccc (CGC)8-10 ccccggggcatggcctgtct	4764
ABCG1	81	(intron 6 376-387)	tcttgcttgagctcaagag (A)10-12 tagccagggtttctgcccag	4765
ABCG1	82	(intron 7 19944-19945)	ctgatgaggagggggggggg (CACCAGGCACGACACTCTGATGAGGAGGGGAGGGGG) caccaggcagcagactctga	4766
ABCG1	82	(intron 7 19944-19945)	ctgatgaggagggggggggg	4767
ABCG1	83	(intron 7 25136-25137)	catgaacttgccctgaccata (G) ccctgtgaggagctagggt	4768
ABCG1	83	(intron 7 25136-25137)	catgaacttgccctgaccata ccctgtgaggagctagggt	4769
ABCG2	1	(intron 1 152)	tcatttgaaagtgggtatgc G/A gttttaaaactgacagttaa	4770
ABCG2	2	(intron 1 614)	agctagtcataataataac G/A ccagagtagtaaggaagaga	4771
ABCG2	3	(intron 1 10002)	cctcatgaatggtatatacat T/A cccaacatatctctttgat	4772
ABCG2	4	(intron 1 10123)	acagtgttcccttgggtgc G/A tatacccaaatccctgcata	4773

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCG2	5	(intron 1 10768)	ataggaataattgagaacag G/A gtctgaagaactctgcagga	4774
ABCG2	6	(intron 1 10791)	ctgaagaactctgcaggaaa T/C g/a aaaatagttccctgctttt	4775
ABCG2	7	(intron 1 10792)	tgaagaactctgcaggaaa t/c G/A aaaatagttccctgctttta	4776
ABCG2	8	(intron 1 14183)	tcacttaaggctttgcaggg T/G gtctaggacacagaaagaga	4777
ABCG2	9	(intron 1 14934)	aaagtgtctttaaatttcc A/G tcttgagtcagtgagctatt	4778
ABCG2	10	(intron 1 14955)	tcttgagtcagtgagctatt G/T aaattcaagcaataagttat	4779
ABCG2	11	(intron 1 17251)	ctgtttgggaacagcaactc A/C atcataggcagagagaaagt	4780
ABCG2	12	(intron 1 17347)	atttcaaacctgtttcacaa G/A ttgttaagctcatcttaagg	4781
ABCG2	13	(intron 1 17626)	gaaggtgcataacaacttcc T/G acataaagctctggagctata	4782
ABCG2	14	(intron 1 18369)	ctattgtctttctgtctgca G/T aaagataaaaactctccaga	4783
ABCG2	15	(coding region 34 (Val 12 Met))	atgtcgaagtttttatccca G/A tgtcacaaggaaacccaat	4784
ABCG2	16	(intron 2 36)	tgtaaaaaagacagcttttta A/G tttacctacagtgaacctca	4785
ABCG2	17	(intron 2 4230)	caaccctaaattggagggcc C/T gggcggtggtgattgagaaag	4786
ABCG2	18	(intron 2 4518)	gttgacagacttttatagtg A/C gggacactgactgcagtcga	4787
ABCG2	19	(intron 2 6278)	atgtatgtaccacgtcttca T/C attcttaaggatgacctta	4788
ABCG2	20	(intron 3 10)	ggcaaatcttctgtgagata A/G gagagtataagtaagcgttt	4789
ABCG2	21	(coding region 421 (Gln 141 Lys))	tgacggtgagagaaaactta C/A agttctcagcagctcttcgg	4790
ABCG2	22	(intron 6 3203)	tcctattctgttttaataaa A/G gcattgaatttaggtttgct	4791
ABCG2	23	(intron 6 3287)	gtcaggtgaaactagagcaa A/G caatctaaaggcaagaatag	4792
ABCG2	24	(intron 9 5974)	tactactaataatggtgtgt A/T taagtcttttatctctaattg	4793
ABCG2	25	(intron 10 1908)	gacgcttatgtgcagcctat G/T ttgatgtctggaaggctga	4794
ABCG2	26	(intron 10 2094)	ccctgagggctgaggtatct G/A gattatttccagacttgcta	4795
ABCG2	27	(intron 11 20)	tgtgagtaggtctttgttct A/G ggaacggggctgtccagcag	4796
ABCG2	28	(intron 11 1447)	tgttcttcaaggaaagcccc C/T gtcaagaaggaaagaaagc	4797
ABCG2	29	(intron 12 49)	atgtcttttagtcttgcctat G/T ggtgaagtcagttgcacctt	4798
ABCG2	30	(intron 12 1566)	tatgcagttacatggacaga C/T acaacattggagaccgaggg	4799
ABCG2	31	(intron 13 40)	gctctgataaggaaattgttt C/T ttctcttcatcttctcctgc	4800
ABCG2	32	(intron 13 1823)	ttactcaagcaggcctgact C/T ttagtatttgcctttttag	4801
ABCG2	33	(intron 14 497)	ctaataaaaacaaacagaa T/C gaaagattgtcactgtaaat	4802
ABCG2	34	(intron 14 815)	taactcttggaaacatttctt A/G aaattttaaactgtttacct	4803
ABCG2	35	(intron 15 110)	ccaggggactgaatttttc C/T gagcctacgttttctcatcc	4804
ABCG2	36	(intron 15 566)	gccgatagtcagtgtgtgt T/A gtttttaattaaacttggaa	4805
ABCG2	37	(intron 15 639)	aacaagaacacttgaataa G/A ttgagaaaaaaccccgtttt	4806
ABCG2	38	(intron 15 1197)	tgagttagctgggattacagg C/T gccaccaccacacctgggt	4807
ABCG2	39	(5' flanking region (-998)-(-995))	gttgggatggctacactcac TCAC/Δ aaagcctgatggcccgtttc	4808
ABCG2	40	(intron 13 405)	ctgctagttttatttttttt T/Δ aacatttttaattatgttt	4809
ABCG2	41	(intron 13 692-702)	tcaatatgtttctgcttacc (T)9-11 aatggttacttaatecta	4810
ABCG2	42	(intron 15 645-650)	aaacacttgaataaG/Attgag (A)7-8 ccccgttttcacataatgtt	4811
ABCG4	1	(intron 1 84)	ggcctgggtgtcccatgttc G/A gaaagtcctgcaccagtggt	4812
ABCG4	2	(intron 2 77)	gaacacagaaggatttctga A/G agggcattgacccccatcct	4813
ABCG4	3	(coding region 679 (Leu 227 Leu))	tgggtgtccctcatgaagtc C/T tggcacaggggggcgtacc	4814
ABCG4	4	(intron 7 95)	ggcctcctaggggttagagat C/T tcaccgtcgctgccttccc	4815
ABCG4	5	(intron 7 158)	cttgccttgggaagtgagt G/A tgaatctaaactgagctctc	4816
ABCG4	6	(intron 8 106)	ccccagagcattgcaacca A/G tgggtgctaggaagaaccta	4817
ABCG4	7	(intron 11 1120)	acgagataagtga t/c ggtcat A/G tggccaggaggaaggggac	4818
ABCG4	8	(intron 11 1173)	gggggacagcttgaacaaga A/G tgtggaggcaggatggacac	4819
ABCG4	9	(3' untranslated region 2)	gagtgacaggcacatacatg A/C gaacaggccatctcagccct	4820
ABCG5	1	(intron 3 40)	ccctggcccccccgccgc C/A cgggggcttaggtacactg	4821
ABCG5	2	(intron 4 841)	gcttggaggcatcttgaatg C/T gcctcatccaaactggactg	4822
ABCG5	3	(intron 4 1145)	gagcaaatccagccacagc G/A tgtaaaat c/a ctgataagtaa	4823
ABCG5	4	(intron 4 1154)	cagccacacagc g/a tgtaaaat C/A ctgataagtaattcagtggt	4824
ABCG5	5	(intron 4 1690)	acagagatgagaaggaggtc T/C gggaatctaccctggctggt	4825
ABCG5	6	(intron 4 1806)	tcttttgttccagaatata T/C tatatctagttttattatgc	4826
ABCG5	7	(intron 4 1878)	atttcagatatgtccattct C/T tgggtgggtcgaagctacat	4827
ABCG5	8	(intron 4 2052)	gggtgtcttggaaacaaaact C/T attaccatagtagtatcttc	4828
ABCG5	9	(intron 4 2108)	tccccctgggggttctctcag A/T tagaggtaatcagtacaggg	4829
ABCG5	10	(intron 4 2230)	agcttctttagtagaaatc G/A gtaagaatttttttttagtc	4830
ABCG5	11	(intron 4 2318)	ggagttacagggctttaagta G/C agcgaagagaaattggaagaa	4831
ABCG5	12	(intron 4 2367)	ttaaatgtggctgggggtta C/T aaattgggtccccattaaag	4832
ABCG5	13	(intron 4 2464)	gattatatgtctttagtggt A/G actcacactgagattgtacc	4833
ABCG5	14	(intron 4 2586)	aaagcatttatgataataa G/A ttcaaaaacccaacactta	4834
ABCG5	15	(intron 6 1318)	cagagacattcaaaagtgcat C/T gctaccctgtgtatcacaca	4835
ABCG5	16	(intron 9 164)	caactattgagttaccaaca T/C gttaatatgaatgagctcac	4836
ABCG5	17	(intron 9 365)	gtaccgttagcttctctttt A/G agctgatttttaggacagcca	4837
ABCG5	18	(intron 10 64)	tcatggagctagtggaactc G/A tgcaggggagagctccaggggt	4838
ABCG5	19	(intron 10 2406)	tcaacaagcctgcttactgc G/A gttagtgtgaccattgtct	4839

Table 1. Demographic characteristics of the study population	
Age (years)	65.0 (SD 10.0)
Gender	
Male	50 (50.0%)
Female	50 (50.0%)
Education (years)	12.0 (SD 2.0)
Marital status	
Married	40 (40.0%)
Single	10 (10.0%)
Widowed	40 (40.0%)
Divorced	10 (10.0%)
Income (USD/month)	1000.0 (SD 200.0)
Health status	
Good	40 (40.0%)
Fair	10 (10.0%)
Poor	40 (40.0%)
Smoking status	
Smoker	10 (10.0%)
Non-smoker	40 (40.0%)
Alcohol consumption	
Drinker	10 (10.0%)
Non-drinker	40 (40.0%)
Comorbidities	
Hypertension	20 (20.0%)
Diabetes	10 (10.0%)
Cholesterol	10 (10.0%)
Arthritis	10 (10.0%)
Depression	10 (10.0%)
Other	10 (10.0%)

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Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCF1	3	(intron 20 69)	tgactttaaccgaccacetc C/T ctctcttctcgggcagaaaa	4905
ABCF1	4	(intron 23 35)	agtgtgccctcatccctgct C/A catggggaccaaagctgtagt	4906
ABCF1	5	(intron 7 342-354)	acagagcggagactccgtctc (A)10-14 gaaaaaaaaaaaaacattt	4907
ABCF1	6	(intron 7 356-369)	cgtctcaaaaaaaaaaaaag (A)13-15 catttcatcagacctgtctt	4908
ABCF1	7	(3' untranslated region 2)	tcagccggcccccagagatga A/Δ gctttccttcccagaagtct	4909
ABCF1	8	(3' flanking region 1067-1068)	attaatttgatcaattgtct (T) aatatgtcgtactcttagatt	4910
ABCF1	8	(3' flanking region 1067-1068)	attaatttgatcaattgtct aatatgtcgtactcttagatt	4911
OAT1	1	(5' untranslated region -1)	gcagctcggactcagctccc G/A gagcaaccagctgcggagg	4912
OAT1	2	(5' untranslated region -2)	gaaggcctcagcccccagcc A/G ctgggctgggctggcccaa	4913
OAT1	3	(intron 3 150)	caatagacaacaccttttctc G/A ggctcatgcgcctgaccc	4914
OAT1	4	(intron 4 211)	ttctctggcttccccactc A/C gttctccagcctgcctgctc	4915
OAT1	5	(intron 5 33)	gagacttcccatgataacct C/T ccagggttccaccccaaac	4916
OAT1	6	(intron 6 168)	gaaccagatgcccccagcct C/T gactcagtcctccatccac	4917
OAT1	7	(intron 1 58-71)	ggaagatgggggctttgtt (A)13-15 gtacatggagaaattaactg	4918
OAT1	8	(intron 3 1306-1319)	aataggttgaggaggagcag (A)12-15 tcaagagtgtggagggggca	4919
OAT2	1	(intron 4 842)	ttgacctccaaaagtgtttg G/A attacaggcatgggcccattg	4920
OAT2	2	(intron 5 183)	ccacatccatcattcgagac A/C a/c actcgtctcagctgcccattg	4921
OAT2	3	(intron 5 184)	cacatccatcattcgagac a/c A/C actcgtctcagctgcccattg	4922
OAT2	4	(coding region 1269 (Ser423Ser))	actagactgctagtgtctctc C/T ggtgagcccagtcctcatagg	4923
OAT2	5	(3' untranslated region 17)	ataaatgtgtacatgagtgt A/G tgaacacacatacataaggt	4924
OAT2	6	(3' flanking region 1386)	tgtagcagccacacatcgcca G/A tgttcacacctgagagagag	4925
OAT3	1	(5' flanking region -463)	ttcctgagaggcaaatccccc T/C tcccctactcgggaggtgcc	4926
OAT3	2	(5' untranslated region -1)	cctgcccacagctctggtctc G/A tcttgcctccagtgccatgac	4927
OAT3	3	(coding region 153 (Pro51))	cctgtccaccactgtcgcgcc G/A ccccacaatgcctccacagg	4928
OAT3	4	(intron 2 177)	gcaccaagacccttggcttc T/C tccactcagagtccaagca	4929
OAT3	5	(intron 2 6201)	gtcctatctctctgtgtctct T/G tgcccagcagcaggttctctc	4930
OAT3	6	(intron 3 79)	tctgtctccaccgtgcaccc G/C caaagaggcaagagctggg	4931
OAT3	7	(coding region 723 (Thr241Thr))	tgccgttggctgcagttaac T/A gtgtccattcccttcttctgt	4932
OAT3	8	(intron 5 524)	tcgaagtacaaaggaaagtt T/C aaagagaagcctgagcctgg	4933
OAT3	9	(intron 7 386)	gaccaatgggttttcagactc G/A aagacaaaaattatgtttat	4934
OAT3	10	(intron 9 81)	attgtcctgtcctctaccca G/A gggagccatcctttatgaac	4935
OAT3	11	(5' flanking region (-661)-(-660))	tacatttgggtccccaggggg (G) aagcggctgatcaggagaga	4936
OAT3	11	(5' flanking region (-661)-(-660))	tacatttgggtccccaggggg aagcggctgatcaggagaga	4937
OAT3	12	(intron 8 211-212)	tctgacttggactggggcaaa AA/Δ gtatggtggtatctgtagat	4938
OATP1	1	(5' flanking region -916)	acagagttagatgtttcaataa G/A tatttgttgtatctgtgaga	4939
OATP1	2	(5' flanking region -843)	tagtgcagcagactatgcctt G/A atgtgtgtgtgtttgggatt	4940
OATP1	3	(5' flanking region -526)	aaatgtgtgctgtatgtta T/C acatctgtacatatatttcc	4941
OATP1	4	(5' flanking region -172)	acaacacacactcaagtat G/A tgtgttattaaaagttagcta	4942
OATP1	5	(intron 1 206)	ttgattcaggcaagttatgc C/G taaatggcttggagagactt	4943
OATP1	6	(intron 1 454)	caacataacaataatttctc G/A taagaaaaatggccattttg	4944
OATP1	7	(intron 1 999)	gtttagcaaggttagatatt A/G atgtggatgttaagacaaa	4945
OATP1	8	(intron 1 1223)	ttgctagaagctagtaggac C/T agctttataaatacacagat	4946
OATP1	9	(intron 1 1326)	aactagtttaggcaaccatg T/C gtttttaggg g/a aaaagcaatg	4947
OATP1	10	(intron 1 1336)	gcaacccatg t/c gtttttaggg G/A aaaagcaatgaggtcatgat	4948
OATP1	11	(intron 1 1498)	atagtttgcctcttaagaata C/T actctgagaaggtttatagt	4949
OATP1	12	(intron 1 5041)	ttatgtctcccgaggagttag C/T tctctaaatgcataaggaga	4950
OATP1	13	(intron 1 9532)	aaagactgggagcacttccc A/G atgacaaatactagactaga	4951
OATP1	14	(intron 2 961)	aaaaagtatatagaaatat A/G agtgtcactcctttctagt	4952
OATP1	15	(intron 2 1110)	gtctactagtgttcaactcc T/C ttagatcttagcctgtatca	4953
OATP1	16	(intron 2 1419)	aaagcctaagaaggatgcag T/C gcaatagcctatgtgagaag	4954
OATP1	17	(intron 2 3339)	tatggtttgcacaaaaactta T/C tcgtatatttgttttttcca	4955
OATP1	18	(intron 3 66)	caggaaatgaagtgtcactt T/C cctctctaggagcaatgctt	4956
OATP1	19	(intron 3 205)	tcagttttgtcaatttacac A/G atggggatttgggacctttt	4957
OATP1	20	(intron 3 6377)	aatgaatagactttgagtta C/T tggatttttagtggataaat	4958
OATP1	21	(intron 3 7238)	tgaatgtcacattttttaa G/A tttgtgttcttatctcata	4959
OATP1	22	(intron 4 1016)	ttttattctggattcatgtt T/C gtggaaattgcagtagtcca	4960
OATP1	23	(intron 5 110)	tccacaatgatgtagtagt A/G tcttggcacagtgtggccttc	4961
OATP1	24	(intron 6 496)	agtgtctgaattataagcca A/G ttttatagtgtgttgggacc	4962
OATP1	25	(intron 7 1934)	aaagtgaaggaaatttaaa G/C tgagaacttgagcctggaatg	4963
OATP1	26	(intron 7 2140)	tagaatgtaccaaataa G/A gcatctctgaggatgggacc	4964
OATP1	27	(intron 7 2365)	tgaatctctctttatcaact C/T gattttctccagactttac	4965
OATP1	28	(intron 8 88)	gcaactcctaagtgtgaagt G/C ttttaggatatatttttact	4966
OATP1	29	(intron 9 534)	tcatattttgtatttttaaa G/A ttatctgggttttactgaaa	4967
OATP1	30	(intron 9 1286)	tattctcttgagataaatca T/C tgaaggagtggctatgtggt	4968

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
OATP1	31	(intron 11 215)	ttcactcctattcctcgcta C/T tttcttctcttattttcttag	4969
OATP1	32	(intron 11 663)	ttcttctcttcttttgagctc T/A aaagtagagttcagttaatc	4970
OATP1	33	(intron 11 999)	atcatcactgcatgagagtt A/G gaattatctaaactttgtgat	4971
OATP1	34	(intron 11 16727)	tttctttttatttacaactt A/G tttacttttccaggtgtatga	4972
OATP1	35	(intron 12 48)	ctatcagaacaattattatta T/G tattattttttattacactt	4973
OATP1	36	(intron 12 686)	tatgtttttgataaaactttgc C/A gtacaaataaagaaaattga	4974
OATP1	37	(intron 12 708)	tacaataaagaaaattgaa A/G tattttccaaataaatcaagt	4975
OATP1	38	(intron 13 418)	tctctgggtctccaaatcat A/G tattttctccctcttta c/a at	4976
OATP1	39	(intron 13 436)	at a/g tattttctccctcttta C/A attttgtgtgaaacaattcttc	4977
OATP1	40	(3' untranslated region 2	gtctttaagaaccttaaaaa C/A ctcttaactcaaaataataa	4978
OATP1	41	(3' flanking region 57)	agtgaactaaagtttttctta C/A aaacaagtgtctgaatcaaa	4979
OATP1	42	(3' flanking region 572)	aatacactatggtttatttat G/A tgtactataaatggagtgag	4980
OATP1	43	(3' flanking region 788)	atttctcaaatgatcagatg C/T atcatatgaaaaagaaagc	4981
OATP1	44	(3' flanking region 1356)	agggtgactgacataaatggg G/A gcagaggacataatgaggtt	4982
OATP1	45	(5' untranslated region (-189)-(-188))	attttctaactctgtattaaa (A) gcgttccagggtatttttcta	4983
OATP1	45	(5' untranslated region (-189)-(-188))	attttctaactctgtattaaa gcgttccagggtatttttcta	4984
OATP1	46	(intron 4 725-726)	tgatctttaaagcggggaa AA/Δ caggcaagtacgctatagtt	4985
OATP1	47	(intron 4 1082-1083)	attgagtcaggaaacccaaa CA/Δ gtttcaaaaatttgaaaaat	4986
OATP1	48	(intron 4 2301)	aatgcatatgcttttttttt T/Δ aatgcagagtgtaaaagga	4987
OATP1	49	(intron 9 241-46)	attgtatgtgcatgtgggtg TGTGTG/Δ catgattgtctttgtgata	4988
OATP2	1	(5' flanking region -2574)	ggataaggcaaccctatgt A/G tcaactgctcaggagagggga	4989
OATP2	2	(5' flanking region -1723)	tctttcagacttcaaaagccc A/G tgatatttcatcagagctgt	4990
OATP2	3	(5' flanking region -1180)	tgcttattttaacaggcataa T/G ctttgggtctcctgagccaga	4991
OATP2	4	(5' flanking region -811)	tatgtgcatatgtgtatata G/A gtaaaagtgtgtatatatgt	4992
OATP2	5	(intron 1 7188)	aatcattttgaaatttaagaa A/G aaaatatgttcagagaaaaa	4993
OATP2	6	(intron 1 7331)	gtgaaatgaggaacaaagt T/C ccaccttttttctcctgaata	4994
OATP2	7	(intron 1 7391)	agagagatgtgaaatagat T/G tttctggggagtaggggaa	4995
OATP2	8	(intron 1 7886)	ttgttagtagaagaaaaatc G/A aagcctaaaactaaagggaag	4996
OATP2	9	(intron 1 7958)	ttgctattatataatttttt T/A a/t aaaaaagatttcttaatat	4997
OATP2	10	(intron 1 7959)	tgctattatataatttttt t/a A/T aaaaaagatttcttaatat	4998
OATP2	11	(intron 1 8036)	ggaaaaaatggggtgaaatt A/T atcaaaagggcagctttattac	4999
OATP2	12	(intron 1 9164)	acatttatattctatataaaa G/T agtcagttgaagtaaaagt	5000
OATP2	13	(intron 2 193)	tgattaagtatttcttttggc G/A aaatttttgatgcttaatat	5001
OATP2	14	(intron 2 1020)	ttgagtaacatttaggccaa G/A tggcagtcataaggaaaaag	5002
OATP2	15	(intron 2 14865)	agaggaattaatcataagag G/T tttatttggctaaagtgaaca	5003
OATP2	16	(intron 2 14931)	gttagttaaataacagaaaa A/T tatcagaaatttttaaaaaat	5004
OATP2	17	(intron 2 15417)	ttctaaaaataagtaagctaa A/T tattctatattataactacta	5005
OATP2	18	(intron 2 20823)	ttgtataagagatacaaaac A/C aattcctactaggggaaata	5006
OATP2	19	(intron 2 20852)	ctaggggaaataaagcttca G/C taaggaggtggcatttaagct	5007
OATP2	20	(intron 2 21360)	ttcaaaagctgtattttctca T/C tagtgctttttgtgaataaa	5008
OATP2	21	(intron 2 21467)	tatacacacaatacctgtcc A/G gaagatgtgtgtataagccaa	5009
OATP2	22	(intron 2 21621)	tatcaataacttatgaagaga A/G ctaactatttctaactaggga	5010
OATP2	23	(intron 2 22760)	ttccccacctcctgttgggt C/G tctctttaaactttctccttg	5011
OATP2	24	(intron 2 23199)	cctatctgcacataacatta C/T aaacttatggcaattata a/g a	5012
OATP2	25	(intron 2 23218)	a c/t aaacttatggcaattata A/G aactcaatacatattatact	5013
OATP2	26	(intron 2 23330)	gcccttgttctgttctctct G/A tacctgctcactacatag	5014
OATP2	27	(intron 2 23673)	ctggagacggtagctcaaac T/C gaggatgaaatagacattt	5015
OATP2	28	(intron 3 89)	ggttatcaactggggtaaat T/G tatctctcacaggcaatttg	5016
OATP2	29	(intron 3 224)	tgctaaatattctataatgc A/G caaagaatgatgtaactgaa	5017
OATP2	30	(intron 4 97)	ccctttaaattaggcagttac C/A ttttgagaagataccacta	5018
OATP2	31	(intron 4 568)	ttcatgatccaaattgtggc A/G acgtattttccaggcaacaag	5019
OATP2	32	(intron 4 599)	aggcaacaagatagaagaag A/G aaagaataagaagcaacaaa	5020
OATP2	33	(intron 4 753)	aaaatagacattattccaag T/A tacciaagttcccggttaaaa	5021
OATP2	34	(intron 4 781)	ttccgggttaaaaattcccaa G/C tataattactgtggaaggaa	5022
OATP2	35	(intron 4 1196)	aaggaccacaatctagatca G/T cattgctctaaatagccat	5023
OATP2	36	(intron 4 1229)	tatgccataatattgtgacac T/C tttgcaactgtgtattctac	5024
OATP2	37	(intron 4 1623)	catctagtgtgaaatggatta G/C attttatttttactacattt	5025
OATP2	38	(coding region 388 (Asn130Asp))	attctaaagaaactaatatc A/G attcatcagaaaaattcaaca	5026
OATP2	39	(coding region 452 (Asn151Ser))	taatcaaattttactactca A/G tagagcatcacctgagatag	5027
OATP2	40	(intron 5 165)	ttatataacacagttcgccc A/T ttaacaacacaggttttaaac	5028
OATP2	41	(intron 5 189)	acaacacaggttttaactac G/A c g/a ttttcaacttctatgcaaa	5029
OATP2	42	(intron 5 191)	aaacacaggttttaactac g/a c G/A ttttcaacttctatgcaaat	5030
OATP2	43	(intron 5 507)	atataactttgttttcattg C/T aaaaggcaaaact a/g ttatatc	5031
OATP2	44	(intron 5 520)	ttcattg c/t aaaaggcaaaact A/G ttatatcatttaagacttt	5032
OATP2	45	(intron 5 856)	agtcatgataaacctaatag A/G ataaaaacaaaaaagaaa	5033
OATP2	46	(intron 5 1157)	acagataatttttacttgggt T/C gtgcttttctgtatgatag	5034

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
OATP2	47	(intron 5 1226)	ccttgattgtaataatctcc A/C c a/c tgccaagagtggggccag	5035
OATP2	48	(intron 5 1228)	ttgattgtaataatctcc a/c c A/C tgccaagagtggggccaggt	5036
OATP2	49	(intron 5 1304)	actgttctcgtggaatgaa G/T aagtcctcacaagatctgatg	5037
OATP2	50	(intron 5 1348)	ttataaatgagagtccct G/A caaagctctcttgctgccc	5038
OATP2	51	(intron 5 1407)	ttgctctctctctatctcc G/A ccatgattgtgagggccccc	5039
OATP2	52	(coding region 521 (Val174Ala))	gtcatatcatgtggatatatg T/C gttcatgggtaatatgcttc	5040
OATP2	53	(coding region 571 (Leu191Leu))	gggagactcccatagtagca T/C tggggctttcttacattgat	5041
OATP2	54	(coding region 597 (Phe199Phe))	ctttcttacattgatgattt C/T gctaaagaaggacattcttc	5042
OATP2	55	(intron 7 33)	agaacaaggtaccatgataa C/T gtctttcttaagcacacatgc	5043
OATP2	56	(intron 7 267)	caaaataaccaaagttaaaa T/A gtctcctcccaactgact	5044
OATP2	57	(intron 7 1260)	gtaatctcacatttctctgc A/G tttaacatttggtaaaacttt	5045
OATP2	58	(intron 7 2273)	ttctcacgtcctatctatgcg C/T gattatgaccttagttact	5046
OATP2	59	(intron 8 207)	gtggaagagaattagggttg T/C acttttttagcaggagaaac	5047
OATP2	60	(intron 8 546)	tcgggagaagtttctcccta T/C gtaattagagtaaatattt a/c t	5048
OATP2	61	(intron 8 565)	a t/c gtaattagagtaaatattt A/C ttttggttaattatctatcta	5049
OATP2	62	(intron 8 668)	taagtaagtgtaaattaggat G/T catcagcatttgacagtgcc	5050
OATP2	63	(intron 8 739)	tggaagaaccattgagagtca A/G taaacaaagagaatgacttg	5051
OATP2	64	(intron 9 112)	attttagtaatacaggataa G/C tataattttctgtattctt	5052
OATP2	65	(intron 9 266)	ttagaggtagtatctgtata A/G ttggatctttataatttagtg	5053
OATP2	66	(intron 9 305)	tgctaagatctgagacaaac C/G cttttgtaattataatcatt	5054
OATP2	67	(intron 11 10224)	tacactgttccataaaaaa T/C tcctctatattattcttagt	5055
OATP2	68	(intron 11 10359)	attaatagattcaacgtgag G/C ttcccttaaaacttttagcta	5056
OATP2	69	(intron 11 10916)	cttatatagaaagaatcca C/G aaaactattttaccttttat	5057
OATP2	70	(intron 11 10997)	aatatattagtttgaacaa G/T gagacttcactaaatataat	5058
OATP2	71	(intron 11 11018)	gagacttcactaaatataat G/A caatgtatttgcagcactgt	5059
OATP2	72	(intron 12 442)	aacattccaaaactttttaa C/T ga c/t t c/a acagcatgacttt	5060
OATP2	73	(intron 12 445)	attccaaaaactttttaa c/t ga C/T t c/a acagcatgactttta	5061
OATP2	74	(intron 12 447)	tccaaaaactttttaa c/t ga c/t t C/A acagcatgactttttaa	5062
OATP2	75	(intron 12 907)	aatgaaaaagagctggcaga T/C tgaacatactgaatgagag	5063
OATP2	76	(intron 13 65)	tatatatatatatatata C/T acacacacatacatatatta	5064
OATP2	77	(intron 13 870)	aattctgagatctctatttc G/A atgtatccaatctgtggcac	5065
OATP2	78	(intron 13 1935)	taaaaaaaagagctctgc T/C tttaacagcaattgagccaag	5066
OATP2	79	(intron 13 2261)	aacgaatctccaaaattttt G/C aacttttatttaatacaaat	5067
OATP2	80	(intron 14 248)	tcaaggataataaccaactt G/A tcaaaaatcagagataatag	5068
OATP2	81	(intron 14 2463)	attgttttactaatatggaa C/G ctctctcaagacataatttt	5069
OATP2	82	(intron 14 2857)	tcacatgttatcttcaggac A/T cctggcaagatgcctctag	5070
OATP2	83	(intron 14 11458)	atctccagaggtcctgtgt C/T tccccaaagtcactgaccc	5071
OATP2	84	(3' untranslated region 22)	ataataaaaacaaactgtagg T/C agaaaaatgagagtactca	5072
OATP2	85	(3' untranslated region 24)	tccttaataaaaacaaatgagt A/G tcatacaggttagaggttaaa	5073
OATP2	86	(3' untranslated region 25)	cagagtttgaactataatc T/G aaggcctgaagctagcttg	5074
OATP2	87	(3' untranslated region 25)	gcctgaagcttagctgtggat A/G tatgtacataaatatctgt	5075
OATP2	88	(intron 1 457-458)	taattggcaaacataaaaaa (A) caggtgtctcaaaagtcacat	5076
OATP2	88	(intron 1 457-458)	taattggcaaacataaaaaa caggtgtctcaaaagtcacat	5077
OATP2	89	(intron 1 753 -7538)	gatcagcattacaaccaaga (G) atggagaatgacattcagga	5078
OATP2	89	(intron 1 753 -7538)	gatcagcattacaaccaaga atggagaatgacattcagga	5079
OATP2	90	(intron 1 10032-10035)	tgtgtgattctatattactt ACTT/Δ gtttcaaatctctctccaca	5080
OATP2	91	(intron 1 10058-10061)	ttcaaatctctctccacaaa TTTA/Δ tttttctattaaattgtaat	5081
OATP2	92	(intron 2 413-423)	acttatttataaaattctttt (A) 11-13 caaaaaacaggatttaaaaa	5082
OATP2	93	(intron 3 1595-1603)	ttgccaagtaattcaagtgc (T) 8-10 gtatttataaaacacttttca	5083
OATP2	94	(intron 4 10-23)	ttcatgggtagtaagtgtt (A) 12-14 cctctgtgcactatcagta	5084
OATP2	95	(intron 5 1567-1572)	gtgaatataaattacttgtta CTGTGA/Δ aattataaaaaataagtag	5085
OATP2	96	(intron 5 1577-1585)	attactgtacttgttaatt (A) 9-10 taagtagaataaataagagt	5086
OATP2	97	(intron 8 1939-1941)	ttctctaactctcttactct CTT/Δ atttcaagcagatgcaactg	5087
OATP2	98	(intron 10 3077-3078)	aaattctttatctacttttt (CTT) ttcctcttttctctgcttct	5088
OATP2	98	(intron 10 3077-3078)	aaattctttatctacttttt ttcctcttttctctgcttct	5089
OATP2	99	(intron 11 11011)	aacaag t/c gagacttcactaa A/Δ tataat g/a caatgtattt	5090
OATP2	100	(intron 12 1160-1169)	agcatgacatggttagagatg (A) 9-11 gcatttttaacatttgttaa	5091
OATP2	101	(intron 12 1310-1312)	tcctcttaataataaaatgt TGT/Δ ctactcaaaaggagaagtct	5092
OATP2	102	(intron 13 9-34)	tacgagcactaggtatgatg (A) 24-27 tatatatatatatatata	5093
OATP2	103	(intron 13 35-64)	aaaaaaaaaaaaaaaaaaaaa (TA) 10-21 c/t acacacacatacata	5094
OATP2	104	(intron 13 1379-1387)	aaaattattccaccacaatac (A) 8-10 caaagtaaaagttaagaac	5095
OATP2	105	(intron 13 1916-1928)	aattctcttaaaaataatgtt (A) 11-13 gtctgc t/c tttaacagaa	5096
OATP2	106	(intron 14 588-596)	caattatactttactctttt (A) 8-10 ctaatttcaaatcatatat	5097
OATP8	1	(5' flanking region -1413)	aataggggcttaataactct G/C aaacttatgatttctcatat	5098
OATP8	2	(intron 1 38962)	atgaaattagtttaaaaaata G/A caaccttaactatactctctc	5099
OATP8	3	(intron 2 253)	acagacttaccacaaagaa T/G tatccttcccaaaatgtcta	5100
OATP8	4	(intron 2 329)	actcatgggttgcaaatata C/G tttttaggaaactttatctc	5101

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
OATP8	5	(intron 2 2568)	ccattctggtgctttcttcc G/A tgaactattttccatcagt	5102
OATP8	6	(intron 2 2679)	ctcttattgctcttcttccca T/C gttttaatctaaataattta	5103
OATP8	7	(intron 2 2753)	caggaaactttcacaaagcc C/A ctaattaatttaagctccct	5104
OATP8	8	(intron 2 3132)	tgggttaatgtaggagagtt T/C accttcacagtttaaatata	5105
OATP8	9	(intron 2 3193)	aatgtcttgggcatatttgc A/G ttcatttggggca t/c tcaagt	5106
OATP8	10	(intron 2 3207)	atttgc a/g ttcatttggggca T/C tcagtcttactagatacaaa	5107
OATP8	11	(coding region 334 (Ser112Ala))	gaactggaagtattttgaca T/G ctttaccacattttctcatg	5108
OATP8	12	(intron 3 76)	agaattttattttttatactt G/A taagtgggcagttacctttt	5109
OATP8	13	(intron 3 2443)	tcaatttcatgttgcctctta C/T agttatagggtattctaaaga	5110
OATP8	14	(intron 4 67)	taatcacgtctataaagttt C/G tgatattctttaacaaaatt	5111
OATP8	15	(intron 4 91)	tattctttaacaaaattgat T/A taagaacaaataggaagaac	5112
OATP8	16	(intron 4 197)	ggtttgaactgcacctgttc G/A cttatgtgcagcttttctcc	5113
OATP8	17	(intron 4 813)	tttaacagataaaaaaaa T/A attttgaacgcaaaaagaa	5114
OATP8	18	(intron 4 974)	atatgcaccttaaaaaaac C/G tggatttttaaatatgtaat	5115
OATP8	19	(intron 4 1003)	taaatatgtaagtacataa G/T gaattattgcatttttgt	5116
OATP8	20	(intron 6 155)	cattaataatcagaataaaa A/G agaaatttagctcctattta	5117
OATP8	21	(intron 6 750)	atccaactggggttttagatt T/G cctctttctgctctctctcc	5118
OATP8	22	(intron 6 780)	gcctctctctccatctgcacc C/T tctcttttctcagcaaaaa	5119
OATP8	23	(intron 6 1248)	ctatgccctgtaattctcaca C/T ttcctcttattttaaaattgg	5120
OATP8	24	(intron 6 1500)	tcgtgtctgtgttagcatat A/G ataactcatcagggtttgtg	5121
OATP8	25	(intron 6 2008)	ataacataaatgagtaaga A/G tatcaaggcagggaatttag	5122
OATP8	26	(intron 6 2087)	actactctctcccatcacac T/C aaaactcatgtgctcccccag	5123
OATP8	27	(intron 6 12305)	tcactatggaggactgcaa T/C cattatcattattttcccaga	5124
OATP8	28	(intron 7 363)	taacaaatgataccagccat C/G atactattctctggttaatag	5125
OATP8	29	(intron 7 411)	cctttattttttgagaaacct G/A gtggatgatattaaga c/a gta	5126
OATP8	30	(intron 7 428)	cct g/a gtggatgatattaaga C/A gtatatagatcactgttaata	5127
OATP8	31	(intron 7 634)	aaaatttatatatatacatat A/G taactttacctaagtattca	5128
OATP8	32	(intron 7 1791)	tgttttttaaaaggttagtga T/C gtgaatagtaaaagcgaattt	5129
OATP8	33	(intron 7 2000)	agttgagcaaatgtctctca G/A gtatcataatgtcacttgaa	5130
OATP8	34	(intron 7 2043)	gtttattgtatccatttttta A/G tggatcaacattgtagttag	5131
OATP8	35	(intron 7 2171)	atttattttgagcaaaaggtc G/A c g/a actct c/t cttagaaagc	5132
OATP8	36	(intron 7 2173)	ttattttgagcaaaaggtc g/a c G/A actct c/t ttagaaagcctc	5133
OATP8	37	(intron 7 2179)	tgagcaaaaggtc g/a c g/a actct C/T ttagaaagcctcacaatt	5134
OATP8	38	(intron 7 2219)	atttgaactttaagttctta T/G ataacttatattttacaaaaat	5135
OATP8	39	(intron 7 2261)	cgatattataatatatttt A/T ttattgaaatagtgtatttt	5136
OATP8	40	(intron 8 150)	acaaaattttctccatcttgt A/G ata t/a catcgttgttttgcatt	5137
OATP8	41	(intron 8 154)	aatttctccatcttgt a/g ata T/A catcgttgttttgcatttga	5138
OATP8	42	(intron 8 1303)	tttttttgagatggagttct C/T gctctgttgccaggctggg	5139
OATP8	43	(intron 8 1372)	aagctccgctctccagggttc T/G ccaccctctctttaagaaa	5140
OATP8	44	(coding region 1272 (Leu424Leu))	tccttctgttttcaacttct A/G tatttccctctaatctgcga	5141
OATP8	45	(intron 10 63)	tcacagatttgattttaataa A/T tacttatcaaatcttccctat	5142
OATP8	46	(intron 10 911)	cttgcccaatctcctaccaa C/T gtattattaaacggcagtgga	5143
OATP8	47	(intron 10 972)	tcctagtttctctgaagata G/A gctacaactttagtaaaact	5144
OATP8	48	(intron 10 1101)	tcctgggtctctgtgtgttcc A/T g t/c agtgaagacctgaaagag	5145
OATP8	49	(intron 10 1103)	cctggtctctgtgtgttcc a/t g T/C agtgaagacctgaaagag	5146
OATP8	50	(intron 10 2027)	ccatttttcatgagtggtcta A/G g/a ttttgtcccggtttcaaaact	5147
OATP8	51	(intron 10 2028)	ccatttttcatgagtggtcta G/A ttttgtcccggtttcaaaacta	5148
OATP8	52	(intron 10 2372)	tgtatttggcaaatgtattt G/T ttaatttttcaaaaactatt	5149
OATP8	53	(intron 11 10538)	caacagaggatcaatgtaaa T/G gaaatctcttaaaattaaaca	5150
OATP8	54	(intron 12 55)	ataaatattaatgttaata C/T taaagactgaatgcaattaa	5151
OATP8	55	(intron 12 1802)	taaaatgaatcggttaaaaca T/G tcatgtataaatcactgtca	5152
OATP8	56	(intron 12 2612)	ataggcatataaatactcttt C/A ttcctctgtatataggag	5153
OATP8	57	(coding region 1833 (Gly611Gly))	aacagctgtggagcacaagg G/A gctttaggatataataatc	5154
OATP8	58	(5' flanking region (-1590)-(-1587))	tacataacatatacctatat CTAT/Δ gttatgtgtctgtcttatata	5155
OATP8	59	(5' untranslated region (-28)-(-11))	agcatcagcaacaattaaaa ATATTCACTGGTATCTG/Δ tagtttaataatggaccaac	5156
OATP8	60	(5' untranslated region (-7)-(-4))	tattcacttggatctgttag TTTA/Δ ataatggaccaacatcaaca	5157
OATP8	61	(intron 4 213-214)	ttc g/a cttatatgcagctttt (T) gtccaaccaaacagaaggag	5158
OATP8	61	(intron 4 213-214)	ttc g/a cttatatgcagctttt gtccaaccaaacagaaggag	5159
OATP8	62	(intron 4 505)	tataactttctctttataaa G/Δ atgcaaaatgttatagcatt	5160
OATP8	63	(intron 4 616)	aatgaagtggaggaaaaaaa A/Δ tgatttcaagttttctgtct	5161
OATP8	64	(intron 4 804-812)	acatccatgttttaacagaat (A) 9-11 t/a attttgaacgcaaaaag	5162
OATP8	65	(intron 4 855)	agattgttttaaccaaatag G/Δ aaactattattcaacacact	5163
OATP8	66	(intron 7 619-628)	ttttatatatgaattaaaa (AT) 4-5 catat a/g taatcttaccta	5164
OATP8	67	(intron 7 1773-1779)	attttctatatattgaactg (T) 7-8 aagggtagtga t/c gtgaata	5165

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
OATP8	68	(intron 8 1270-1290)	tagtgtgcccaccottctctc (T)19-23 gagatggagtct c/t gctc	5166
OATP8	69	(intron 10 665)	aactcaaggctttttttt T/Δ ccatgtgacacatctcgt	5167
OATP8	70	(intron 11 247-250)	aaaaatcttaaggcacacac TGAT/Δ tgacagttgccttgattgta	5168
OATP8	71	(intron 12 1622-1630)	aaataaattgttgacctc (T)8-10 atttttctaagggctcgctgt	5169
OATP8	72	(3' untranslated region 2464-2465)	cctgatgccttttaaaaaaa A/Δ tgaacaccttttgatgtatt	5170
TAP1	1	5'flanking - 673	agctaagagtcacagcacc G/C ctttttccaccagcctcgcg	5171
TAP1	2	5'flanking - 646	ccaccagcctcgctgctcgt T/G tcccttcacggacactctag	5172
TAP1	3	5'flanking - 563	ttgcaagcgttgctgtctac A/C ggccacctccctcgctcctc	5173
TAP1	4	5'flanking - 236	gctttgcgcgcggcgctaac G/T tgtgtagggcagatctgccc	5174
TAP1	5	intron 3 + 408	aaggaaactgaggccaagac C/T ctaaatgctgaaactgcaca	5175
TAP1	6	exon 4 + 153	ccctcaccatggtcaccctg A/G tcacctgctctgcttttc	5176
TAP1	7	intron 4 + 289	gtatttcttttagcatccaag G/T ggcatagctgtgtctcttct	5177
TAP1	8	intron 4 + 291	atttcttttagcatccaaggg C/G catagctgtgtctcttctc	5178
TAP1	9	intron 5 + 1139	ttcttctcaggttaagtactg C/T ggttctttgtgtctctctca	5179
TAP1	10	intron 7 + 375	gtctctgcccctgtctttgc C/T gcttctctatctctactcc	5180
TAP1	11	3'flanking + 71	agcgcaacttttcagctgcgg G/A tgtctctctttttatcatcc	5181
TAP1	12	3'flanking + 129	aactgcacacaccttttccct T/C aagcttttttaattctctatga	5182
TAP1	13	3'flanking + 459	cattcaggaggagccaggtc G/A tgtgacgtcgacagttgctg	5183
TAP2	1	intron 3 + 8	tctcctttggcaggtaggtg G/A tgggcagctgggtccatttg	5184
TAP2	2	intron 4 + 104	cttcaccctgatgccaggac C/T tggggatgcttttctcttctg	5185
TAP2	3	intron 10 + 219	gcagcagttgtgtctctctc A/G tgggcagcccgctcaggtcc	5186
TAP2	4	intron11 + (317-319)	atgggtgccaggtggatgtg GTG/Δ tccatctcattctcgtcttt	5187
TAP2	5	exon 12 + 19	agctgcaggactggaattcc T/C gtggggatgcacagtgctg	5188
TAP2	6	exon 12 + (356-357)	aggtgggtgtgggtgtgggtg GG/TGGTGGGTGGA ggcgtctctgtctc	5189
OCTN1	1	intron1+6602	aggcgagccaggttatgtgg C/T gaaggataaggcctcttccc	5190
OCTN1	2	intron1+6790	gacaaaaggggaaaaccttc C/T gtgataggcaggtttgtgga	5191
OCTN1	3	intron1+14019	cactgtctcccactgggccc G/A ccatgtcactgttaaccaca	5192
OCTN1	4	intron1+14136	ccggtttcttaagaaaagcc T/C tttctaaaggaccctctta	5193
OCTN1	5	intron1+14266	agctttccaaaaagacactt G/T cggcaccataactccccaaa	5194
OCTN1	6	intron1+14412	cttggggcaaacggccactg C/T gtgtgcattggctctctctgt	5195
OCTN1	7	intron1+15776	acataggagacactctcttc G/A gatctcagttatcagaacaa	5196
OCTN1	8	intron1+15817	ctgtgctctctgcgaataagc A/G gactactctggatactgtaa	5197
OCTN1	9	intron1+15889	agagccagtttttggagccccc G/A tctggcaagcaggcagggccc	5198
OCTN1	10	intron1+16063	acctctgtctgtctgcagaat A/G aggtgtgatataaataatgtg	5199
OCTN1	11	intron2+1105	atatttccacaaggtctcttg C/A gtacactgctccactgtcttt	5200
OCTN1	12	intron3+1022	cttctgtcaagttgccagga T/C ggaaatattccaaactctact	5201
OCTN1	13	intron3+1217	tccccttctctgcagggggaa G/A gagcgggggcaagattttctt	5202
OCTN1	14	intron3+1596	aagccagagaagctctctcc G/A tgggaatgggaacaaggtgg	5203
OCTN1	15	intron3+1720	ggagcctccaaagcctcccc G/A tgtgagcgggtgagggcagg	5204
OCTN1	16	intron3+2104	tatgagactcgtgtgtgtgg G/A ttctcaggtctgaaagtta	5205
OCTN1	17	intron3+8323	cttttccccttttctaagtg G/C tgatagtttgaaacttaact	5206
OCTN1	18	intron4+926	tttttggaaactcacaattta G/T actagacctcatggttgccc	5207
OCTN1	19	intron4+1055	cacctgtctgacgagatagc G/A caggtcaggtgggctcactc	5208
OCTN1	20	intron5+ (1197-1202)	caacaacaacaacaacaaca ACAACA/Δ ttggagtgctcttaacacttc	5209
OCTN1	21	intron5+ (2071-2083)	gttctgctcattgctcatgc (T)11-13 caaaaaaagaactaaggca	5210
OCTN1	22	intron5+2781	tgatcattcttagaaaaag G/A acactcacattttggagagga	5211
OCTN1	23	intron6+ (882-917)	toctactctatgatggcagc (AC)15-18 gatgatcgtcagaactgta	5212
OCTN1	24	intron6+924	acacacacacacacgatgat A/C gtcagaactggttagatttag	5213
OCTN1	25	intron7+511	attattgatagtaaatagaa T/C acatatttcttaataataag	5214
OCTN1	26	exon8+124	ggtoagggaacatggcggtgg G/A ggtoacatccacggcctcca	5215
OCTN1	27	intron8+3514	acacacacacctgaaacat G/A tatgaattctcaggaaaaggt	5216
OCTN1	28	intron8+3902	aagcaagatgaggatctgtt T/C ttctcctgtgtgagtaaagc	5217
OCTN1	29	intron8+ (4064-4089)	gtgaacataaacttagttg (T)18-26 gagtctcatagcctgtgga	5218
OCTN1	30	3'flanking+115	aaccaaatgattatatgcag T/A attctctatccagaaaacctt	5219
OCTN2	1	5'flanking - 225	cggcgctagaggagcaggtt C/T ggaactggaccaccaaggcct	5220
OCTN2	2	5'flanking - 124	gctggcagaggccgggcttc G/T ccaggtccccaggacaggcc	5221
OCTN2	3	5'flanking - 13	ggcgccgctctgctgccc C/G gggggcgcccttgcggccca	5222
OCTN2	4	intron 1 + 232	ggtggtcagtcgtgctctcc G/A tctgtatggccactttgaag	5223
OCTN2	5	intron 1 + 314	atggcctctgtgtgtccagga C/T ttactctagttggggttggg	5224
OCTN2	6	intron 1 + 5055	catgtggtacactagacat G/A tctgactgttgatagctga	5225
OCTN2	7	intron 1 + 6437	gaagcttggcctcacacaca G/C aggcgggcacccctgtcatca	5226
OCTN2	8	intron 2 + (173-174)	tagtaagaagagccaacaaa TC/Δ atctgactccgtaattcttg	5227
OCTN2	9	intron 2 + 608	agcaggttatttgtataatt C/A taaagcttttaactcaagga	5228
OCTN2	10	intron 2 + 4370	taatttattgatatccaagt G/A cctctataatagatgctca	5229
OCTN2	11	intron 5 + 969	caccagaaaggggtctctgt C/T gcaaggttcaggcaggagt	5230
OCTN2	12	exon 10 + (1028-1044)	ttagctcctctggtttgtgtc (T)16-18 aaaaagaaactcactctgga	5231
OCT1	1	intron 1 + 7715	tagtctgactcacacatgg G/T tctgtgcttttctctctct	5232
OCT1	2	intron 2 + 97	ggtggagacatgaccagtt G/A gaattaaactgcagaagctgc	5233
OCT1	3	intron 2 + 797	gtggagtgtgtgaaacact C/G tttaaaagagtgtggggagg	5234

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
OCT1	4	intron 2 + 1768	ctggaactggagagggctctg T/C gggcactgcccggctgagct	5235
OCT1	5	intron 3 + 1244	gcagatggtaaaggagcaga C/T gcggaagcgacggctcaggg	5236
OCT1	6	intron 4 + 865	agcgtccagtggttaggaag G/T ctccacaggtggcaatccca	5237
OCT1	7	intron 4 + 1028	gtcatctctgctcttctccc A/G cttcttcatttttatagtac	5238
OCT1	8	intron 4 + 1040	cttctccacttcttctcatt T/G tatagtactattggtattat	5239
OCT1	9	intron 4 + 1485	agcctgcccttcccctgcct C/T gtccttggtgaacagggtac	5240
OCT1	10	intron 4 + 1997	tgagggattacagccccaac G/A tggggaggcgaggtgcact	5241
OCT1	11	exon 5 + 9	tggtgttcgcaggtgtgtgc C/T ggagtccccctgggtgctgt	5242
OCT1	12	exon 5 + 20	ggtgtgtgcggaggtccctc C/G ggtggtgtgtatcacaaaa	5243
OCT1	13	intron 6 + 379	gaggaagtccattccctcat A/G tctaaacacctagagacct	5244
OCT1	14	intron 6 + 2125	tattgacccaaatctgttct C/A acaatgtaaatatgactgta	5245
OCT1	15	intron 6 + (2935-2953)	tttctccatctgcgaggggc (T)18-20 cttcagttctgactcatgc	5246
OCT1	16	intron 7 + (6-7)	ttttatctcacctggtaagt (TGTAAGT) tggttaagttgtctgctttc	5247
OCT1	16	intron 7 + (6-7)	ttttatctcacctggtaagt tggttaagttgtctgctttc	5248
OCT1	17	intron 7 + (1780-1781)	gttttcttttcccttttttt (T) catggagaaagacagagaa	5249
OCT1	17	intron 7 + (1780-1781)	gttttcttttcccttttttt catggagaaagacagagaa	5250
OCT1	18	intron 8 + 3247	ccaggccaacaattccatt G/T tcatggccactggggccaagg	5251
OCT1	19	intron 8 + 10521	cccttaaccaatgtaacgcca G/A tggcagatccctcattctga	5252
OCT1	20	intron 10 + 393	tcagattcttttagtaacttt G/C ttcacaaaattcttttgaca	5253
OCT1	21	3'flanking + 1755	tgaatgatgtttttcaaatg T/C gtattaaaaatgtcctctct	5254
OCT1	22	3'flanking + 1799	ctttcttagaattctcttgg G/Δ caaaactcttgaggaagccc	5255
OCT2	1	intron 2 + 1329	tggcagcagaagggaagg G/Δ ataaaagttggagggcacagc	5256
OCT2	2	intron 2 + 1867	cctctgtcaaggttaagtact C/Δ attattcttcccccaaggc	5257
OCT2	3	intron 9 + (340-343)	cagcagggccctaacctctct CTCT/Δ gctgatttccacccttctctg	5258
OCT2	4	intron 9 - 396	atacataattcattactttt A/G ttgtctagaaatgacctcaag	5259
OCT2	5	intron 9 - 386	cattacttttatttgctaga A/C atgatcccaagtttctgactt	5260
OCT2	6	intron 9 - 86	atagaaaaatgctaaaaaa A/Δ gtttttaacaaaaataaggg	5261
OCT2	7	intron 10 + 1725	tggaagaggcccttgaatcc G/A agcggaggtcacacactcgc	5262
OCT2	8	intron 10 - 195	caagataatttttaggaataa C/T tctgtctgacatgagttatca	5263
OCT2	9	exon 11 + 328	gttttctggaggggtttttt T/Δ ccatctttgtatttttttaa	5264
OCT2	10	exon 11 + 427	aggcaaacaaaatagaaaa A/T gtgtgaaaaacagttaagtt	5265
OCT2	11	exon 11 + 455	aaacagtaaaagttgggagag G/A agcatctatttttcttaaaga	5266
OCT2	12	3'flanking + 34	agaatgtatgtcaagaattt T/A agataggcctttcagtaaca	5267
NTCP	1	exon 1 + 307	tatggcatcatgcccctcac G/A gccctttgtgctgggcaagg	5268
NTCP	2	intron 1 + 607	cccagcaccactccagata G/C gccagcccatctcagccac	5269
NTCP	3	intron 1 + 702	gcagaaatcagcaagggtc G/A ctctggagagcgcagcacac	5270
NTCP	4	intron 1 + (3950-3966)	cacatcacctaacagcttgc (T)14-17 gagaataggcatgtaaga	5271
NTCP	5	intron 1 + 9597	aaggacatattattcaggct C/G tgagtgatcataatttatttt	5272
NTCP	6	intron 2 + 4808	cctatggagaagcaactacc C/T ggggccacttgtctcagcag	5273
NTCP	7	intron 2 + 5032	acacctgggagactagcagag G/C cagctttccaccaggatca	5274
NTCP	8	intron 2 + 5046	gcagaggcagctttccacc A/T ggatcatatcaaatatgtg	5275
NTCP	9	intron 3 + (8-21)	gcctcaatggagcgttagtta (T)12-15 aagaaagggtctcactctgt	5276
NTCP	10	intron 4 + (484-495)	taataataaccagaataaag (A)10-13 gattcctcaactctagtac	5277
NTCP	11	intron 4 + (728-754)	tgaccttaacaccaaattt (A)25-27 caggacattcaaaaccactt	5278
NTCP	12	intron 4 + 747	taaaaaataaaaaa A/C aaaaaaacaggacattcaaa	5279
NTCP	13	intron 4 + 1339	ccccagtggaacactaaat C/A aaagcaactgtatttcttgg	5280
NTCP	14	intron 4 + 1545	accagggacaagaagggtta G/C atcaattgggggtggagg	5281
NTCP	15	3'flanking + 559	caagacaatatagttttcgg G/A tatcagtttggcaaatgtgc	5282
PEPT1	1	exon 1 + 25	ctgccaggagcacgtccgc C/T ggcaggtcgcaggagccctg	5283
PEPT1	2	intron 1 + 88	cgagggccgggagggcgcaa G/A ggtacggcgggcggggaagc	5284
PEPT1	3	intron 1 + 106	aagggtacggcgggcgggga A/T gcggggcgacccgaaggccc	5285
PEPT1	4	intron 1 + 248	cgaggttgatcctctggccc G/A cccgcccgtggggcaactgta	5286
PEPT1	5	intron 1 + 326	tggaaggggaggggaccag C/A gggtagcggcgaggggcgga	5287
PEPT1	6	intron 1 + 1238	tttagcatttccagcagatc C/T aatcccagagctgttagag	5288
PEPT1	7	intron 1 + 3001	tcttatatgctgggaagaa C/T gtcagtaagaaaaagcagc	5289
PEPT1	8	intron 1 + 5673	ttgggaagtgccacagccac G/C gggcacagggacaggtctt	5290
PEPT1	9	intron 1 + 5679	agtgcacagccacggggca C/G agggacagggtcttccacag	5291
PEPT1	10	intron 1 + 5917	aaattcacaaaatgtacttc C/T ataagaaggctcgtaaaag	5292
PEPT1	11	intron 1 + 5966	ctaggcatttagaacttcta C/T aatctgcccctagtgcacaa	5293
PEPT1	12	intron 1 + 9255	tggtcatttccagcctcttc A/G gcctatgatttttagatagt	5294
PEPT1	13	intron 1 + 10278	catgacccatgtaggcgga A/G aagcagccctgtagcagcag	5295
PEPT1	14	intron 1 + 20251	aagaagagcctgtgtttatt C/T agtgattgcaatgtgtggg	5296
PEPT1	15	intron 1 + 20509	aaacaccacttctgcatttg C/A gctttctaaagtagcaatcc	5297
PEPT1	16	intron 1 + 20532	tttctaagatagcaatctg T/C tgacacagggtacattaagat	5298
PEPT1	17	intron 3 + 55	agagcgggagtgccataac C/Δ agtccctaactttgtttcccc	5299
PEPT1	18	intron 5 + 1720	atcctctcttttactgaaaa C/A aataaagctacaaaagacc	5300
PEPT1	19	intron 5 + 1790	gctactgttttatgttttcc G/A gatggtaaatattatagatgg	5301
PEPT1	20	intron 5 + 1860	agtttgcatctgactatcac G/A ctgcattcctgtgagctggc	5302
PEPT1	21	intron 5 + 1943	aggccactgagggaacctg G/A ggaagagagggccttctac	5303
PEPT1	22	intron 8 + 1478	tgttttcagatcttagtagt A/G catggaataggaccgttttc	5304

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
PEPT1	23	intron 8 + 1898	ttaaatattagtggtaaaag A/G aaacatagactcaatctctt	5305
PEPT1	24	intron 10 + 388	ttaaatagtttagacatttt C/T gattttctaaagaaaactgc	5306
PEPT1	25	intron 11 + 985	atccataaggtactcagtg C/T tggcctgtatgaagaactca	5307
PEPT1	26	intron 11 + (1022-1045)	ctcaaacaggggtagatttc (T)20-24 gagtcaagagttctcactctg	5308
PEPT1	27	intron 11 + 1320	tgtgagccactgcacctggc C/T aatttctgactttctatga	5309
PEPT1	28	exon 16 + 107	tggagagatggtgacacttg G/C cccaatgtctcaagtaagta	5310
PEPT1	29	intron 18 + 6048	tttgttgttgggttttttt T/Δ gttgttgttgtttgttttg	5311
PEPT1	30	intron 18 + (6141-6142)	tcactgcagcctccgcccc (T) gggttcaagcaattatctg	5312
PEPT1	30	intron 18 + (6141-6142)	tcactgcagcctccgcccc gggttcaagcaattatctg	5313
PEPT1	31	intron 18 + (6241-6242)	tatttttagtagagacgggg (G) tttcaccatattggccaggc	5314
PEPT1	31	intron 18 + (6241-6242)	tatttttagtagagacgggg tttcaccatattggccaggc	5315
PEPT1	32	intron 18 + 12102	gtgggaattcttagctaaagg C/T cgtgtggtctgtctcaggt	5316
PEPT1	33	intron 18 + 12203	gacctgagtttaattcatag C/A cattttctcccagcacctaa	5317
PEPT1	34	intron 18 + 12307	gaaaggttaaatattcttt A/G cactgtgaggtgtacacta	5318
PEPT1	35	intron 20 + 79	tcacaaacacttaggacata A/G tatgatttaactagagtgat	5319
PEPT1	36	exon 23 + (348-370)	tcttttttcttttcttttc (T)18-23 gagacagagttttgctcttg	5320
PEPT1	37	exon 23 + 790	ccacattgttcattcttccct A/G tcacacaaatgatgttattt	5321
PEPT1	38	3'flanking + 2	aaataaatttctgttcttaa G/A cctaagtggttcatgtatctc	5322
EPHX1	1	intron 1 + 110	tgcaaaatgtgtcttactag C/T ttctagtgcataaaatattg	5323
EPHX1	2	intron 1 + 143	aaatatttgggtgagctcttc G/A ctgtgctgggcccagtcacca	5324
EPHX1	3	intron 1 + 1097	aatccagagagggagataga T/G tggaggttcaaggggtgaca	5325
EPHX1	4	intron 1 + 1717	ttccaaagacagagcgagggg T/C gctgtggggcggtgtttgc	5326
EPHX1	5	intron 1 + 1772	aaactgatgtcttctctctcc G/T tctgggtcctaactgcagtg	5327
EPHX1	6	intron 1 + 2054	gaaatgtaacagggcaacact A/G tggacacagaaagttagata	5328
EPHX1	7	intron 2 + 1414	atttccaaaaatctgttttggg G/T gtaactgaacacttgggaa	5329
EPHX1	8	exon 3 + 174	taccttcacttcaagactaa G/A attgaaggtatgtttgcaaa	5330
EPHX1	9	intron 3 + 6583	ctgtcaaatccatgaagggg G/C ggcgggggacctaaaggttg	5331
EPHX1	10	intron 4 + 34	agagggttccataactgcgcc G/A tctctgccaaaggttgggcc	5332
EPHX1	11	intron 4 + 63	aaggggtggggccgggtgtcc C/T accaggctctctctccggcg	5333
EPHX1	12	intron 5 + 154	gcagtgctgagggcacgttg G/A cttggatcctctctgtctga	5334
EPHX1	13	intron 5 + 276	tgtgtgaccaaagctctggga T/C agccctgagcagaactcccc	5335
EPHX1	14	exon 6 + 130	gatgtggagctgtgtgtacc C/T gtcaaggagaaggtattcta	5336
EPHX1	15	intron 8 + 206	gggtgcctgggtcccgggcg G/A cctcagtagcctccccagt	5337
EPHX1	16	intron 8 + 353	tggccctcccagaaaagaga A/G ggcctcagtgaggggagag	5338
EPHX1	17	3'flanking + 708	aggtgcagactcatgcactc A/G gccctgaagaggtgagagag	5339
EPHX2	1	5'flanking - (523-522)	aaagtcaactggatatgcccc (C) tccccccgcccccaacacgg	5340
EPHX2	1	5'flanking - (523-522)	aaagtcaactggatatgcccc tccccccgcccccaacacgg	5341
EPHX2	2	5'flanking - 522	aaagtcaactggatatgcccc T/C cccccgcccccaacacggt	5342
EPHX2	3	5'flanking - 521	aagtcaactggatatgcccc C/T cccccgcccccaacacggtc	5343
EPHX2	4	5'flanking - 516	actggatatgccccctcccc G/C ccccccaacacggtcttatg	5344
EPHX2	5	5'flanking - 515	ctggatatgccccctcccc G/C ccccccaacacggtcttatgt	5345
EPHX2	6	intron 1 - 74	tggctgtcttctcaatgaata T/C gaacagtgtctgtttccatg	5346
EPHX2	7	intron 3 + 72	gagccttaggtcagaatcca T/C tgaagttagctttgagatca	5347
EPHX2	8	intron 4 + 473	gtgtgtctctactttaatct A/G caaaaggtgattgaatggag	5348
EPHX2	9	intron 5 + 276	caagagtggagtggttcaagg C/T catcctgacctcacttttga	5349
EPHX2	10	intron 8 + 8	tctgtctctcccggtgggtg T/C gctgtcttgcagctgtctta	5350
EPHX2	11	intron 9 + 1573	atgtctgtgaagactgatga C/T gatggacgggtgcactgtctc	5351
EPHX2	12	intron 10 + 207	gaacaggatggagatgagct T/C gtttattgtcttttaatga	5352
EPHX2	13	intron 12 + 911	tgaagagacctcgacatgtc G/T catccacatactacaggga	5353
EPHX2	14	intron 12 + 2425	atcttctcagctgagcaaac C/T gaggtctcagagggcttaacc	5354
EPHX2	15	intron 12 + 2460	ttaaccccaactggcccaag G/A ccaggtacatgattgggtca	5355
EPHX2	16	intron 12 - 281	aagtcctttcaagagattat T/C ataagttagtaccttctcatt	5356
EPHX2	17	intron 12 - 268	agattattataagtagtacc T/G tctcattataggaatattga	5357
EPHX2	18	exon 13 + 50	cctgagtcggactttcaaaa G/T cctcttcagagcaagcgatg	5358
EPHX2	19	intron 13 + 1739	ttgtctgaacaggggttttca G/T atgagcatatttcttttga	5359
EPHX2	20	exon 14 + 33	atgcataaagctctgtgaagc G/A ggtaagagacatgcttggga	5360
EPHX2	21	intron 14 + 314	ggatttgagacttacctcta T/C gggggctcactctgtgtatgc	5361
EPHX2	22	intron 14 + 878	attcccttattccttcacac C/T gtctgtcactcattcatca	5362
EPHX2	23	intron 14 + 948	gcacaggctgggtatgaagc T/C ggggctgcatgctcagctac	5363
EPHX2	24	intron 15 + 259	agaggggttttactactttt C/T agtcatggctcctcagagaa	5364
EPHX2	25	intron 16 + 459	tctctatttgtcaagcagaa G/C atgagtttccaatctctggg	5365
EPHX2	26	intron 16 + 645	gtaaagtgaacacactgttac G/A tgccagacttctgcccagac	5366
EPHX2	27	intron 16 + 985	gtcattatcatcatatgacc G/A atgaaaatgacaaactgca	5367
EPHX2	28	3'flanking + 12	aggtggccttacacacatct T/C gcattggatggcagcattgtt	5368
EPHX2	29	3'flanking + 374	tgttcacggagaaatgcacgg C/T atggggatgaacctttccc	5369
EPHX2	30	3'flanking + 544	tagccacctgcctttctccc G/A gcttccctagcagagtttgc	5370
COMT	1	5'flanking - 1287	cgtatgatattccccattct G/A agtccagaataacctagaaat	5371
COMT	2	5'flanking - 1217	tgtgagtatgggaaggggaa G/A cttttctgtctgtgttccc	5372
COMT	3	5'flanking - 503	caggggtcctcaggaggacga G/A tgtgtatcctccattgtctc	5373
COMT	4	5'flanking - 425	gagaagttgggaagctctggc C/T agtggggccggtgctctgtg	5374

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
COMT	5	5'flanking - 277	cccagccccagtttccccac C/T tgggaagggggctacttgbg	5375
COMT	6	intron 1 + 12058	ctggcccatggaaggagg G/A agggggccccgacggggcca	5376
COMT	7	intron 1 + 12070	agggagggggagggggcccc G/A cgggggccacagtaaaggagt	5377
COMT	8	intron 1 + 18831	tgtgtatgttcttgggtaaac C/T agcccttgggtttacacatc	5378
COMT	9	intron 2 + 832	cctctcctttggccaccgt G/C actaccccccaactccggggc	5379
COMT	10	intron 3 + 90	ggagaagctgttatcacc G/A ttccagggggctgggaacc	5380
COMT	11	intron 3 + 425	ccccagggtgggctgggtcgg T/G gattcagagagggcagctct	5381
COMT	12	intron 3 + 671	ggctcctgctctttgggaga G/A gtggggggccgtgctgggg	5382
COMT	13	intron 3 + 676	ctgtcttttgggagaggtgg G/T gggcgtgctggggatcca	5383
COMT	14	intron 5 + 75	tcagcctcagcctctccaaa G/C agccaggcattccagtagag	5384
COMT	15	intron 5 + 310	accagacacaggggcagaaa C/T ggcacaggaccaaggagatg	5385
COMT	16	intron 5 + 346	agatgggtgggggaaggccc G/A ctctggggccagcctgctct	5386
COMT	17	intron 5 + 3023	aaggcagccgctgctcaa G/A gcttaggccattgtctcct	5387
GAMT	1	intron 1 + 429	ctcggaagctgagctcagg G/A agacagctgtccccgggggtg	5388
GAMT	2	intron 5 + 1411	ggtagcctgggtgccatccc G/A accagagacgcaggtgcc	5389
GAMT	3	3'flanking + 626	cactgacctcttgcctga G/A agaaggccggctcctgtgct	5390
PNMT	1	5'flanking - 367	aagaggtgaatggctgctgg G/A ggctggagaagagatggg	5391
PNMT	2	intron 1 + 35	ctgaggcagcaggggacaaga G/T gtcgtcggggagtgaaagca	5392
HNMT	1	5'flanking - 211	cagaggcagatgacagctct C/T cgtaaaagatttcactgtg	5393
HNMT	2	intron 1 + 5409	aatataactgatataattgg A/G acatttcatgttggcctagt	5394
HNMT	3	intron 2 + 2561	cacttgtgcttgggacagaa A/G agaaggcctacaagaaaaag	5395
HNMT	4	intron 2 + 2895	caatcagaaaatgtaagaaaa A/C ctccaagaaaaatttaagt	5396
HNMT	5	intron 2 + 3977	accaaacttggagtgtaaa G/A ttatgcatgtatgttcatgt	5397
HNMT	6	intron 2 + 5296	ttacatagtgagtttggag T/C cccaggattttatttccct	5398
HNMT	7	intron 2 + 13317	caacctcatgaattcttag C/T tgggatgggtccctataaca	5399
HNMT	8	intron 2 + 14682	gtagatgagcaaatgagttc A/A ggagagatttaaatcccta	5400
HNMT	9	intron 2 + 15406	gtctatgcatctcatgcc G/A tctaaccagctgtctacctta	5401
HNMT	10	intron 2 + 28943	atgtgactttaaacttcaggt A/G tatcaatatcccttgaatgt	5402
HNMT	11	intron 4 + 49	cagaagaagacttttcaga A/G tatatatataatgaatatct	5403
HNMT	12	intron 4 + (1942-1943)	tttgagaaaaatttaaggta (A) tcttctatggcccacttcca	5404
HNMT	12	intron 4 + (1942-1943)	tttgagaaaaatttaaggta tcttctatggcccacttcca	5405
HNMT	13	intron 4 + 2405	ccctgtgaccaaagcagataa C/A ctcatgctttatttagtcca	5406
HNMT	14	intron 5 + (80-81)	cctgtgtttgaaagaagctt (TT) atatatatttgccttcattat	5407
HNMT	14	intron 5 + (80-81)	cctgtgtttgaaagaagctt atatatatttgccttcattat	5408
HNMT	15	intron 5 + 235	ctttcttttgggaaaaatg T/C ctttgccttctatatatgaa	5409
HNMT	16	intron 5 + (702-703)	tacttacaggttgatttttag (AT) acacagcagactctgtcttc	5410
HNMT	16	intron 5 + (702-703)	tacttacaggttgatttttag acacagcagactctgtcttc	5411
HNMT	17	intron 5 + 749	ttacaccagacccatactt T/G aacaccatagtccacaaaat	5412
HNMT	18	intron 5 + 1101	gtaggcagcctattcttgat T/G atattcatcaatcacaaga	5413
HNMT	19	intron 5 + 1137	acagaaaaagtattgtagac G/A gaaataacaattcattgaga	5414
HNMT	20	intron 5 + 1348	aaggagcatgaatagtcca C/G aagtaactgagaactgatta	5415
HNMT	21	intron 5 + 1673	caaaagaaaggagtaaaaga C/G tcaacaatcagttagctttt	5416
HNMT	22	intron 5 + 2022	attttatttggggctttcta C/T gtctctctctcctaagccta	5417
HNMT	23	intron 5 + 2285	tgctacttaactctttaa G/C atccagagtaaatgatggag	5418
HNMT	24	intron 5 + 4159	taccagttgacccagcaacc C/T tcttatagagtattttaa	5419
HNMT	25	intron 5 + 4501	aatgatccacaaaattacta C/G tcattgttttcttccaatga	5420
HNMT	26	intron 5 + 5251	cacacacacacacacaca C/G caaatggaagcagccagaca	5421
HNMT	27	intron 5 + 5802	gaaaaagaaaatctggctta C/T atcatgttgaaaacaaaagt	5422
HNMT	28	intron 5 + 6189	tccaattccaccttctccta G/C agcatatcctgcagttacct	5423
HNMT	29	intron 5 + 6297	gtcttgggttcatctctttag T/A taaattagatctgggaactt	5424
HNMT	30	3'flanking + 458	tatgtcactctcaagaactc C/T tataagaccaagagtcact	5425
HNMT	31	3'flanking + 993	ctgaaaatgaacactgaacc G/A ttaatcactatgatgtac	5426
HNMT	32	3'flanking + 1793	gtggagcacagcatttttag G/A cttgatatttgccttattata	5427
NNMT	1	5'flanking - 228	ataatttctctgacgagctc A/T agtgctccctctggtctaca	5428
NNMT	2	intron 1 + 44	cccactaatgtgagtcata T/C agatggagctcagggcacg	5429
NNMT	3	intron 1 + 149	ggataaaaacgaatattgg G/A tagcgattccacagtttaca	5430
NNMT	4	intron 2 + 158	agataggcccatgtgtgtgc G/A tgttagtaaatttgtgtatg	5431
NNMT	5	intron 2 + 433	gctgtagccatccaagccta T/C agaacttggctgtgagtgtg	5432
NNMT	6	intron 2 + 10826	atcatctgactgtgaagttc C/T agttctgtgtgaactcaagt	5433
NNMT	7	intron 2 + 13630	atttcatggagggaagtcca T/C ggtagaagcaggctgctagg	5434
NNMT	8	3'flanking + 71	ggctcagtggttggggccca A/G tgggtcatcttaggacgggac	5435
PEMT	1	intron 1 + (297-299)	attgtgtgagactcagaggt TGT/A cctgttagtcttggggatt	5436
PEMT	2	intron 1 + 817	tcatgaagcctgttaaggcac A/G tctctgcccccaagcagcttc	5437
PEMT	3	intron 1 + 830	aaggcacatctctgccccaa G/A cagcttctaataccagttctt	5438
PEMT	4	intron 1 + 1035	gagttctctgaaggagctaa T/C accagtttagtgttttgaaga	5439
PEMT	5	intron 1 + 1573	agtgggcaggggagactaac C/T ggggtgtgtgaggggtgggct	5440
PEMT	6	intron 1 + 1759	gatttttcttaagaaagaa A/G gaaagaaacatacaacatac	5441
PEMT	7	intron 1 + 2768	gcattcttgcgtccacagge C/A ggggcacctccaggattcag	5442
PEMT	8	intron 1 + 2785	ggccggggccacctccagat T/C cagaagatgactccagtagg	5443
PEMT	9	exon 2 + 162	agctcagcagacctcctggc C/T gtggtggtagctccttcttc	5444

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
PEMT	10	intron 2 + 4598	cctgtgggttttttttttttt t/Δ cttcattttcttggttgctg	5445
PEMT	11	intron 4 + 39	actgtccagacgggagtatc C/T cactgttggtagcccccac	5446
PEMT	12	intron 4 + 1317	accgtccccagctggcccca G/A cctcctgacatgggctctg	5447
PEMT	13	intron 4 + 1355	ctggagccaggctgcagccg A/C agtgccctggccatcctggcg	5448
PEMT	14	intron 4 + 5925	gtccaggcactgtggcccta C/T gtgggagtctccagtctcca	5449
PEMT	15	intron 4 + 6028	ggcagtggtcccaaggaccag G/C atggactccctctctcacc	5450
PEMT	16	intron 4 + 6078	atctgtaccctcgcggactc C/T acctggcttcgtgccatcac	5451
PEMT	17	intron 4 + 6089	cgcggaactctacctggcttc A/G tgcoatcaccccgccagat	5452
PEMT	18	intron 4 + 6379	tcaggtgtccctccctcat G/A cctcctcaccctgccctctc	5453
PEMT	19	intron 4 + 7339	tgtaaggaatcctgcccaaga C/T ggcagatgcacacggggtca	5454
PEMT	20	intron 4 + 7619	ctcctgcacatgtgctccag A/G gaggaaagcatttgacagg	5455
PEMT	21	intron 4 + 8858	ggcatgtgtgtgtgtgtgta T/G gtgtgtgagtgtgtgcattg	5456
PEMT	22	intron 4 + 9029	tttctggaccagaaagcgctc G/A tctctgcoagggcctcttg	5457
PEMT	23	intron 4 + 9056	gccagggcctcttgcacttg C/T gggaaagctgagctgagctg	5458
PEMT	24	intron 4 + 9512	ctgagctggggcagcagcatt A/G cctctgtgtgctgtggcact	5459
PEMT	25	intron 4 + 9523	agcagcattactctgtgtgc T/C gctggcactggccttggtgg	5460
PEMT	26	intron 4 + 9622	gacaaagtgtacaacaaggt G/A tctcgaactgggtcagctca	5461
PEMT	27	intron 4 + 10776	ccattcctgggtctctcttg G/A aggtgaatgaatccatg	5462
PEMT	28	intron 4 + 10912	tctgccccactttgtcaga G/C gtgcaacaagggccttcagga	5463
PEMT	29	intron 4 + 11590	ggacactggcctgatgcaga G/C gtgtgtgtctctctcctgcag	5464
PEMT	30	intron 4 + 12090	ggccagggcaccctaccag G/C ctgagtcctcactgtccagc	5465
PEMT	31	intron 4 + 12263	taaccgccttccagatgga G/A cgggctgctcatgggactta	5466
PEMT	32	intron 4 + 12448	tctgggtccctctcctgctt G/A tagttctctgggtctaaatc	5467
PEMT	33	intron 4 + 12730	tgggaccagtgcgcaccaca C/T ggcocaaaggaactgtgtgt	5468
PEMT	34	intron 4 + 13240	gggtctccaggcacacagcgg G/A ccagtagcacctgtcgttt	5469
PEMT	35	intron 4 + 13494	tccttggaactcagagatgg T/C acctcctgcgaggtggggc	5470
PEMT	36	intron 4 + 13817	aactctccctctgctgtgag A/G cagatcttggagcctcgccc	5471
PEMT	37	intron 4 + 14773	cgcctctgtgtctcatgccc C/T ctatgctctcactgctctg	5472
PEMT	38	intron 4 + 14951	gtcctgagggccctccccc G/A gagcctggggtgccctcaca	5473
PEMT	39	intron 4 + 16896	gctgtgactgtcttggagac T/C gggctctggcgggctgtgtg	5474
PEMT	40	intron 4 + 19439	ccaggagcctctgaggcagc G/A ggggcttctcaaccacacac	5475
PEMT	41	intron 4 + 19557	attttgtcagcatgtcacgt C/T cctttcataatgaagcaagg	5476
PEMT	42	intron 4 + 20051	acagcactgcgggagccacg A/G catctgcagacgcatttgat	5477
PEMT	43	intron 4 + 20816	tggactctctggcgtccatc C/T agccacttcagtgccagctg	5478
PEMT	44	intron 4 + 21196	ggctggctgggcccctgggag C/G atcgtgacaggttttagtgg	5479
PEMT	45	intron 4 + 21528	acaggtgggagccgagggctc G/T ggaagtgggcgggctgagc	5480
PEMT	46	intron 4 + 21596	ccgcttcccgctgctgtggc C/T gtgacagaaagtgtccact	5481
PEMT	47	intron 4 + 22672	agcctccactgccttctgtg C/T tgaggggagggggccgggtg	5482
PEMT	48	intron 4 + 22713	tctaacgctgtctctcttgt A/T ctgaaacacaaacacctct	5483
PEMT	49	intron 4 + 23010	tgccgggcagcggggagggga G/A ggcagtggttcccccaagt	5484
PEMT	50	intron 4 + 23588	gtgcaggcgcctctgcacccc C/T gcagccaaagtcttggcgga	5485
PEMT	51	intron 4 + 23627	gacactgccttgagccagga C/T ggtgaggtgggacgcttcc	5486
PEMT	52	intron 4 + 23941	tgaggggttgggactctaca G/A aggaagtgagactcacgggg	5487
PEMT	53	intron 4 + 24091	gacacctcttctactgtcagc G/T ctgagacacgcccctgccct	5488
PEMT	54	intron 4 + 25348	caggccagttggaatcctac G/A tagagtgaagcattctcagc	5489
PEMT	55	intron 4 + 25603	taagcagttaacactgatgc G/A tgatgaaaattccaacagca	5490
PEMT	56	intron 4 + 31540	cctccaggtggcaggaacac T/C gtgaggagcatgcaacgtgc	5491
PEMT	57	intron 4 + 31637	gtgggctgggacgcccaggac G/A gtgaggggttcaaggtgtg	5492
PEMT	58	intron 4 + 31642	ctgggacgcccagggcggta G/A gggcttcaaggtgtgtttgt	5493
PEMT	59	intron 4 + 35593	ggaggagctgaaagacttg G/A gctcgggatcaggtgtgtca	5494
PEMT	60	intron 4 + 35647	actttgagccaccacgcac C/A tgtccgtgcgtgagggagac	5495
PEMT	61	intron 4 + 35862	tcccagtggtggtctctgcc C/T cgtctcagccagcactcag	5496
PEMT	62	intron 4 + 35882	ccgtctcagccgagcactca T/G cggccaggggtggctggactc	5497
PEMT	63	intron 4 + 37141	ccacaggccggatgccttga T/C acttctcagctgcagggctg	5498
PEMT	64	intron 4 + 38862	tggaagagccacctcagaca C/G caaggacgggcatgccatgg	5499
PEMT	65	intron 4 + 38872	acctcagacagcaaggacgg G/T catgccatgggtcccggcag	5500
PEMT	66	intron 4 + 39140	atgtctcaaatctccctccc C/T gggaaatctaggcacaggtc	5501
PEMT	67	intron 4 + 39635	caggcccaggagcaggtggg G/T cctcctcacaggagcagggc	5502
PEMT	68	intron 4 + 39713	actctgagcatgctggctcc C/T tcttcttccagggcagca	5503
PEMT	69	intron 4 + 40436	cctggttgtgtctcggaccc G/A gaggcagacagaggagcct	5504
PEMT	70	intron 4 + 47485	acaatgactgttgagccct C/T gagcaggctgtgtcactgtg	5505
PEMT	71	intron 4 + 48131	actggggatcctgaatccc G/A cctcctgatgccaagtggagc	5506
PEMT	72	intron 4 + 48558	cacagtgtgaactgttaggc C/G acagccacatcttgcggag	5507
PEMT	73	intron 4 + 48702	gagatggggggcgttcggga G/A gcaaaagcaggaaggcagaa	5508
PEMT	74	intron 4 + 50302	gcattgtcatgggagagcc T/C gtcccatctgagtgaggacc	5509
PEMT	75	intron 4 + 54102	ggccgcgtgctcctgcagcc A/T tgggctctctgagcttct	5510
PEMT	76	intron 4 + 54220	cccagggacagatcttctcc G/A ccagacgtctcttctgctc	5511
PEMT	77	intron 4 + 54371	gcagataatgtgcagctggg G/A tgcattgtgtgtgtgctcc	5512
PEMT	78	exon 5 + 79	tggcctgctactctctaaagc G/C tcaccatctctgctctgaac	5513
PEMT	79	intron 5 - 6796	ggaggaagtgcagctctctac A/C gatggtggctcccagcttcc	5514

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
PEMT	80	intron 5 - 6636	ttttctctctcaccttttg T/C gttcagaggcagaggtgtgc	5515
PEMT	81	intron 5 - 6448	gttggggccaggtctctgacag G/A accctcgggaccagctcctg	5516
PEMT	82	intron 5 - 5218	ggagccctggctgaagaagc C/G ttacgaccaaggcctggagg	5517
PEMT	83	intron 5 - 4824	ggacagggccgggggttgagc G/A gctgcatgaaggaggagg	5518
PEMT	84	intron 5 - 4249	tcaccagagtgatttctctcg C/A ggcaggtgcctggggtagcc	5519
PEMT	85	intron 5 - 4230	gaggcaggtgcctggggttag C/T cactgggagggtccatgag	5520
PEMT	86	intron 5 - 4182	ggagagtaagggtggggggg G/A cacttaggacagggaaagctg	5521
PEMT	87	intron 5 - 3369	ccaggtggggcggtgtgcct G/C tggcctggtgtgtggccag	5522
PEMT	88	intron 5 - 2625	cagggaagctgggcccgtga C/T gagctgggcttttggccac	5523
PEMT	89	intron 5 - 1200	attattgtgagcatgggaag A/T gcacatttgggtcacacatgt	5524
PEMT	90	intron 6 + 606	gcctggctagacgccaccca A/G tgaccctgatgatggcagca	5525
PEMT	91	intron 6 + 1229	tttggtccaggaagggggac G/A gcagccaggagcgtctggtat	5526
PEMT	92	intron 7 + 716	atggagatgtgctcccccg C/G gggtcagaggacctgcggtc	5527
PEMT	93	intron 7 + 1537	ctctgggggacgcataagcc G/A cctccagaggacatcagcca	5528
PEMT	94	intron 7 + 1718	gggcttcacagtgcttgagc T/C ccccgccatgtaggacccca	5529
PEMT	95	intron 7 + 2695	ggctttgggggacctggac C/T catttctagaaaacagcctt	5530
PEMT	96	intron 8 + 140	ccagggctccaggtcagag C/T ggccatggttagcttacaatg	5531
PEMT	97	3'flanking + 179	tacttaggagcgctcagggg C/T tcacctggccatggccatgg	5532
PEMT	98	3'flanking + 394	gatgacactgtcattcctaa A/G tgaatggcctgtgtgctgacc	5533
ALDH1A1	1	intron 1 + 564	cattattttctcagccaagt T/C tgttgccattggagcagatg	5534
ALDH1A1	2	intron 1 + 710	gtcttgagagtaactctgaa C/T tttgctgtttcacactgct	5535
ALDH1A1	3	intron 1 - 3868	ccctttttatattccagaata C/G agcctaaactcttctctctg	5536
ALDH1A1	4	intron 2 + 2933	taagtatgctatactatatt T/C gatagataactatactata	5537
ALDH1A1	5	intron 2 - 1646	caatgtgattaaactgaatgc C/T gcaaatatgcactgtatatg	5538
ALDH1A1	6	exon 3 + 54	caggcttttcagattggatc C/T ccgtggcgtactatggatgc	5539
ALDH1A1	7	intron 3 + 157	taggccccttaacattgaac T/G attctcaaatagtaactctgc	5540
ALDH1A1	8	intron 3 + 339	tgagctctcttagaatgat G/A ttaggttttattcaagcattt	5541
ALDH1A1	9	intron 3 + 655	agcagtttagatgagtcagag C/A ataataatgtgggggaggg	5542
ALDH1A1	10	intron 3 + 735	gaagccaatttaacataaac C/A aataccaagatcaggtttca	5543
ALDH1A1	11	intron 3 + 863	gcaagtatgggtaatacaag G/A accatttattactcaaatat	5544
ALDH1A1	12	intron 3 + 1757	agatgacaaagatttcttcta T/A ttcaaaaattccctagcaca	5545
ALDH1A1	13	intron 5 + 90	ttctctaaacagatggatg C/A ttatgtatttgttaaatgtg	5546
ALDH1A1	14	intron 6 + 213	caggaaagccaaacaaaagg T/C ttgggtgtcaaacagctcaact	5547
ALDH1A1	15	intron 6 + 1323	ttttgaattaaattcttata C/T tgaattcttttaacttttta	5548
ALDH1A1	16	intron 7 + 638	gcaaaagaaagtgttggaag C/A atactgtaccatgcataaaaa	5549
ALDH1A1	17	intron 9 + (1462-1463)	aatggaattctatgtttttt (T) gttgtgattattttatctatc	5550
ALDH1A1	17	intron 9 + (1462-1463)	aatggaattctatgtttttt gttgtgattattttatctatc	5551
ALDH1A1	18	intron 9 + 1757	tgatctagaatttagtttct A/G taaatgaatagaatccagtg	5552
ALDH1A1	19	intron 12 - 1383	aatcccacttattactctcc T/G gagagcttcaagtcctata	5553
ALDH1A1	20	3'flanking + 40	ttttaagtacaagttttggt T/C acagtgattttctctgttca	5554
ALDH1A2	1	5'flanking - 716	cagggtactctattctgagc C/G cgaggcgagggggactcgca	5555
ALDH1A2	2	intron 1 + 314	cggtcccgactgcgcgggg G/Δ aaggcgtcggaaccgcttag	5556
ALDH1A2	3	intron 1 + (664-675)	ttttgaactgaagaacttac (T)11-13 ataacgaactgtgacatctt	5557
ALDH1A2	4	intron 1 + 1370	gcattgcagcttagaagtttt A/G ttttatgaggggtctcttaacc	5558
ALDH1A2	5	intron 1 + 1557	ggtagcttttttcagaattta A/Δ ttgggaagctcttccagttc	5559
ALDH1A2	6	intron 1 + 1934	tcagctcttttagtgagactt C/G taaattttctaaagacaagca	5560
ALDH1A2	7	intron 1 + (1971-1980)	agcatgtgggcaagcagta (T)9-11 aaactgtgaagcagagaagct	5561
ALDH1A2	8	intron 1 + 2295	tactgtaagacaatatgtta T/C tgtttttgtcttctgtaaac	5562
ALDH1A2	9	intron 1 + 2387	ttgggcccacatagagtca C/T tacttaaaataaatgaccag	5563
ALDH1A2	10	intron 1 + 2841	aggaatgtgcttttttaaac T/Δ agatggtgttagtcaaggag	5564
ALDH1A2	11	intron 1 + 3035	gacttttataattttgtata A/G ctgatattataggaatacac	5565
ALDH1A2	12	intron 1 + 3319	aaagagttatgttttttttt T/Δ ctgcatctgatattatagg	5566
ALDH1A2	13	intron 1 + 3474	ttgtctttttattttatcat T/C taaactctgtttttctgggg	5567
ALDH1A2	14	intron 1 + 4186	ccctccaaacctttaactaa G/C attgtctgttttgggtcataa	5568
ALDH1A2	15	intron 1 + 4222	cataaattgtcagtcacaaact A/G catgttaataagaggacttca	5569
ALDH1A2	16	intron 1 + 4254	aggacttcaggttttttttt T/Δ aaatacttttccataactat	5570
ALDH1A2	17	intron 1 + 4397	ccctccactacatgggctt A/G tgttaccatgtggaattatc	5571
ALDH1A2	18	intron 1 + 5935	aactccaggttgcaaataga T/C gtttctggtatttttaagtag	5572
ALDH1A2	19	intron 1 + 6206	ttttgaaagccctcttagca T/G ttctttaatttctttattga	5573
ALDH1A2	20	intron 1 + 9559	agataaattgatgaattatt C/T actctgtgtgctgtgatagat	5574
ALDH1A2	21	intron 1 + (9631-9632)	taaaaagaatttctaaaaga (AAGA) ccttttttttgaataactct	5575
ALDH1A2	21	intron 1 + (9631-9632)	taaaaagaatttctaaaaga ccttttttttgaataactct	5576
ALDH1A2	22	intron 1 + 12731	ctgaaatagaacacttttcag T/A gtacctgtgcagagcagtgaa	5577
ALDH1A2	23	intron 1 + 13442	cagtgctcataaagatccagc G/A gaaatcaaaatgtttcatat	5578
ALDH1A2	24	intron 1 + (14173-14176)	tctaaaaataaataaata AAAA/Δ gagaaaattaagtttaagat	5579
ALDH1A2	25	intron 1 + 14586	actcatttattgggtcaaac C/G cttcttcaaccttaggatag	5580
ALDH1A2	26	intron 1 + 14595	ttgggttcaagacctcttcca A/G ccttaggatatgcattgagg	5581
ALDH1A2	27	intron 1 + 14711	gtttgagacattaacttcta A/G tccaactgaagatgctagtt	5582
ALDH1A2	28	intron 1 + (15327-15337)	gaagagcacagtagaagac (T)9-11 aaccttagcaataactattga	5583
ALDH1A2	29	intron 1 + 17258	atcagtcacatgtgtgggc A/G tacaacacttaatttaaaat	5584

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ALDH1A2	30	intron 1 + 18277	taatacaaatcatttgaagc A/G ttctactatataaaaaacaaa	5585
ALDH1A2	31	intron 1 + 18734	ctttgagcaccctactgcatt T/A taagtgcgtttaagatgtgg	5586
ALDH1A2	32	intron 1 + 19081	ttaatcacctcaatctttaa C/T gaatttcttgattttcttt	5587
ALDH1A2	33	intron 1 + 21514	aatcaggatattgggggttc G/A ttctttattctgccacaaa	5588
ALDH1A2	34	intron 1 + 21732	cattttaaaatagtgcttta A/G taggacttggtgttaaaagt	5589
ALDH1A2	35	intron 1 + 21865	tggcataggtttaaaaatgt C/T tgttgtaggactcttttcca	5590
ALDH1A2	36	intron 1 + 26282	taaagaaggagaaaaaaa A/Δ ctaatctgagactttgcagg	5591
ALDH1A2	37	intron 1 + 27805	ggatgatgctacccaaggaa T/C tgcacacttccagacagtac	5592
ALDH1A2	38	intron 1 + 28204	tcactccatttttaactgt C/G ctctcctaagtgtgtggttaa	5593
ALDH1A2	39	intron 1 + 28521	tcctttgttacacttctttaa T/C cggggtatcagataatcttc	5594
ALDH1A2	40	intron 1 + 49478	gaataaaaggataggacat G/T ggtaagaccactttttccct	5595
ALDH1A2	41	intron 1 + 49834	gcctctcaattttctcatgt G/T taatagagagaaaacctgc	5596
ALDH1A2	42	intron 1 + 50351	gactgactgggttcataagtt C/G agaaatttcactgtggtgtc	5597
ALDH1A2	43	intron 1 + 51181	tgattattaccatagtagttc C/T gtaacacttggccgttgact	5598
ALDH1A2	44	intron 3 + 654	ttaacctctcttgagtaaaa G/A gaatccttcagaaccagg	5599
ALDH1A2	45	intron 3 + 668	gtaaaaggaaatcctcagaa C/T cagaggggatgtacggacc	5600
ALDH1A2	46	intron 3 + 712	catacacttctgtcccggtt G/T ccctgtcattctgtgagcca	5601
ALDH1A2	47	intron 3 + 1273	tattcactagtgtaaaaagg T/A gtttcatgggtgaagaaattc	5602
ALDH1A2	48	intron 3 + 1743	ccacacctaaatgagattcc C/T gttttaaacactctcaagct	5603
ALDH1A2	49	intron 3 + 2891	tgcacatatatactcattgt A/G gtttttactaggaactagac	5604
ALDH1A2	50	intron 3 + 2919	ctaggaactagaccacactg G/A cagtactagaaatcttttta	5605
ALDH1A2	51	intron 3 + 3054	tggaaagtctctggggaactta G/C tatctctccatttctcttc	5606
ALDH1A2	52	intron 4 + 290	cattgtgctagattaggtgc T/C ggggtaggtatgaaggggca	5607
ALDH1A2	53	intron 4 + 380	ctccttgccctcctgaacaa T/C ataagatctactctttggaa	5608
ALDH1A2	54	intron 4 + 461	gattatggctgattttcagtt G/T tcttttaataattttctct	5609
ALDH1A2	55	intron 4 + 506	tctatatttctcgaacggcc G/A tgaattactttcataatcta	5610
ALDH1A2	56	intron 4 + 1952	ttggtcccccactccactgt C/G atttcattattaaaacaaca	5611
ALDH1A2	57	intron 4 + 2079	ctctatttggcctaaccgta C/T cttggttttcttttacttcc	5612
ALDH1A2	58	intron 4 + 2519	ttgggtcataagagctctct C/G catggtgtctcaaacagatg	5613
ALDH1A2	59	intron 4 + (2840-2851)	tttgtctctgcatacttggc (T)11-13 cacagtgaagtctggaatat	5614
ALDH1A2	60	intron 4 + 7231	aataggatacaaatacacaa A/T gatagtgttcagatccttaa	5615
ALDH1A2	61	intron 4 + 7958	taaaatcgtttttattgtta C/T taggtatataaaattgtcta	5616
ALDH1A2	62	intron 4 + 8090	tctgattttatcactgttta C/T agattgcttagtcatactca	5617
ALDH1A2	63	intron 4 + 12823	tgttagcctgtagctaaatg C/T ttttcaaatatgtgaaagg	5618
ALDH1A2	64	intron 4 + 12939	atgagggtccgacttttaaga T/C ttttgctacattttcttcc	5619
ALDH1A2	65	intron 4 + 14935	tattgatggagttcttttta T/G aaatggacttttacccttct	5620
ALDH1A2	66	intron 4 + 15321	gcattttgggtgtctgagaga C/T atatccagaaatatgctatg	5621
ALDH1A2	67	intron 4 + 15412	tttcaagtttatctctgttt T/G tttttttttttttttttttg	5622
ALDH1A2	68	intron 5 + 1888	aatccaaacatctgtacttt G/T tagtggacagatttatgtc	5623
ALDH1A2	69	intron 7 + 9166	gaaaagctactttattcaaa G/A ataaaagtattttaagaaaa	5624
ALDH1A2	70	intron 7 + 9914	aagctggagaaaaactagg C/T ttttctcaacagtgtattcc	5625
ALDH1A2	71	intron 7 + 18942	tttggagggggaactaatccc G/A tgacttctaggttatctct	5626
ALDH1A2	72	intron 7 + 19820	ttcaccctcatttttaggtt A/G ggggaggtggcttgctacag	5627
ALDH1A2	73	intron 7 + 19826	cctcatttttaggttagggga G/A gtggcttgctacagttttag	5628
ALDH1A2	74	intron 7 + 19913	cgtgaatcattcagttatttt A/G tttaaaaatcaccagtttgaa	5629
ALDH1A2	75	intron 7 + (20110-20111)	catgatttattctctaacta (ACTA) tgctaagtcaaaagattctgc	5630
ALDH1A2	75	intron 7 + (20110-20111)	catgatttattctctaacta tgctaagtcaaaagattctgc	5631
ALDH1A2	76	intron 7 + 21857	acaatgaaaattaagaagg A/T gaagagggaagaagcagaga	5632
ALDH1A2	77	intron 7 + 21929	tacaagacacaggcatcttt A/G actagtttactgggatctct	5633
ALDH1A2	78	intron 7 + 23308	ggctttgacttcggaacct G/T tgggttataacaaagtactg	5634
ALDH1A2	79	intron 7 + 23554	gacattgggtgaaaaccagg C/T tggtttaggagtgctctgtcc	5635
ALDH1A2	80	intron 7 + (23701-23703)	catctgagatttgccttctg GTG/Δ tttaccgagtttagtgggtgc	5636
ALDH1A2	81	intron 7 + 26479	gatacatgaacaatttgggtt T/C atcctcatgatattcttcaa	5637
ALDH1A2	82	intron 7 + 26561	taaaggccacaatgcagtga T/C tgaaatctccagttacattt	5638
ALDH1A2	83	intron 7 + 26662	tttcttagtctcttccatca C/T gaaactaaagctgtcttcca	5639
ALDH1A2	84	intron 8 + 76	tttatatctccacttttgat G/A ggacactagcaaaagattt	5640
ALDH1A2	85	intron 8 + (700-711)	accatctcattcagtgatc (T)11-12 ccttccacttgttggcaggc	5641
ALDH1A2	86	intron 8 + 724	ttttttttccctccactgtt T/C gccaggcagagctgctttcc	5642
ALDH1A2	87	intron 8 + 800	cagattgcttgaatttcagc C/A ccagcttggaaatttgcagag	5643
ALDH1A2	88	intron 8 + 1251	gatttctgtgaaaattgaga G/A gatctggcaacctggggctc	5644
ALDH1A2	89	intron 8 + 1627	ggccctcccccaggcaaac G/A gtgagaaatggctgtttcc	5645
ALDH1A2	90	exon 9 + 141	tggagcgggccaagaggcgc G/A tagtggggagctcccttgac	5646
ALDH1A2	91	intron 9 + 778	aaccagctctggacagatccc T/C tgtagcttgtgaaagtgtag	5647
ALDH1A2	92	intron 9 + 801	tagcttgtgaaagtgttagga A/G gtgaaggctggctcacttc	5648
ALDH1A2	93	intron 9 + 868	tctgaaggcctctgtgactt T/C agtgggggtggggaggccac	5649
ALDH1A2	94	intron 9 + 1338	aatttttgcctcttttact A/G tcaatacaacttgcctaagtt	5650
ALDH1A2	95	intron 10 + (227-229)	ctatgtgcttatgattatta TTA/Δ gccaacagaacaatcagaat	5651
ALDH1A2	96	intron 10 + 316	ctaaatgtgggtcactggga T/C gttaaccaggagagagaatc	5652
ALDH1A2	97	intron 10 + 368	ctttacatctgtgcaagaga G/A ggacaaggagcaaatcagcc	5653
ALDH1A2	98	intron 10 + 660	gtaaacttgcattgaaatgt G/A gaaagcaggttaaggaaatga	5654

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ALDH1A2	99	intron 11 + 104	tggggaataccaaaagcaac C/T aaagttcaccagaaaagggg	5655
ALDH1A2	100	intron 11 + 229	aaacttctaaaagaaatacc A/G tgccagtcagattatgtgct	5656
ALDH1A2	101	intron 12 + 117	catacattcaacaacattt C/T gtggagcacatgtactata	5657
ALDH1A2	102	intron 12 + 691	gataggggaagatcactgtga A/G ctggaaaaatctgggaaacc	5658
ALDH1A2	103	intron 12 + 1934	catcttgtctagattgcacg T/C ttgtttgtttgtttgtctct	5659
ALDH1A2	104	intron 12 + 1973	ctacttaccocccaaaacatg T/A ttctctttctttaaagacc	5660
ALDH1A2	105	intron 12 + 2722	ccagagtgcactccagtatac C/A tcaactgcccaggaccacag	5661
ALDH1A2	106	intron 12 + 3855	cacttgaaagcaaccataat T/C gtgaggtttctgatgctgta	5662
ALDH1A2	107	intron 12 + 4185	ttgtcttaagcgaaatgaac T/C atacggacagagaaacagcc	5663
ALDH1A2	108	intron 12 + 4991	acaggaacacttagacatgc A/G acccactccaccctccgctc	5664
ALDH1A2	109	intron 12 + (5018-5019)	cccaccctccgctcttggggg (G) aggaaagcacactactgtcc	5665
ALDH1A2	109	intron 12 + (5018-5019)	cccaccctccgctcttggggg aggaaagcacactactgtcc	5666
ALDH1A2	110	intron 12 + (5051-5052)	actgtcccaagaactaata (A) ctgaaccagtgtgctgtgt	5667
ALDH1A2	110	intron 12 + (5051-5052)	actgtcccaagaactaata ctgaaccagtgtgctgtgt	5668
ALDH1A2	111	intron 12 + (5300-5302)	ttaaagtttttaaaaaactt CCT/Δ taaaactactcatgagatg	5669
ALDH1A2	112	intron 12 + 5405	catccagagactgtgtgtc G/C caggtgataaactgcacctc	5670
ALDH1A2	113	intron 12 + 5435	aactgcacctccccaggact C/A ccgctgcactcacatgcagc	5671
ALDH1A2	114	3'flanking + 449	tttgggcccgggaacaatttt T/C caaggttgaataagccaaatt	5672
ALDH1A2	115	3'flanking + 597	acctgggatattctctgaccc A/C atctgtgtttctttttacc	5673
ALDH1A2	116	3'flanking + 669	atagagactggaaagtcacat C/T gtgcagttccacgcttctga	5674
ALDH1A2	117	3'flanking + 1122	cgctgctccactgagctctc T/G gtcacacccattcttggccc	5675
ALDH1A2	118	3'flanking + 2214	tgcagctgttaaaagaatc T/C gtaaatgggtgacgtactac	5676
ALDH1A3	1	5'flanking - 1425	cagtgtagccagccgat C/T ggtcaaggctgcccgcctcg	5677
ALDH1A3	2	5'flanking - 1379	ccattatccccctttccccc C/T ctcagctgtgcactccaggc	5678
ALDH1A3	3	5'flanking - 1270	aacttaccctctctaccagc T/A ctatccagaaggacaccagg	5679
ALDH1A3	4	5'flanking - (1214-1213)	acggaggcctcaaacaggga (GGA) aaataaggagaccctcccc	5680
ALDH1A3	4	5'flanking - (1214-1213)	acggaggcctcaaacaggga aaataaggagaccctcccc	5681
ALDH1A3	5	5'flanking - 1103	gcacagcttttgcagagat C/T cgctgcctccggtctttgttc	5682
ALDH1A3	6	intron 1 + 986	gccttaactttcccccactt T/G ggcttctcttgatttttgc	5683
ALDH1A3	7	intron 1 + 1462	gtacaggatttcaaaatact G/A tatatagaaccagacagta	5684
ALDH1A3	8	intron 1 + 1661	cctgtgtcttgggtgggtgc G/A caacctttgcagttaaagg	5685
ALDH1A3	9	intron 1 + 2360	agaggatagaagtcctctt A/G atttagagggcctcttctt	5686
ALDH1A3	10	intron 1 + 2516	tgaaaacataattcttttga G/A tttagctgagtgccctgttg	5687
ALDH1A3	11	intron 1 + 2624	cctgagacaccttacagctc C/T gtccctgctccatgtcatc	5688
ALDH1A3	12	intron 1 + 3255	tttcatctttctacaaatgg G/C cccctcttccgtgcactc	5689
ALDH1A3	13	intron 1 + (3643-3656)	gcttcagaggtttttgtggg (T)12-14 aacattctatcaacttttaa	5690
ALDH1A3	14	intron 1 + 4265	ccaaaagccctctctttttaa T/C atgacattaataagacaatt	5691
ALDH1A3	15	intron 1 + 5187	caagatggataagacgtcac C/T taaggtccttagcatgtga	5692
ALDH1A3	16	intron 2 + 43	ctotaagtaattcaattatg G/T atgaccaaggataaggaaa	5693
ALDH1A3	17	intron 2 + 127	cagggcctgggctagctgcg T/C gaattggcatgtggttctca	5694
ALDH1A3	18	intron 2 + (285-300)	aggaagggttttctttttt (T)16-17 atcaattatttggacctgga	5695
ALDH1A3	19	intron 2 + 778	cggtgtcagataggtcttgg A/G ttttatcttgcccatgagtt	5696
ALDH1A3	20	intron 2 + 1216	actcggtagagtcactcctg A/C ctggtgtccacatccactc	5697
ALDH1A3	21	intron 3 + 81	acatgggggtatgggaaaaa A/C gatcacggctctggtttgt	5698
ALDH1A3	22	intron 3 + 236	gctcagctcttttgaccaagt T/G gttgtctataggcagttgag	5699
ALDH1A3	23	intron 3 + 1467	ggcccgggtgttagggaggga G/T atctcctttctgaccttga	5700
ALDH1A3	24	intron 3 + 1725	ccacatgttccccgggtgag A/G gtgactcctccagggttaa	5701
ALDH1A3	25	intron 3 + 3777	gccagaagtagatgcccca A/G ttcagctgctgcattactgg	5702
ALDH1A3	26	intron 3 + 3829	caagtcactgggcccgttagc G/C tccgtgctgcaccttgaag	5703
ALDH1A3	27	intron 3 + 4299	tcaatttccacagccacact G/A gccagcctggccgagaaggga	5704
ALDH1A3	28	intron 4 + 84	agagccccctcgtactgttt C/G cctaaggcaccattcccaac	5705
ALDH1A3	29	intron 4 + 126	ccactcctctccaaatggt A/G ctgccaattcttcttctaag	5706
ALDH1A3	30	intron 6 + (290-291)	tagagaattttcagggggg (G) tcaaccaaggaggagccaaa	5707
ALDH1A3	30	intron 6 + (290-291)	tagagaattttcagggggg tcaaccaaggaggagccaaa	5708
ALDH1A3	31	intron 6 + 705	aacagctggtgatgagccaa T/G ttccactttctcttgggtga	5709
ALDH1A3	32	intron 7 + 56	ggggcgtgttatttgacacc C/T gtgagcttttctcttgacag	5710
ALDH1A3	33	intron 7 + 1107	gatgctgttactctctctgg A/G gacagacactgcctgtgga	5711
ALDH1A3	34	intron 7 + 1610	aagagccacacagaccacc C/G cctactgggtgtgtggaat	5712
ALDH1A3	35	intron 7 + 1820	cacctgtaagtggagcggct T/C agaccaaggatccaggatg	5713
ALDH1A3	36	intron 8 + 963	gagaaggacaggaggaggga C/T acaggctctcagggaaggaaa	5714
ALDH1A3	37	intron 8 + 1824	accattcttattccactaagc G/A tgtcccccagaatcttattc	5715
ALDH1A3	38	intron 8 + 2384	cgctccctctgccccctccc C/A tccagtggaactggcagtg	5716
ALDH1A3	39	intron 9 + 24	atccccctggtgtgtgtgaa A/C ccatggtgctgtctagggg	5717
ALDH1A3	40	intron 9 + 91	gcctacaggggtccctctccg T/C gaaaggaatgtgacctgtc	5718
ALDH1A3	41	intron 9 + 219	actgaggcatgggaggagg C/G gctattcccagggcagaaagg	5719
ALDH1A3	42	intron 9 + 435	ccagacggagagagcctggg G/A caggagaatgtatctccagg	5720
ALDH1A3	43	intron 9 + 1472	ttgactttttagggccagata C/T accgatttcttccaagagaa	5721
ALDH1A3	44	intron 9 + 2038	taacaatgtgttctactcgg G/A ctctccaggaggtgtggagt	5722
ALDH1A3	45	intron 9 + 2124	caaacagggctctccagatg G/A catatgccacagcagccagg	5723
ALDH1A3	46	intron 9 + 2154	agcagccaggaggacctgc G/C gttggcggaagccctgtgt	5724

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ALDH1A3	47	intron 9 + 2197	cttttggcccccagggagg G/A gaagagcagctcagcagcat	5725
ALDH1A3	48	intron 9 + 2466	ttcttagtttctcatgtttc C/T ctctagaatgttttcgtgtg	5726
ALDH1A3	49	intron 9 + 3655	gatttggtcaagtgccatgca C/T gggttatgccctctctctg	5727
ALDH1A3	50	intron 9 + 3954	gggtgcgcttttgacaactg C/G tcagtagcgtgttcacaagc	5728
ALDH1A3	51	exon 10 + 88	tggaaatgcgggggctcagcc A/G tggaaagacaaggggctcttc	5729
ALDH1A3	52	intron 10 + 8	tgccaaagaggaggtacaag G/A gggtctgtggcaaggctacga	5730
ALDH1A3	53	intron 10 + 307	ctctctgatttttctaacaca A/C ccggtcccccagtcagtcac	5731
ALDH1A3	54	intron 10 + 378	gtgggttttgccaggaatca G/A ttcaagaacctgtggattca	5732
ALDH1A3	55	intron 10 + 975	aatattgtgtcattctctcc C/G ctggtagtattatggaaac	5733
ALDH1A3	56	intron 10 + 1088	cagtgccaggagccaggggg C/T ctctccagatgactctgag	5734
ALDH1A3	57	intron 11 + 105	ttgtttacattgtatattat A/G taccagccctgtctcagtg	5735
ALDH1A3	58	intron 11 + 274	agggctccagtcactgtgcc T/G gtggccctgtgctgtactg	5736
ALDH1A3	59	intron 11 + 1088	cagtgccaggagccaggggg T/A ctctccagatgactctgag	5737
ALDH1A3	60	intron 12 + 96	ctccaatctgtctgacacccc G/A tccccccacacccgcgctc	5738
ALDH1A3	61	intron 12 + 1537	gggccttggttggggccttt G/T tgggtctctcttttagagatt	5739
ALDH1A3	62	intron 12 + 1660	gtccccctccacactcagtc C/A tgetttgtagtcacatccctg	5740
ALDH1A3	63	intron 12 + 5642	tctgtgctaactgtctgcttc T/C ctcatgccccctaggctggc	5741
ALDH1A3	64	exon 13 + 104	gggtctcttctcaaacatc G/C gacggcggaatgtggcagat	5742
ALDH1A3	65	exon 13 + 281	ataggttgctgtgaaatcg C/T agtccgtcctggggaggag	5743
ALDH1A3	66	3'flanking + 743	gtgagcaggaactgtagga G/A aagatattttccctcattt	5744
ALDH1A3	67	3'flanking + 1145	gcctccagctacccccacc A/G cctcaggaggggtcattcca	5745
ALDH1A3	68	3'flanking + 1185	aacctagggtgtctgagaatc T/C ggggtgggattaccagcaaaa	5746
ALDH1A3	69	3'flanking + 1600	acaccacgcccctgcaaatg T/C tgggaaactgtcgtgggcaa	5747
ALDH1A3	70	3'flanking + 1847	caggagccctgcggctgccc C/G ggttctgtgaaatggcagtg	5748
ALDH1B1	1	intron 1 + 134	cgttgcactgtaggactctc C/T ccacgtcccccaatccccatc	5749
ALDH1B1	2	intron 1 + 367	gcagttccccggtatagaga A/G ggtccggtccttccccctgt	5750
ALDH1B1	3	intron 1 + 405	tgtgggtgaactgtaaaaaa C/T tgcctgtattcaggaggata	5751
ALDH1B1	4	intron 1 + 2002	cttcaactaatctgggaaca C/T tacactctgtttaattttca	5752
ALDH1B1	5	intron 1 + 2157	tgggaaagctgaaaaggat G/T ctgagacctgtggtggggg	5753
ALDH1B1	6	exon 2 + 192	ccgacggtcaaccctaccac T/C ggggaggtcattgggcacgt	5754
ALDH1B1	7	exon 2 + 265	cgtgaaagcagcccggaag C/T ctccgcctggggctccccat	5755
ALDH1B1	8	exon 2 + 329	gcggggccggctgtctgaacc G/T cctggcagacctagtggagc	5756
ALDH1B1	9	exon 2 + 614	acttgccccgcactcgcca C/T aggcacactgtggttatga	5757
ALDH1B1	10	3'flanking + 168	aaagtgcactgtgaagacc G/A tagagaaaaactctggttcc	5758
ALDH1L1	1	intron 1 + 252	cgcagcgcaggactggccc G/C ccgaggatctggccggcgcc	5759
ALDH1L1	2	intron 1 + 544	ctcaggggctgcgtggagt C/T ccagctccagccactgcct	5760
ALDH1L1	3	intron 1 - 6596	cagatttttcttaaggtgca C/G tagccactgaggatattttt	5761
ALDH1L1	4	intron 1 - 6513	caattatggtttatcttagg G/A acatgtttatagagatagta	5762
ALDH1L1	5	intron 1 - 6478	atagttattcttacttagctt G/A cattctaaaattttgtccct	5763
ALDH1L1	6	intron 2 + 240	gtggcattaggtcctggag A/G agggctatagagaagccag	5764
ALDH1L1	7	intron 2 + 1326	gaggaggagaccggagagga G/C agccagctccagtcaggggcc	5765
ALDH1L1	8	intron 3 + 386	gtcctaactctaacttccact G/A ccgctgctctgggcagcaca	5766
ALDH1L1	9	intron 4 + 271	gggcccgttcaatagacaag G/C aaggctaaaaggcaggactg	5767
ALDH1L1	10	intron 4 + 356	taggattctatttctctctc C/T ttcaactcgttgattctcctt	5768
ALDH1L1	11	intron 4 + 608	gtgctctgataggctgtctc A/C gtcacatgcttctgctggg	5769
ALDH1L1	12	intron 4 + 664	ggtcacatggcctgagcgcc A/G gggcggtcagtcacctggg	5770
ALDH1L1	13	intron 4 + 785	gagggtctgttgcctctgcc C/G gaggacaggctggcagggaac	5771
ALDH1L1	14	intron 4 + 874	ccctggggagcccttctgt T/G tgggcgcagcaggaagagca	5772
ALDH1L1	15	intron 4 + 1349	tcctcaggctcttctgtcac G/A tggggccagactccttggct	5773
ALDH1L1	16	intron 4 + 1799	ctggggctgggaaggagga G/A ggtcctattgctggggatag	5774
ALDH1L1	17	intron 4 + 1815	ggcagggtcctattgtggg G/A atagcaaccactggatctc	5775
ALDH1L1	18	intron 5 + 272	aaagcccacaggagataag A/G gtgggagttagggggcaaaa	5776
ALDH1L1	19	intron 5 + 301	tagggggcaaaacgtcagcc G/A tagtgcgagcagctctcaag	5777
ALDH1L1	20	intron 5 + 343	caagggtgtgaggagacgtgc G/A ggtctctggagcaatagcca	5778
ALDH1L1	21	intron 6 + 926	cctgcctgggctactggctt C/T gggggcttcttctcaccac	5779
ALDH1L1	22	exon 7 + 41	aacgctgaacacttcaggcc T/C ggtgccgaggagagacgctt	5780
ALDH1L1	23	intron 7 + 305	cctagaatcagagagaagcc C/T tcccaggagcctgggttca	5781
ALDH1L1	24	intron 7 + 837	gtccggacaacccccatggg C/T gtggtacccccagcgtgtt	5782
ALDH1L1	25	intron 7 + 866	cccagcctgtgtgtgtgtc C/T ggcctaccagagtgggct	5783
ALDH1L1	26	intron 7 + 884	tccggcctaccagagtggg C/T gtggcagtagtggggcctggc	5784
ALDH1L1	27	intron 7 + 1118	aatgttccagaaaatcatgc G/C aggcagtaagggcagaggaa	5785
ALDH1L1	28	intron 7 + 1168	aaagtaaaaggttcaggagaa G/A tctagcctggggctgtctcc	5786
ALDH1L1	29	intron 7 + 1451	cagggcacccacagcatctg T/C ccagagacctgcaaaagacag	5787
ALDH1L1	30	intron 7 + 1489	caggaatgcaagaaggcaa T/C taagtgtcttaaggaggaaac	5788
ALDH1L1	31	intron 7 + 1579	tcagggtgggaggggagtga G/A gagagaccagctgagcacac	5789
ALDH1L1	32	intron 7 + 1691	ctggctgggctttagcttgc A/C gaaagctccagaacatcttt	5790
ALDH1L1	33	intron 8 + 1632	tcagggttgcatttgttccac T/C gtgcacattcagagttccag	5791
ALDH1L1	34	intron 8 + 1799	gctcaagtctctcttagct G/C ttacccgtgcagccccctaa	5792
ALDH1L1	35	intron 8 + 1986	ggtggaggggcctggcctgt G/T gctgttcaggagaacgctcc	5793
ALDH1L1	36	intron 8 + 2002	ctgtggctgttcaggagaac A/G ctccaagagcctgctgtggg	5794

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ALDH1L1	37	intron 8 + 2627	aaagaggagagccgggggtg C/T ttgtgccaggggttggggga	5795
ALDH1L1	38	intron 8 + 2646	gcttggtgccaggggttgggg G/A aactgggttctgattgggct	5796
ALDH1L1	39	intron 8 + 2925	ctgctgccctccataggtcc C/G agactgaatccttcagagga	5797
ALDH1L1	40	exon 9 + 4	caggtcttctgttgcagagt G/T ttggcagcggatcctcccc	5798
ALDH1L1	41	exon 10 + 109	cagctgttagtgaggaagct G/T cgaggggacgatgaggaggg	5799
ALDH1L1	42	intron 10 + (671-672)	tggcattttcctctgtctga (AG) gtcctcttagcccccctaa	5800
ALDH1L1	42	intron 10 + (671-672)	tggcattttcctctgtctga gtcctcttagcccccctaa	5801
ALDH1L1	43	intron 11 + 8	caccgatggaagtgtgagt G/A agggccagcaccctctctcc	5802
ALDH1L1	44	intron 11 + 447	atgagccaaagcagccctat G/A gtatgatacacacgtgaacat	5803
ALDH1L1	45	intron 11 + 601	ctcaaatgagtcatttgag A/G ggagttaatgaaagactcat	5804
ALDH1L1	46	intron 11 + 639	catctgcacagggagagggga G/A ggggtaggggacacagacag	5805
ALDH1L1	47	intron 12 + 66	ctgggcagtgccagggggg G/A actctctgtggagccctttt	5806
ALDH1L1	48	intron 12 + 478	ctattaaaaaaaaaaaaaa A/A ttttaagccaggagaaaggg	5807
ALDH1L1	49	intron 12 + 684	tcctgggagaagagaggggtg C/T gggcagatgagccgagaaca	5808
ALDH1L1	50	intron 12 + 767	cgctaggggtgcgaagcca A/G gttatgggtgtgtcccaacg	5809
ALDH1L1	51	intron 12 + 1014	tcataggttcagtcctcctt C/T gcaagccctcaattctaga	5810
ALDH1L1	52	intron 12 + 1359	ctggttctgtcctcagctcag C/T acagcagaggctgggtctag	5811
ALDH1L1	53	intron 12 + 1734	gggtgttcacaggtctgtgtg G/T tcagtagggccggccgagcc	5812
ALDH1L1	54	intron 12 + 1901	ttcagcagcctaactgaatt G/A acaatagaatagtcctgcaa	5813
ALDH1L1	55	intron 12 - 470	gggatggggccacctctcca T/C ctctggagatgccaggctca	5814
ALDH1L1	56	intron 12 - 334	aagggcagcctcttggggcca T/C gaccccttctgtctgtcag	5815
ALDH1L1	57	intron 12 - 325	ctcttggggcctagccctt T/C gctgtctgcagcaagtgggt	5816
ALDH1L1	58	intron 12 - 221	gaagggaagcaggggaagatc G/C aggaaggagagaggggacag	5817
ALDH1L1	59	intron 12 - 4	cccgtctccctcaccctgg T/C caggttggcagatctcatgg	5818
ALDH1L1	60	intron 13 + 34	tcccaccagtgtagcaca T/C gcagactggccagccatcat	5819
ALDH1L1	61	intron 13 + 58	gactggcccagccataggg A/G gaactccaaggccagcacag	5820
ALDH1L1	62	intron 13 + 125	ccacaactggtgtgttggaa T/C gacacctgtttattagcttg	5821
ALDH1L1	63	intron 13 + 126	cacaactggtgtgttggaa G/A acacctgtttattagcttg	5822
ALDH1L1	64	intron 13 + 281	acctgcattccagcaggttc T/G ggtgttgacagagttcagtt	5823
ALDH1L1	65	intron 13 + 299	tcgggtgttgacagagtcca A/G ttccgtgtggatgcagggtc	5824
ALDH1L1	66	intron 14 + 121	catttatcaaacagccatcc A/G tgtgtctcttgagcactgc	5825
ALDH1L1	67	intron 14 + 167	gccaggcattgttgttaagga C/T ttgaggacaattgtatttaa	5826
ALDH1L1	68	intron 14 + 205	taatctcccagtaaacactgg A/C tcagtcaggtccacgggtggg	5827
ALDH1L1	69	intron 14 + 219	cactggatcagtcaggtcca C/G ggtgggaacaaagagtaaac	5828
ALDH1L1	70	intron 14 + 2275	tctcatctgtgatgcattccg T/C cagacctctgtcccagcct	5829
ALDH1L1	71	intron 14 + 2431	agaatgactgagtgatcaga C/G cttagagagcccagcccgg	5830
ALDH1L1	72	intron 14 + 2660	agccaagcatttcttggggga C/T accaagaaccttctgttgg	5831
ALDH1L1	73	intron 14 + 2740	aaactccacctcaccgtcca T/C gcagctccccaggagcgtca	5832
ALDH1L1	74	intron 14 + 2756	tcactgcagctccccaggag T/C gtcagagggcagagagggg	5833
ALDH1L1	75	intron 14 + 2805	ccgcacagcaggagaatggc T/C ccaaggaggaggagggacggg	5834
ALDH1L1	76	intron 14 + (3636-3637)	tctcctgggtgtgtgtgggg (G) tgtggggcagctccccatc	5835
ALDH1L1	76	intron 14 + (3636-3637)	tctcctgggtgtgtgtgggg tgtggggcagctccccatc	5836
ALDH1L1	77	intron 14 + 4347	tccaggacagaaacagcagg C/T gtgagctgcctctcagaggg	5837
ALDH1L1	78	intron 15 + 380	atgtcccttatgtgtgttccc A/G agaccagaaagtcctggagag	5838
ALDH1L1	79	intron 15 + (1055-1056)	gccacaatctgcagctactc (C) tcccagcttctgtctgggct	5839
ALDH1L1	79	intron 15 + (1055-1056)	gccacaatctgcagctactc tcccagcttctgtctgggct	5840
ALDH1L1	80	intron 17 + 15	gaaaaggtgcgtgctgggg G/C tggagcagaggaggggctgc	5841
ALDH1L1	81	intron 17 + 44	aggaggggctgctgtgagt C/T gcctgggacatggcagtgct	5842
ALDH1L1	82	intron 17 + 51	gctgtgtgagtgccctgg G/A acatggcagtgctgtccaca	5843
ALDH1L1	83	intron 17 - (2224-2223)	ctggtgtcatctcccagact CT/Δ gtcactaaaccacaatatga	5844
ALDH1L1	84	intron 18 + 140	agcgtcatcacaaagcatagc G/A tggcaggcagcaggcttagg	5845
ALDH1L1	85	intron 19 + (51-52)	tgggtcactgggacagcagc GC/Δ ctggtggagggggtggag	5846
ALDH1L1	86	intron 19 + 399	tcaggtcagcctgggctga C/A catggacaggggcccctggag	5847
ALDH1L1	87	intron 19 + 608	ccaccagatttatccactca A/G ccacacctgggaagagcaggc	5848
ALDH1L1	88	intron 19 + (669-670)	atgggcatcctgagtcctcc (C) ttgggaggtttgtaagcct	5849
ALDH1L1	88	intron 19 + (669-670)	atgggcatcctgagtcctcc ttgggaggtttgtaagcct	5850
ALDH1L1	89	intron 19 + 1794	gtcctgtctgggggtcttaa G/C ggagtcagtagactccaca	5851
ALDH1L1	90	intron 19 + 1969	tgatcggggtgcggtttggg G/T cgacaggacaggagcagaga	5852
ALDH1L1	91	intron 19 + 1972	tcggggtgcggtttggggcg A/G caggacaggagcagagaata	5853
ALDH1L1	92	intron 19 + 2083	tgagaagagcagaggggtgt G/T ccgggtgtctgagtcacacc	5854
ALDH1L1	93	intron 19 + 2119	acacctgtgtctgattagg G/T tgattaggggtgcagagttt	5855
ALDH1L1	94	intron 20 + 1388	ttacctcttcccactccg C/T tggactgtgagttccatgag	5856
ALDH1L1	95	intron 20 + 1564	cccagggaaccaggaaacagt G/A ggagccatccccgccctg	5857
ALDH1L1	96	intron 20 + 1873	tcagtgttaaaacatcattt G/A tgtatgtatgaaaaaatattg	5858
ALDH1L1	97	intron 20 + 2427	actaggattggatggacttg G/C gatcaggtctcagctctgtc	5859
ALDH1L1	98	intron 20 + 2458	cagctctgtcactgcccaac C/T ggcgggccccatttccctcaa	5860
ALDH1L1	99	intron 20 + 2544	ccaggtgggagagccatctg C/T agcgtggtgacacccatcac	5861
ALDH1L1	100	intron 20 + 2573	gacacccatcacaggggtgc C/T gtgacccgggtgcttatgtcg	5862
ALDH1L1	101	intron 20 + 2574	acacccatcacaggggtgc G/A tgacccgggtgcttatgtcg	5863
ALDH1L1	102	exon 21 + 33	agccaactgttttcacagac G/A tggaaagaccacatgttcata	5864

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ALDH3B1	11	intron 6 + 263	cagaccctcatacgtgaccc T/C gctgccccccaggctcttag	5935
ALDH3B1	12	intron 6 + 1298	gtagacagagctggactcca T/G ccttgggtgataagggatcc	5936
ALDH3B1	13	intron 6 + 1411	gccagggtcacaagcagagg C/T gggaggagccaaggggtttg	5937
ALDH3B1	14	exon 7 + 185	acctgctggcccccgacta C/T gtcctatgcagccctgagat	5938
ALDH3B1	15	exon 7 + 339	tgccggcattgtctgggtgc G/A gcgtgtggccattgggggcc	5939
ALDH3B1	16	intron 7 + 249	ccagggtccagggtctcagc G/A tgctaagatgaatcccatc	5940
ALDH3B1	17	intron 7 + 277	atgaactccatccaccac C/T ggctatcctgaaagctgta	5941
ALDH3B1	18	intron 7 + 498	gaccaaggtcggggattct C/T tgtgtccacagggcctgag	5942
ALDH3B1	19	intron 8 + 14	cagccaggtgggggtgcgc C/T gggctgggcagggtcaggag	5943
ALDH3B1	20	intron 8 + 49	caggagcccgagtggtgg C/T acaagtgggtggcagcagg	5944
ALDH3B1	21	intron 8 + 111	tcaggactttgggatggtgg A/T cctcttggtctgtctctgc	5945
ALDH3B1	22	intron 8 + 3219	atcctgatggggctcaaggc A/G gcctcagcacatcctgttc	5946
ALDH3B1	23	exon 9 + 33	gtgctgacccagaccagcag C/T gggggcttctgtgggaaca	5947
ALDH3B1	24	intron 9 + 946	tcaccagggccccagagctgac C/A cttcttggtggcctggccc	5948
ALDH3B1	25	intron 9 + 1067	aggctcccaagcctgggtc C/T cttctggccccaccatctct	5949
ALDH3B1	26	exon 10 + 137	ccgcaatcgccgcgcgcgcct G/A aggatgctgctgtggccat	5950
ALDH3B1	27	exon 10 + 397	cgctcccaaccatgagagcc G/A aggtgggaggcatgggaac	5951
ALDH3B1	28	exon 10 + 1198	ctcttcccatgtgtctcat C/T ctcttggggccccaccctc	5952
ALDH3B1	29	exon 10 + 1475	cagggttggaactgagtttc G/A tctctgtctctctgtgctga	5953
ALDH3B1	30	3'flanking + 15	cctggcaatacttacatctc A/G gtgatttcttctgtgcat	5954
ALDH3B1	31	3'flanking + 60	caacaggactctggaccaag G/C ccttggcgtttgggtaacaat	5955
ALDH3B2	1	intron 1 + 98	agggaagggtgtgtgtccc G/A tggcccggtgggtcagggggc	5956
ALDH3B2	2	intron 1 + 157	atggctgcaggggcatggg T/C acggggcttgcctcaggagag	5957
ALDH3B2	3	intron 1 + 354	tctgtggacagacaaggatt C/G ggtcgggggaccagggtcg	5958
ALDH3B2	4	intron 1 + 851	tatgacaggtccatcaggcc T/G caccttctgtgtgtcttat	5959
ALDH3B2	5	intron 1 + 894	ctcagcatctgccccacag T/G gcttttgacacgttggttc	5960
ALDH3B2	6	intron 1 - 463	aaagaacctccagagtcct C/G gtttagtcccagaaggagg	5961
ALDH3B2	7	exon 2 + 61	gccttcaactgaggcgccac G/A cggccggccaggttccgggc	5962
ALDH3B2	8	intron 2 + 8	ggacctgcataagtggtggc A/G tggagagtgggccccggcag	5963
ALDH3B2	9	intron 2 + 23	gggcccgtggagagtggggc G/C ggcaggggctggagcagcgt	5964
ALDH3B2	10	intron 2 + (180-181)	ttcactcctgaacactcaca (A) gccaccctgtgatgcaggct	5965
ALDH3B2	10	intron 2 + (180-181)	ttcactcctgaacactcaca gccaccctgtgatgcaggct	5966
ALDH3B2	11	exon 3 + 72	gactacgctctcaagaacct T/G caggcctggatgaaggatga	5967
ALDH3B2	12	intron 8 + 375	ctgcagcatcctaaccctac C/T gtcgcgactcaaggctgccg	5968
ALDH3B2	13	intron 8 + 463	aatcacccccatggcacc C/A accgtcactgagaggtgtct	5969
ALDH3B2	14	exon 9 + 33	atgctggagcggaccagcag C/A ggcagctttggaggcaatga	5970
ALDH3B2	15	exon 10 + 428	aggtgtctctactcaccaca C/T cctcccaattccagccctt	5971
ALDH5A1	1	5'flanking - 1303	gaattgattaaactctact G/A ttatcacttctgcatatgt	5972
ALDH5A1	2	5'flanking - 301	gtgaaaaggtgacagcagtc C/T gcagggtgcatctactggcga	5973
ALDH5A1	3	5'flanking - 221	ggtcgcgccaggagagaagc C/T gcgcggcgcttagggcaagg	5974
ALDH5A1	4	5'flanking - 175	agggcgccgcggcggtgcag C/G gagaagagcgggagagagg	5975
ALDH5A1	5	5'flanking - 174	ggcgccgcggcggtgcagc G/A agaaagacgggagagagg	5976
ALDH5A1	6	exon 1 + 106	gcggcctgtgctcctgcctcc G/C ggcctgcgcggcgccggcc	5977
ALDH5A1	7	intron 1 + 326	cctaaccctggagggcggg G/A agaaaggggaggggtgtcag	5978
ALDH5A1	8	intron 1 + 5551	gtctgtacaaaaaaatttt T/G ttttaattagctgagcatga	5979
ALDH5A1	9	intron 1 + 5555	gtacaaaaaaatttttttt T/A aattagctgagcatgatcat	5980
ALDH5A1	10	intron 2 + 306	gttttggtgttttttttttt T/A aaactgtttttgtacattt	5981
ALDH5A1	11	exon 3 + 107	cggagacattatccacacc C/T ggcaaggacagggcgggccc	5982
ALDH5A1	12	intron 3 + 201	gtggtgagcagtgagtggaat G/T atgcatttctaatgcctga	5983
ALDH5A1	13	exon 4 + 42	atcacccggaaggtggggc C/T gccctggcagcggtgtgac	5984
ALDH5A1	14	intron 4 + 2306	atcgtgtcttataaatcagtt T/C tgetaggtataaaatccttg	5985
ALDH5A1	15	intron 4 + (2334-2346)	tataaaatccttggtcaca (T)11-13 acttgattatcttaaatga	5986
ALDH5A1	16	intron 4 + 2456	tataagtcacacttttttttt T/A acctagatcacaaaaagtg	5987
ALDH5A1	17	intron 4 + 2501	tttggtttttttcccccttt A/G tctttaaagaccaataatgt	5988
ALDH5A1	18	intron 4 - (64-46)	atctattttttctcttttc (T)16-18 cagtttggttaattgttggc	5989
ALDH5A1	19	intron 4 - 27	ttcagtttggttaattgttg G/C cacatgtttgtgtttctct	5990
ALDH5A1	20	intron 5 + (4621-4624)	tttgaatagataaacactta CTTA/Δ tatggttgaataaataagac	5991
ALDH5A1	21	intron 5 + (4677-4678)	accatgacaagtcctaccct (C) accccaacctgactcactc	5992
ALDH5A1	21	intron 5 + (4677-4678)	accatgacaagtcctaccct accccaacctgactcactc	5993
ALDH5A1	22	intron 7 + (432-443)	aaaaatgatgttaaaaggc (A)10-12 tgaatacaaaaagtcattt	5994
ALDH5A1	23	intron 7 + (3243-3244)	cagtccttgtgtgtgtgt GT/Δ cccccaaacactgtctgga	5995
ALDH5A1	24	intron 7 + 4987	tttttgaaaaagaaaaaaa A/Δ tggaaactagttatagttttc	5996
ALDH5A1	25	intron 8 + 2717	gatcacctggaaactcacagg C/T gtggtaggagacgtgcagcc	5997
ALDH5A1	26	3'flanking + 2711	cagtgtgtgcttggggaag G/A agccagcatgtgaaatgatg	5998
ALDH5A1	27	3'flanking + 2777	gtccatggtgtgcgttata G/A aatgtttgtctaagctgaact	5999
ALDH6A1	1	5'flanking - 1303	ctctaaagcagaaccaagag G/C aaaagcatgggagtatacca	6000
ALDH6A1	2	5'flanking - (1273-1270)	ggagtataccaaaacactt AATT/Δ gttacttgaaatgacttgca	6001
ALDH6A1	3	intron 1 + 437	tgccattgtctccttcccc A/T cctacttctactatccgttg	6002
ALDH6A1	4	intron 1 + 835	gttccccccccaaatcagc T/Δ cttctagtgtcacacacct	6003
ALDH6A1	5	intron 1 + 1294	atatttctgtgcgatctc T/C gttctgttctagtatctttt	6004

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ALDH6A1	6	intron 1 + 1447	gagtcattgagaaccttaag A/G aagtattttgtccttttcca	6005
ALDH6A1	7	intron 1 + 2536	agtcttgccatctcttttcta T/C gttaggcactgacataggct	6006
ALDH6A1	8	intron 1 + 2703	caggagaggaaggaggttct G/T ataaaggatagcaagtag	6007
ALDH6A1	9	intron 1 + 2802	gcaacaatgctaattgggtgt T/C tcttaggaatgaagaaaag	6008
ALDH6A1	10	intron 2 + 2333	gtttgtttgtttgtttgttt G/Δ ttttttcagccaaactgtaa	6009
ALDH6A1	11	intron 4 + 138	gaactctctccctgtactgc A/G tctctccagctcttattctt	6010
ALDH6A1	12	intron 4 + 200	aaagagggaacattcttgcat T/C aatttctatttgtgtgtctt	6011
ALDH6A1	13	intron 5 + 291	ggcaagtcagtgtaacctgc G/A ccccttcattggcctgaacc	6012
ALDH6A1	14	intron 7 + 209	tcccggttcaagcgattct C/A ctgcctcagcctcccgagta	6013
ALDH6A1	15	intron 8 + 287	gcctctctgagcagcttgac C/T acaggtgcgggcccacacct	6014
ALDH6A1	16	intron 9 + 877	gatacaaaatataaacata C/T agacatatttgggaggcaaa	6015
ALDH6A1	17	intron 9 + 885	aataaatacagacagata T/G ttgggaggcaaaaggagtaa	6016
ALDH6A1	18	intron 11 + 40	ttttgtcttttcttttaaga A/C atttcttaagatattcag	6017
ALDH6A1	19	3' flanking + 520	cctgcaaaagttttcttttagc C/T cctcttttatcccaatac	6018
ALDH6A1	20	3' flanking + 1026	cgtgttgggtcaggtgtgtct T/C gaactcctgacctcaggtag	6019
ALDH6A1	21	3' flanking + 1035	caggctgtgtctgaactcct G/C acctcaggtgacccctgc	6020
ALDH8A1	1	5' flanking - (837-836)	gctgaacattgttaatat (AT) tcattagccaattgtgttcc	6021
ALDH8A1	1	5' flanking - (837-836)	gctgaacattgttaatat tcattagccaattgtgttcc	6022
ALDH8A1	2	5' flanking - 702	gggactctgaagccttgcta C/T atgtgtcacacatgtttttg	6023
ALDH8A1	3	5' flanking - 642	gcacatctaggaagatgtga G/A cagccactgtggcccggt	6024
ALDH8A1	4	5' flanking - 84	atgctctctgagagcgtcag G/T tgcctccacattcactga	6025
ALDH8A1	5	intron 1 + 5437	gcattggtgaaatggagcg T/C gttctttgtttcttatggtta	6026
ALDH8A1	6	intron 1 + (5836-5855)	gtgagaatccatctaaaaaa (CAAAA) 4-5 atgaggtgtgtggagacct	6027
ALDH8A1	7	exon 3 + 146	cactacacggtgccccccc G/T gtgggagtcggtgagtgctg	6028
ALDH8A1	8	intron 4 + 1033	aggctcttttctctatgtcac C/T ccacggccaggcaggagtg	6029
ALDH8A1	9	intron 4 + 1037	ctttttgtctatgtcaaccca C/T gggcaggggcaggagtgctgg	6030
ALDH8A1	10	intron 4 + 1662	tctctctctgagaccaagaac G/A tctggatagatgatgagtaa	6031
ALDH8A1	11	intron 4 + 2046	agtccttgggcattttaaacag A/C ctgacagataaaccttctt	6032
ALDH8A1	12	intron 6 + 1146	ttttccagatgcaagagact C/G ccttgttctctctctctctg	6033
ALDH8A1	13	intron 6 + 1744	ttcttcttcttcttcttctt C/T tttcttttttaacatgtact	6034
ALDH8A1	14	intron 6 + 9802	tgagtgtaattcttaacttt A/T ctgtttattagctctatgaa	6035
ALDH8A1	15	exon 7 + (1089-1098)	tacagtgagacctgtcttt (A) 9-10 tgcgtgcaaaacaaaaataa	6036
ALDH8A1	16	3' flanking + 848	ctcagctgagtcctccttgac T/C ttaatcactttagtgaagaa	6037
ALDH9A1	1	exon 1 + 121	actgtgtgggtatggcggg G/A tgggtgggagaatgtgtgt	6038
ALDH9A1	2	intron 1 + 67	cgcggttttcccgccagcc C/G cgttctctgtgttctgacg	6039
ALDH9A1	3	intron 1 + 103	tgcagcgttgacttgagcac A/G agacagtgacagtgagagtg	6040
ALDH9A1	4	intron 1 + 1818	gaatttttgagaaaaaa A/Δ tgttcttttaggggtgcctt	6041
ALDH9A1	5	intron 2 + 5891	tcaggaacaggaaagtaaga G/A gtttacatttctaaattctt	6042
ALDH9A1	6	intron 2 + 6398	atcaaaaaacacttgtctgat T/G atcgtgtctgtaacctgcct	6043
ALDH9A1	7	intron 2 + 9677	atgacgctgagtttgggtgt A/G ttcttttgttttcttgcct	6044
ALDH9A1	8	intron 2 + 9991	gggagaagtgaggacctac C/T ctggcttcttaattcttcat	6045
ALDH9A1	9	intron 2 + 10198	ttgtcagagacacttttgat A/G atccttaactactatatacag	6046
ALDH9A1	10	intron 2 + 10256	ttagtagataacttttttt T/Δ gtaaggatggagaataatag	6047
ALDH9A1	11	intron 2 + 11382	catattcaatttttttatgt T/C ctttagaccaagaagagca	6048
ALDH9A1	12	intron 2 + 11455	taaacctttaagctcatcat C/T ggaccatctattgtaattct	6049
ALDH9A1	13	intron 2 + 12044	atttaaaagtgaagctattt C/T tagttttaaaaattgagcag	6050
ALDH9A1	14	intron 3 + 334	ctatttagcaaacctttttt T/Δ gacagtgtataaagttttca	6051
ALDH9A1	15	intron 3 + 368	gttttcaacaattgatattg G/Δ aaggttggttagggcctagga	6052
ALDH9A1	16	intron 4 + 191	ccctcaaggagcttatagtt T/A aggttgatcacacatcatgtc	6053
ALDH9A1	17	intron 4 + 557	tagaaaaaattgtaattgta A/G aaagcattactgttaggaca	6054
ALDH9A1	18	intron 5 + 830	agttcaagatgattttgtag G/C ttcagggcctagttgactta	6055
ALDH9A1	19	intron 5 + 838	atgattttgtaggttcagg C/T ctgattgacttagcatgcaa	6056
ALDH9A1	20	intron 6 + 120	agaaaagtgcacaaatagt A/C caaagaattccatgtacct	6057
ALDH9A1	21	intron 6 + 2569	attaaaaatctgctttaaata T/C ttttttggggagaggacac	6058
ALDH9A1	22	intron 8 + 1414	ccgatcttcaaaaaattagc T/C ggggtgtgtgtgtcacactg	6059
ALDH9A1	23	intron 9 + 664	aaagtctacattttttttt T/Δ ataacttcatggtcaagagc	6060
ALDH9A1	24	intron 9 + 2170	taatgcacacattttttttt T/Δ ctctcatagggacatccaacg	6061
ALDH9A1	25	exon 11 + 587	aaaacaaaaacaaaaaaa A/Δ ccttgttctttataggttc	6062
ADH1	1	(5' flanking region -55)	atcatgtgtgggaactggaat C/T gggtgttattcaagcaaaa	6063
ADH1	2	(intron 1 268)	acatttgcggtaaagcgata A/G tttattccaagctaatactg	6064
ADH1	3	(intron 3 443)	aatgga g/c gctacatggctat G/A gctgaatgagcatgacctt	6065
ADH1	4	(intron 6 56)	tacaacttgaggatgctatt T/G aggtgcagaaatattgttt	6066
ADH1	5	(intron 8 74)	gtctagcagaaaaatgaaa G/A tggaaaggatgagaaaaatta	6067
ADH2	1	(intron 2 340)	ctattttttaaagcgtgcat T/C ctacataagacttaaatat	6068
ADH2	2	(intron 3 91)	aaggcaatgagagacgaaag T/G gcttgacaaagtcaccg	6069
ADH2	3	(intron 3 205)	atgtattgtaccctcaaac A/G ttatgtaccgagtatctact	6070
ADH2	4	(intron 7 108)	acaattgacaaggcaagatt T/C tgaacacaaatcaaaaataa	6071
ADH2	5	(intron 3 1721-1723)	actgcatagaaatttaagaa GAA/Δ cttgttttatctctctccag	6072
ADH2	6	(3' untranslated region 2305-2306)	gttaaatgcttccccactctc AG/Δ gggaaggatttgcattttga	6073

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ADH3	1	(5' flanking region -254)	tgagagaagagaagcaggaa C/G ttgagagaggaggaagagag	6074
ADH3	2	(intron 2 355)	tatgcattcttctatatattat A/G caagacaaaaatttttaggat	6075
ADH3	3	(intron 3 32)	acactcaggggaacatgcctt G/A gtccaccatcacagatttag	6076
ADH3	4	(intron 4 6)	ctgcttgaaaaatgagtaag C/T ttctgatgctttctttgcac	6077
ADH3	5	(coding region 453 (Thr 151 Thr))	agcaccttctccacgtacac A/G gtggtgagtagaagtcagt	6078
ADH3	6	(coding region 815 (Arg 272 Gln))	ttcgtttgaagtcacgtgc A/G gcttgacaccatgggtatgat	6079
ADH4	1	(5' flanking region -482)	acagccagagaccagaacc A/G tcagggtggttgtaggact	6080
ADH4	2	(5' flanking region -437)	catcaggtgggacaaaaaga G/A tagctccttagcagtgaacta	6081
ADH4	3	(5' flanking region -234)	actcaagcatatgtgcaacc A/G agtaccatgaaaagaatttgt	6082
ADH4	4	(5' untranslated region -3)	ggtaagttaaatggcgatt C/G tgaggagtagaaatttccct	6083
ADH4	5	(5' untranslated region -2)	ttcaataaaaaaagaa T/A ttaaaaaatcttgagctca	6084
ADH4	6	(intron 1 707)	ttatatttgaattaaaaat A/G taatttgaggctagaaaaaa	6085
ADH4	7	(intron 5 619)	tcaaagaggatctcacaat T/C ggacatctcaacctgttat	6086
ADH4	8	(intron 5 1755)	tttagcgcacaattactca T/C taataaaaaatcttgaagctca	6087
ADH4	9	(intron 5 3425)	actgagactctggagcaata T/C attaagaatcatactgaaca	6088
ADH4	10	(intron 1 1181-1189)	ggtaaacctttaaatacactg (T)9-11 caagaataaaaaatgtaat	6089
ADH4	11	(intron 5 2828)	tccagtcaaaagtcgacctaa A/Δ ttccaggaggtgttctctcc	6090
ADH4	12	(intron 7 15)	ttggtggtcagtttttttt T/Δ ctctcatagctttaaattctt	6091
ADH5	1	(5' flanking region -115)	taactgctgtaaaagtacac G/A g/a ggaagccctttcccgacaa	6092
ADH5	2	(5' flanking region -114)	aactgctgtaaaagtacac g/a G/A ggaagccctttcccgacaa	6093
ADH6	1	(intron 3 249)	tgaactgggacttgaaagta C/A aaatgagacaaaaatttatg	6094
ADH6	2	(intron 6 1072)	taacccctatactgtattgc A/G tcacttttaacaggcagct	6095
ADH6	3	(coding region 885 (Val 295 Val))	gtctgtgtggttgttgggt G/A ttgcctgccagtgttcaact	6096
ADH6	4	(intron 7 1292)	gttgagaacactgccttagt C/A ccgtctgtgtgcttagaatt	6097
ADH6	5	(intron 7 1616)	ctatcacagaataatccgca T/C agaactaagcagattacg	6098
ADH7	1	(5' flanking region -528)	tgtgcagacacagaaagttt T/C acttaactttctacacctaa	6099
ADH7	2	(intron 1 361)	tcagtagcatgtgtgcact C/T gctgcagtagttcaatggga	6100
ADH7	3	(intron 3 183)	aaactcaaccttttagaaggc A/G aaccttacgggtgtttataaa	6101
ADH7	4	(intron 4 76)	tgaattgaattaaataac G/A tgtatttgatgtatcaaca	6102
ADH7	5	(intron 6 615)	tggcatagcgtaaagagact T/A ggaataatggaataaagcca	6103
ADH7	6	(intron 8 532)	aagtctaacacatcaccaa T/C ttagtatgccattgtactat	6104
ADH7	7	(intron 8 651)	gctgctatttattcaagta G/A gccacaaaatttccctattt	6105
ADH7	8	(intron 8 727)	ttcagatccctgtgaagccag G/A tattatttttaccattttta	6106
ADH7	9	(intron 8 1207)	tctccacatttggcttagcc T/C acaggatcatcatattatga	6107
ADH7	10	(intron 8 1691)	tcctctatctcattgccac G/A ctctattgttttaattcagtc	6108
ADH7	11	(3' untranslated region 13)	atttacattttgtgaaggcta T/C aattgtatctttttaagaaaa	6109
ADH7	12	(3' untranslated region 14)	gatatagtaaatgcactccc T/C agagtaataattcacttaaca	6110
ADH7	13	(3' untranslated region 15)	aaacacttggttatgagttaa C/G ttggattacattttgaaatc	6111
ADH7	14	(3' untranslated region 18)	aatataaacatagagctaga A/G tcatattatcatcattatca	6112
ADH7	15	(3' flanking region 865)	tacatcaaaagaaataaatc C/T aagaaggataaaacacattt	6113
HEP27	1	(5' flanking region -191)	tcagcactctgtgtctagct A/T aaggtttgtaaatgcaccaa	6114
HEP27	2	(5' untranslated region -1)	gaacccatcaattccgtaca C/A attttggtgactttgaagag	6115
HEP27	3	(intron 1 1941)	aaatttaccctaacaccgct G/C actctctgaccttttctgtt	6116
HEP27	4	(coding region 289 (Ala 97 Thr))	ttgtgtgccacgtggggaag G/A ctgaggaccgggagcagctg	6117
HEP27	5	(intron 4 1070)	tgctcagttcagagatca T/C gactcttttctctgaaactg	6118
HEP27	6	(3' flanking region 362)	ggctttgtgtgtgtccatt A/G tctgaactgggctgtgctgg	6119
UGT1A1	1	(5' flanking region -1337)	tctttcccttttgacttcaa A/C tcagtcacagaatttcccc	6120
UGT1A1	2	(coding region 211 (Gly 71Arg))	cctcgttgatcacatcagagac G/A gagcattttacaccttgaag	6121
UGT1A1	3	(intron 1 2925)	gcatttgggaagggaataatc T/G aattaaaaagcctaaactaaa	6122
UGT1A1	4	(intron 1 3442)	agactcggccttttccagat G/T agcttcagtgtaagagtgagg	6123
UGT1A1	5	(intron 1 3512)	ttaagtaagcattttaccaa C/T gctcagaagaaagaaacttga	6124
UGT1A1	6	(intron 1 3665)	tcttgctacaacaaaaaa T/C gcagcatggtgtgtgggagg	6125
UGT1A1	7	(intron 2 15)	cagacagtaagaagattcta T/C accatggcctcatatctatt	6126
UGT1A1	8	(intron 4 574)	agattttaaactccaattta C/T ataaaaagttgccataatag	6127
UGT1A1	9	(3' flanking region 125)	tatagaggttcacacacaca C/T gccttcattgctgtgcatg	6128
UGT2A1	1	(5' flanking region -1602)	ataacatcttctgcagagaa A/C ctccaatggaaatacactca	6129
UGT2A1	2	(5' flanking region -1480)	tacagattatcttgggtgat G/C ggagagcttagaagagacat	6130
UGT2A1	3	(5' flanking region -1406)	atttcagaagattttataac A/T tgaaaaggatcactctg c/t tt	6131
UGT2A1	4	(5' flanking region -1388)	acatgaaaaggatcactctg C/T ttatttcacagacatattgat	6132
UGT2A1	5	(5' flanking region -935)	aaattattcaatctcttggg G/A cagtggtttcttttcttctg	6133
UGT2A1	6	(intron 1 535)	cattgatcagggtgatttat C/T catgctaagcttatttattt	6134
UGT2A1	7	(intron 1 642)	tatattgatcatgttgatac A/C ttatatacacatatttgctta	6135
UGT2A1	8	(intron 1 1448)	aggtgcttacaggcaacatc C/T acatagcagctgtgtggctgg	6136
UGT2A1	9	(intron 1 2000)	gacacattagcttctttctt A/G cagatctctgtttctaaaaa	6137
UGT2A1	10	(intron 1 3118)	cttaaaattctttaaagaa T/G cattgcacaaaatttatatc	6138

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
UGT2A1	11	(intron 1 3191)	ataaatagaacaactcccta A/T gtttacttctctgcagtga	6139
UGT2A1	12	(intron 1 3770)	atcaccagataatttactat C/T cattaaggagtaggtcatca	6140
UGT2A1	13	(intron 1 4584)	tgattgggttagaatcttga A/C aaatcttctagtatcatcc	6141
UGT2A1	14	(intron 1 4854)	tactctgtgcattgtaata G/A cctatcacttggtgctgccc	6142
UGT2A1	15	(intron 1 -19146)	ctgtttaaattctcattcaa C/T gggcacatgggttaaaataaa	6143
UGT2A1	16	(intron 1 -19085)	tagacaaagaccctttcaat A/C aacaaagttagaatgtgtt	6144
UGT2A1	17	(intron 1 -18346)	atggcaatatttttagaata G/A ttaactcccaataatgaata	6145
UGT2A1	18	(intron 1 -18218)	tatatcattatttttaactta T/G agatagcactagccctaatt	6146
UGT2A1	19	(intron 1 -17937)	ctcctaataatttggactca C/T cactatttctcagcactatc	6147
UGT2A1	20	(intron 1 -12585)	ttccacacagggacaagtca A/G cagaggaaatttttcttgc	6148
UGT2A1	21	(intron 1 -11430)	aacaaagggtttattttctta C/G agttctgaggttagacgtc	6149
UGT2A1	22	(intron 1 -10761)	tttaaaatagcatgtattt T/G ccacttttaaaactatatac	6150
UGT2A1	23	(intron 1 -381)	aaatcctccctccttcttcc C/T ttccacaggcccaactctac	6151
UGT2A1	24	(intron 1 -329)	ttcccttttctccttttctcc A/G tctctctctcttctctctc	6152
UGT2A1	25	(intron 1 -41)	ttttctctcagcaaacata T/A aagctaatttctcctcaccata	6153
UGT2A1	26	(intron 2 263)	caccttgatactggacttgg T/C gggacagaaacacagatcat	6154
UGT2A1	27	(intron 2 454)	agaaagcccatgaaataag G/C cagggttttttaggttttaat	6155
UGT2A1	28	(intron 2 554)	aaaaacttttttaggtgac A/T atgggtgagtttagtttctga	6156
UGT2A1	29	(intron 2 1113)	ctgcaggcaagctctagtga A/T tgtttattataggaaataat	6157
UGT2A1	30	(coding region 922 (Gly308	gtgtgtgtgtgttttctctg G/A gatcaatggtcaaaacett	6158
UGT2A1	31	(intron 3 -217)	aagcttagaagtataaata T/C caaaacaataatactatact	6159
UGT2A1	32	(intron 3 -194)	aaacaataatactatactg G/A tagactattatagacaagact	6160
UGT2A1	33	(coding region 1171 (Val391Ile))	acggagtcctcatgtgtgga G/A ttcccatgtttgtgatcag	6161
UGT2A1	34	(intron 5 1546)	tttttaaaattcagaaactc A/G g/a ttatggtgtattcttaca	6162
UGT2A1	35	(intron 5 1547)	tttttaaaattcagaaactc a/g G/A ttatggtgtattcttaca	6163
UGT2A1	36	(intron 5 2505)	taattgacttttattaatac G/A tacatgttgataagtcata	6164
UGT2A1	37	(intron 5 2639)	tagactattacaaagtgtt A/G gttgctgacaaatttgttca	6165
UGT2A1	38	(intron 5 4009)	gaatccaggctggaaacttt C/A ttccagacacaaacaaaa	6166
UGT2A1	39	(intron 5 4311)	atcacagactgtcttttcc G/A tcacaaacatacagatgtgt	6167
UGT2A1	40	(intron 5 4616)	acttttttatgtctacattt G/C atcatactgtgttaagcata	6168
UGT2A1	41	(intron 5 4717)	tgcaagaatttatattttctc C/A acgtaactatggccttaaac	6169
UGT2A1	42	(coding region 1524 (Gln508Gln))	gctatattttgggtcataca A/G tgtgtgtgtgttttctgtca	6170
UGT2A1	43	(3' untranslated region 1	aaggagtttaacaaaaaac G/A tctcccatcctgtttccaaa	6171
UGT2A1	44	(3' flanking region 685)	aatctagaaaataattatca T/C ttttataaaatttttagtca	6172
UGT2A1	45	(intron 1 (-18967)~(-18965	ctcccaattagattgattag TAT/Δ gagttctcgggggttactggt	6173
UGT2A1	46	(intron 1 (-18862)~(-18803	aatacattcttcccccctca (AC)14-17 atgcttactggcctattta	6174
UGT2A1	47	(intron 1 (-17463)~(-17447	aaacttagaaacctctatcc (A)16-27 gtaagaaaaatggcagagaa	6175
UGT2A1	48	(intron 1 -10860)	attcaatgcaacttttttt T/Δ gtaatggcagaattagaaca	6176
UGT2A1	49	(intron 2 528-538)	ctgttaggaaacaaattgggt (A)8-10 cttttttgagttgacA/Tatg	6177
UGT2A1	50	(intron 2 1514-1533)	ttgtgtgtatgtgtatgttt (GT)9-11 tattttaatgaatttaatac	6178
UGT2A1	51	(intron 5 916-917)	gcttagtatattatataat AA/Δ gtctatatataatagcttagt	6179
UGT2A1	52	(intron 5 1163)	caatatttatgtcatttttt T/Δ ctccacatttactctgtttcc	6180
UGT2A1	53	(intron 5 3819-3838)	agacagacagacacacaaac (AC)8-12 tcaacacatgtaaaactacc	6181
UGT2A1	54	(intron 5 4785)	tatcttcaatgaaaaataaaa A/Δ caaaaattgtctaatttctg	6182
UGT2B15	1	(5' flanking region -277)	cgaacagggcaggagcctct C/A acttgcactgtttcttaaca	6183
UGT2B15	2	(intron 1 670)	catcaaaagaaaataggggcc A/T aattaagggagagacatat	6184
UGT2B15	3	(intron 1 775)	ctaatttatattaagatctta A/C gatgaaccaagacagtagta	6185
UGT2B15	4	(intron 2 2183)	cagagtttccacatgttggc C/T aggtgtgtcttgaactcctg	6186
UGT2B15	5	(intron 2 2430)	tatttcaaaagaaataagact C/G ttgccaaaaagatcaagtg	6187
UGT2B15	6	(intron 2 4806)	aaaaaattactccaatagct C/T ctga c/g ttctctatcttagat	6188
UGT2B15	7	(intron 3 129)	ctaatttatctcagacatctg T/C tcaaa g/a caaaaacatatatg	6189
UGT2B15	8	(intron 3 424)	caataacaataagcaggtat T/C gaaaaaactttgaaatgcat	6190
UGT2B15	9	(intron 3 493)	ggc t/a gtttttacttcccatg C/T attggaataggtctatttag	6191
UGT2B15	10	(intron 3 906)	gccctctctgaatgatctat G/A caagtttttgcgtgaaacac	6192
UGT2B15	11	(intron 3 1036)	tcagtaccttagtttggtag T/C agacatggttaatgactggct	6193
UGT2B15	12	(intron 3 1544)	aataaatatataaggttatta C/G taatttgcactttttttatt	6194
UGT2B15	13	(intron 3 5550)	gtgtgtgtgaatcaatgtgtg C/T tgccttggggcagtagtcca	6195
UGT2B15	14	(intron 3 5720)	ttttttaaagtttaatttt C/A ttggggatttccctgcaggg	6196
UGT2B15	15	(intron 4 134)	atcaaaatttaactactttat A/G tttattttccagctcttagta	6197
UGT2B15	16	(intron 5 6627)	ttttaatgttgatatcttta T/C atttatecttcagctataaa	6198
UGT2B15	17	(coding region 1568 (Lys23	tttccgaaagcttgcacaaa A/C aggaagaagaagaagaagag	6199
UGT2B15	18	(3' untranslated region 1	ggatttaaatcgtacttttag C/T tggaaattattctatgtc a/t at	6200
UGT2B15	19	(3' untranslated region 1	ag c/t tggaaattattctatgtc A/T atgatttttaagctatgaaa	6201
UGT2B15	20	(intron 2 1980-1981)	aagagagtagcagaataagg (AGG) acaagggataaatgactagt	6202
UGT2B15	20	(intron 2 1980-1981)	aagagagtagcagaataagg acaagggataaatgactagt	6203
UGT2B15	21	(intron 3 605-618)	ctagccaaagtagatttagag (A)11-15 cttgtctgctctgctgactt	6204
UGT2B15	22	(3' untranslated region 1957-1968)	aagtataatttaaaaaaagc (A)11-14 tacaactcttttttttaaac	6205

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
UGT8	1	(coding region 677 (Pro226	gcagaagtacaacctgctgc C/T ggagaagtcctatgtatgatt	6206
UGT8	2	(coding region 741 (Ala247	atgctgtgtactgacgttagc A/G ctggaattcccaagaccac	6207
UGT8	3	(intron 2 53-54)	ttgacaatcaatctcctt GT/ Δ ttagtgcacaggtccagta	6208
GSTA1	1	(5' flanking region -266)	ttgcaaaagagcaaaatct C/A ggtgaaatgtattgtgtaaa	6209
GSTA1	2	(intron 2 1220)	gagacacaggtttcctaag A/C tatgacaacaccataactag	6210
GSTA1	3	(intron 4 1813)	aaaggcaccactggtgagtg A/C attattttgcatcacctga	6211
GSTA1	4	(intron 5 732)	gaagagtgttgcataaggg T/C ggagtcactgccccaggag	6212
GSTA1	5	(intron 6 333)	ttatcccatatgtgccaca A/G tgagccggtctgagcagagc	6213
GSTA1	6	(3' flanking region 412)	ctttcttatgcatgtgcaaa A/C caatgattctgtctgtgtg	6214
GSTA4	1	(intron 1 280)	gcattggtggaaggtgggt C/T ggatcgccccggcctggc	6215
GSTA4	2	(intron 3 176)	ggaaatcacttcttattcaa T/C agttccataaaaagctggccg	6216
GSTA4	3	(intron 4 94)	acaccacatttactttatgt C/G ttacatagtttagtgagatca	6217
GSTA4	4	(intron 5 1062)	cacacttgtgcacatgcaga C/T acccatgggcatccaagagt	6218
GSTA4	5	(coding region 487 (Thr 163 Ala))	catagtgtattttactccaa A/G ccattttagctctagaagag	6219
GSTA4	6	(intron 6 595)	tgagctctgagagcaaatga G/A agatgtt a/g gccccaaaca	6220
GSTA4	7	(intron 6 630)	taaacatcaccccaaggat T/A cctaccattctccttctgag	6221
GSTA4	8	(intron 6 3943)	tcttctgtagtatcctaacc T/C tttttgttagccttaaaagt	6222
GSTA4	9	(3' untranslated region 10	taataacacaccgaatgtcta G/A taaatgactctcctctgagc	6223
GSTA4	10	(intron 5 370-371)	gtgtctgaacagctgtctca (TA) gctgacatcctcctgataa	6224
GSTA4	10	(intron 5 370-371)	gtgtctgaacagctgtctca gctgacatcctcctgataa	6225
GSTM1	1	(5' flanking region -694)	tacgaagtggctaatattca C/T agtacttagccagatgaccg	6226
GSTM1	2	(5' flanking region -661)	gatgaccgaaggactcagta C/T ccgagggcccttaacagaaa	6227
GSTM1	3	(5' flanking region -658)	gaccgaaggactcagtacc C/A agggcccttaacagaaaaca	6228
GSTM1	4	(5' flanking region -656)	ccgaaggactcagtaaccga G/A gggcccttaacagaaaaca	6229
GSTM1	5	(5' flanking region -537)	tagaggggagactaaagccct G/C ggagtagctttcggatcaga	6230
GSTM1	6	(5' flanking region -525)	taagccctgggagtagcttt C/G ggatcagaggaagtcotgct	6231
GSTM1	7	(5' flanking region -465)	aattaaattcccaggttggg G/A ccaccacttttttagctgac	6232
GSTM1	8	(5' flanking region -383)	gcggagagaaggctgaggga C/T accgagggcaggaggagaa	6233
GSTM1	9	(5' flanking region -382)	cggagagaaggctgaggga A/T ccgagggcaggaggagaa	6234
GSTM1	10	(5' flanking region -378)	gagaaggtctgagggaaccg C/T gggcaggaggagaaaggag	6235
GSTM1	11	(5' flanking region -343)	agggagagaagccttctgccc G/A ttaggatctggctgtgtct	6236
GSTM1	12	(intron 2 118)	tgctggagctgcaggctgtc T/C cttccctgagccccggtag	6237
GSTM1	13	(intron 3 233)	agtgtgtgcccgggtctctc T/C ctgctcttctgtattgggaag	6238
GSTM1	14	(intron 4 26)	tgtgtgtgtgtgcaatgtgt G/A gggggaaagtgccctcctcc	6239
GSTM1	15	(intron 5 140)	actatcagcagttattctca C/T gactccaatgtcatgtcaac	6240
GSTM1	16	(intron 5 577)	ctgccacccattagaagga A/G ctttctactttccctgagct	6241
GSTM1	17	(intron 5 645)	gctggtctggatccagaggg T/A gccaggtgcttgggctctcc	6242
GSTM1	18	(coding region 519 (Asn 173 Lys))	caccgtatatttgagcccaa G/C tgcttggagccttcccaaa	6243
GSTM1	19	(coding region 528 (Asp 176 Asp))	tttgagcccaagtgccttga C/T gccttcccaaatctgaagga	6244
GSTM1	20	(intron 7 2421)	cagcaccgtgtagaatcttc A/G taagtgttagctgttactgt	6245
GSTM1	21	(3' flanking region 42)	atttgcctctggccatctac C/T cagactgtctgtctgtctgt	6246
GSTM2	1	(intron 1 7)	ggaacatccgggggtgagc C/G agggctccgtggggcggtggg	6247
GSTM2	2	(intron 1 45)	gggacgggggtgcgtggggg C/T ggggaaagtgtggagcagctg	6248
GSTM2	3	(intron 3 70)	gactgcattctcctctccca G/C cttagaggtgttaagatcag	6249
GSTM2	4	(intron 3 224)	agcagggccctgtgtctctc T/C tgcccttgcatatggggaag	6250
GSTM2	5	(intron 5 100)	ttgatctctctgtgtgagtt C/A ttggtcttgctgactctaag	6251
GSTM2	6	(intron 5 341)	tcctcttggtgggttctatgg T/C ctggctggcttcaggagtag	6252
GSTM2	7	(intron 5 696)	accttttagctagacacagag C/T gctgatttgtgcatttaca	6253
GSTM2	8	(intron 5 723)	ttgtgcatttacaatccttt A/G gctaggcagaaaagttctcc	6254
GSTM2	9	(3' untranslated region 10	ctcagccccagagctgtcccc G/A tgttgcatgaaggagcagca	6255
GSTM2	10	(3' flanking region 139)	ttctgtctgggcatagtaagg C/T gcttgagaattcttgcctcc	6256
GSTZ1	1	(5' flanking region -546)	agcagggcccccagccgcac C/A gcctcgaagcgcgtgagcc	6257
GSTZ1	2	(5' flanking region -321)	tgtctgaccagccgccccgc T/C aaggagtcacaaagaggcag	6258
GSTZ1	3	(intron 1 2890)	aaaatactgcataaaaacca G/A gccacgctctgttgggggga	6259
GSTZ1	4	(intron 1 2896)	ctgcatcaaaaaccagggccac G/A ctctgttggggggacaccaa	6260
GSTZ1	5	(intron 2 255)	tctcccaacactgtctctca A/G agcccttgggcaaccatgtt	6261
GSTZ1	6	(intron 2 1560)	caccactgtttaagccctg G/C gggggcagagttaaacacaa	6262
GSTZ1	7	(coding region 94 (Lys 32	ccttgaaggcatcgactac G/A agacggtgccccatcaatctc	6263
GSTZ1	8	(intron 4 297)	agaaggaggagtttgcctggc C/T ctgtccctctgggtccaggg	6264
GSTZ1	9	(intron 6 94)	tatctgaaccagctccccag G/A ctgcttgggctgacagtt	6265
GSTP1	1	(intron 1 269)	ctccccgggctccagcaaa C/G ttttcttgttgcgtgcagt	6266
GSTP1	2	(intron 2 134)	ccccgggctccttctctgtt C/T cccgcctctcccgccatgcc	6267
GSTP1	3	(intron 5 438)	gtgtgtgctgctgctgtgc G/A tgtgtgtgctgctgtgtgtg	6268
GSTP1	4	(intron 6 162)	cccgtggctgagtcctcag C/T cccctcgccctgcagatctc	6269
GSTP1	1	(5' flanking region -103)	taaaagtggtcccaggcgct C/T gtgcccaccaatggggcaca	6270
MGST1	1	(promoter region -1879)	ttaataaatgtttattcaat T/G aaaccaactgctaattctc	6271
MGST1	2	(promoter region -508)	tctggaccctgaacaggagg G/C gacatcgtgacaaagcaat	6272

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
MGST1	3	(promoter region -314)	cctggagatttttaactttct G/A cgaagtttttaaaacaact	6273
MGST1	4	(promoter region -131)	atcagcaggcgatggttact G/C tggcggggttaaatcaggtga	6274
MGST1	5	(intron 1b 36)	ggagaaggggacgcgcatca A/G aggggtggcaggcagggaagg	6275
MGST1	6	(intron 1c 456)	ccccctgggaacgggttctcac C/T tgtgccccacttccccagtc	6276
MGST1	7	(intron 1c 719)	gcccgcaagcattgctgtat A/G gcacccaggcctccagtgag	6277
MGST1	8	(intron 1c 985)	cgagtaaaatttttctaccg C/G tttgttttagagtgtgtct	6278
MGST1	9	(intron 1c 1428)	gtaaaggggaagggcgttcc T/A caactgagaagtgaagattc	6279
MGST1	10	(intron 1c 2914)	ctcatcagggtgtgtgcaga T/G gcttgggtgctggccagtcctc	6280
MGST1	11	(intron 1c 4274)	attgtaataagattaacaaag G/T tgatgaaagtagtgatcata	6281
MGST1	12	(intron 1c 4276)	tgtaataagattaacaaaggt G/T atgaaagtagtgatcataat	6282
MGST1	13	(intron 1c 4767)	gccttctctcttcagcacatt C/T ccaattatacttccaattcc	6283
MGST1	14	(intron 2 2379)	ttctcaaatcttcattatata G/C tttcttcaacccaaagttt	6284
MGST1	15	(intron 2 2767)	tttaactatagatgccttct T/G ctctctctgtgtttgattta	6285
MGST1	16	(intron 2 2974)	tcactgcagcctcaacctct C/T gggctcagggtgactcctcaa	6286
MGST1	17	(intron 2 3083)	aaaaaattgttagataggg T/G actccctatgttccccaggc	6287
MGST1	18	(intron 2 3106)	tcocctatgttgcacaggctg A/G tcttgaaattctgggctcaa	6288
MGST1	19	(intron 3 1495)	gtcagacaatggcctcagc G/A tctctctcttgcagaatatg	6289
MGST1	20	(intron 3 1703)	ttctcttctaagaagaagtc T/C gtgcagatacttagcagaaa	6290
MGST1	21	(intron 3 2528)	ttttggagacacttttcaga G/C agagcgtttccagcatcttc	6291
MGST1	22	(intron 3 2557)	tcacgcatcttcccttcca T/C ttttaagttagacttttttt	6292
MGST1	23	(intron 3 2731)	atacacataggaacaatta A/C ctaaaaacttaaggtaatat	6293
MGST1	24	(intron 3 3032)	agagacatttagaataatatt C/A cctttaaaggttagagaataa	6294
MGST1	25	(intron 3 3045)	atatattccctttaaaggta G/C agaataacccttcaactgaga	6295
MGST1	26	(intron 3 3289)	ggtttatagtggttccccccc T/A ccccgccccaaaagaccca	6296
MGST1	27	(intron 3 3976)	ggaaagctgggggaactgttt T/C cctggaacagagtcctcaaaa	6297
MGST1	28	(intron 3 4288)	ccatttctattgtcaactgc G/A taacacaggcgtagaagtg	6298
MGST1	29	(intron 3 4298)	tgtcaactgcgtaacacagg C/T gtagaagtggacattgtttt	6299
MGST1	30	(intron 3 4429)	attggagggtgacgatatctc T/C gtgatgctgggggagaaatc	6300
MGST1	31	(intron 3 4519)	tttaataaaaaatggtaatt C/T tgtcttttcttcccatctc	6301
MGST1	32	(intron 3 4817)	attgctatagaagagagtaa C/T gtaaagcagaaatagttttc	6302
MGST1	33	(intron 3 6077)	tttgaattagtgtctttaa T/C agttatctttttccacagag	6303
MGST1	34	(3' untranslated region 60)	gggttaaacccattttgaata T/C tagcatttgccaatatcctgt	6304
MGST1	35	(3' flanking region 147)	tatttgcttctctctctctc C/T tgttttcttttctctgaaa	6305
MGST1	36	(3' flanking region 237)	cagcagctttttcctatgaa C/T aagacattctccaaataact	6306
MGST1	37	(intron 1C 904-923)	tgcgattatcttggtaatt (A)16-19 ggcaaatcagtcacaaattg	6307
MGST1	38	(intron 1C 3433-3434)	ccccttcaataactagaacaa (AA) gcagacacattaaatgttac	6308
MGST1	38	(intron 1C 3433-3434)	ccccttcaataactagaacaa gcagacacattaaatgttac	6309
MGST1	39	(intron 1C 5146)	actatttcaattttttttt T/Δ ggagggggagacagagcttc	6310
MGST1	40	(intron 2 552-563)	cccagcattataagaatgac (T)10-12 aagtgcagatgtggggagg	6311
MGST1	41	(exon 3 172-173)	tagcatttggcaaggagaa AA/Δ tgccaagaagtatcttcgaa	6312
MGST1	42	(intron 3 152-158)	agaaaactggatgtctgaa TTGACA/Δ (GTCCAATAT)	6313
MGST1	43	(intron 3 2198-2200)	ggatttttagattctcctcta CTA/Δ tcttttccgaccttccaccc	6314
MGST1	44	(intron 3 2567-2568)	ccctttccatttttaagtta (A) gacttttttttttcaactct	6315
MGST1	44	(intron 3 2567-2568)	ccctttccatttttaagtta gacttttttttttcaactct	6316
MGST1	45	(intron 3 2571-2580)	tttccatttttaagtttagac (T)9-11 caccctctctctgttacttcag	6317
MGST1	46	(intron 3 3288-3289)	ggtttatagtggttccccccc (C) tccccgccccaaaagaccc	6318
MGST1	46	(intron 3 3288-3289)	ggtttatagtggttccccccc tccccgccccaaaagaccc	6319
MGST1	47	(intron 3 4682-4683)	tcctcttcatgtctctatgt (GAGATGTTGTGGCTCACAT)	6320
MGST1	47	(intron 3 4682-4683)	agtcacatctctttgtgagac	6321
MGST1	47	(intron 3 4682-4683)	tcctcttcatgtctctatgt	6321
MGST1	48	(3' flanking region 1359-1)	acacacacacacacacacac CC/Δ tgctctggagttgggcaact	6322
MGST1	49	(3' flanking region 1889-1)	ttagaatagtttcttaactat ACT/Δ tttactcccaagagaagctt	6323
MGST1L1	1	(5' flanking region -105)	tgctgcccgtgcccgtggggc G/A gggcggtggcggtgctggct	6324
MGST1L1	2	(intron 1 277)	agtgtctgtgagagaagcag G/A ttctggagggtggagtggtg	6325
MGST1L1	3	(intron 2 8030)	ggggttatagacagacccctc C/G gccccaccacacatatgca	6326
MGST1L1	4	(intron 2 8499)	gtatggcaggagtggggtcc C/T ggcaagccatagaggtatgg	6327
MGST1L1	5	(3' untranslated region 46)	cgccacctgtgaccagcagc T/G gatgcctctctggccaccag	6328
MGST2	1	(5' flanking region -46)	ggtcagcattcaagtcag A/T agcgccatttatcttccctg	6329
MGST2	2	(intron 1 176)	ggtcacccatgcccgctgct A/C cctcctctcccaaggggcgaag	6330
MGST2	3	(intron 1 204)	tcccaggggcaagcagagac T/C gagaacattccagagattag	6331
MGST2	4	(intron 1 373)	ttacaagtgttccaaaggaa A/T cgtgcctgtcttcaaacctg	6332
MGST2	5	(intron 2 -3245)	ctctgtgatttgccacctc G/A gcctcccaagtgctgggat	6333
MGST2	6	(intron 2 -1998)	aggccgaggtggcggtatca T/C gaggtcaggagatcgagacc	6334
MGST2	7	(intron 2 -1640)	tgttatttccctgcatagcc A/G taatataaagtatgaattt	6335
MGST2	8	(intron 3 41)	actgtgttctaagtatgact A/G tgatgcttaaacgattaaag	6336
MGST2	9	(intron 3 453)	atcagagtgtatgtgtcag A/G tatatgaacttttgcttcat	6337
MGST3	1	(5' flanking region -520)	acaaaaagcccttaacagc A/C taaatccattcacttcggga	6338
MGST3	2	(5' flanking region -355)	cgcttaaaaccgctacgggtg G/A ctctgctggggacaaattat	6339

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
MGST3	3	(5' flanking region -234)	ctgggggagtagatatatgt T/A tttagagaatgagaggagtaa	6340
MGST3	4	(intron 1 74)	agcctttgagcaggcaactcc C/T atatttcagcctatgacgagc	6341
MGST3	5	(intron 1 682)	agaaaatgccctctctttat G/C tggggtggcagcagcgagcc	6342
MGST3	6	(intron 1 832)	cgagtttacagctacataa T/C agcgtcgggggcaagtaagt	6343
MGST3	7	(intron 1 1919)	aataaaattcctgagtttct G/C tcaactgcctcttacagtacc	6344
MGST3	8	(intron 1 1991)	tgtaattaggcaacaggaaa A/G ttgtactatctttcaaatgc	6345
MGST3	9	(intron 1 4458)	tcttccatcctcctaacata T/C agttagcttccactctccaa	6346
MGST3	10	(intron 1 4676)	tgaatatgcaatgcaattgt C/G gggggatagttacttttcat	6347
MGST3	11	(intron 3 278)	cagcatgacccatctaaacc G/C atgttgactctcccaggcct	6348
MGST3	12	(intron 4 423)	cttgccctttttgtgtgggg T/G gtggggtgttcacagagaag	6349
MGST3	13	(intron 4 506)	gtgcagagaagaaacaaag T/C ggggaagggtgaaaggggat	6350
MGST3	14	(intron 4 -162)	tcacagatattttattttcc C/T gactgaaactaacttaattc	6351
MGST3	15	(intron 4 -130)	acttaattctacctaatttg C/G gtggggagtagttggccaaa	6352
MGST3	16	(intron 4 -105)	ggagtagttggccaaatcat C/G aaattgttaactttttgcta	6353
MGST3	17	(intron 4 -65)	aacatattgtgtaatacaacc C/T taggtgttaaaaaaggtttg	6354
MGST3	18	(intron 5 105)	atcccagcaactttgggaggc G/C aaggcaggcagattgcttga	6355
MGST3	19	(intron 5 197)	aaaaaatcaaaaattagcc G/A gatgtgtgtgtgcacacctg	6356
MGST3	20	(intron 5 222)	tggtgtgtgcacacctgtagt C/T ccagctactctgggaggctga	6357
MGST3	21	(intron 5 374)	tcttatgctactatattttt T/C tcttgggaatttgagaaaa	6358
MGST3	22	(3' untranslated region 51)	atgacttacctttattttcca G/T ttacattttttttctaaata	6359
MGST3	23	(3' flanking region 166)	agtcgtattgtgtgtatgta G/T gtatagtcagtcacacatga	6360
SULT1A1/ST	1	(5' flanking region -1597)	gcagagtaaaagggaactcact C/G aagaagaggaaactgggggt	6361
SULT1A1/ST	2	(5' flanking region -1491)	gaggggtatattcatgaaga G/T tccaggaaaaggttaagatt	6362
SULT1A1/ST	3	(5' flanking region -1376)	cggtttcattatgttactgat C/T a/g taca a/g tgagatcctaggt	6363
SULT1A1/ST	4	(5' flanking region -1375)	ggtttcattatgttactgat c/t A/G taca a/g tgagatcctaggt	6364
SULT1A1/ST	5	(5' flanking region -1370)	catatgttactgat c/t a/g taca A/G tgagatcctaggtgaaacc	6365
SULT1A1/ST	6	(exon 1B -65)	aaccctgcattccccacaca G/A caccacaatcagccactgc	6366
SULT1A1/ST	7	(intron 1B 442)	gagccacccctgcctaggcct G/A tgcttttctgtagtcatcag	6367
SULT1A1/ST	8	(exon 1A -197)	gctgggggtcccagcaggaa A/G tggtagacaaaagggcgctg	6368
SULT1A1/ST	9	(exon 1A -159)	ctbgctgggcaggagacagc A/C caggaaaggtcctagagcttc	6369
SULT1A1/ST	10	(exon 1A -95)	gagaccttcacacacctga T/C atctgggctctggcccgaca	6370
SULT1A1/ST	11	(intron 1A 60)	ctggttttcagccccagccc C/T gccactga c/g tggcttttga	6371
SULT1A1/ST	12	(intron 1A 69)	agccccagccc c/t gccactga C/G tggcttttgaagtgccggca	6372
SULT1A1/ST	13	(intron 1A 174)	tgtgatgggtgtaagggaac G/A ggctgtgctctggccctga	6373
SULT1A1/ST	14	(intron 6 11)	catgaaggaggtgagaccac C/G tgtga a/t gcttccctccatgt	6374
SULT1A1/ST	15	(intron 6 17)	ggaggtgagaccac c/g tgtga A/T gcttccctccatgtgacacc	6375
SULT1A1/ST	16	(intron 6 35)	gaagcttccctccatgtgac A/T cctggggcccgccactcac	6376
SULT1A1/ST	17	(intron 6 71)	ctcacaggggaccacagg T/C caccagcccccctcccttg	6377
SULT1A1/ST	18	(intron 6 108)	ttggcagccccacagcagg C/A cc g/a gattccccatcctgct	6378
SULT1A1/ST	19	(intron 6 111)	gcagccccacagcagg c/a cc G/A gattccccatcctgctctct	6379
SULT1A1/ST	20	(intron 6 270)	ctccctgccaaaaggtgtgc C/T acccagggccacagtcagtg	6380
SULT1A1/ST	21	(intron 6 488)	ttttacttttctgtaatcag C/T aatccagacctccactgagg	6381
SULT1A1/ST	22	(intron 6 509)	aatccagacctccactgagg A/G gccctctgctgctcagaacc	6382
SULT1A1/ST	23	(coding region 600 (Pro 201 Pro))	ccctctgctgctcagaacc C/G aaaaggagagattcaaaagat	6383
SULT1A1/ST	24	(coding region 638 (His 213 Arg))	gactctggagttttgtggggc A/G ctccctgccagaggagaccg	6384
SULT1A1/ST	25	(coding region 645 (Leu 215 Leu))	gagtttgggggcaactccct G/A ccagaggagaccgtggactt	6385
SULT1A1/ST	26	(coding region 902 (Gly 301 Ser))	gctgtgagaggggctcctgg G/A gtcactgcagagggagtg	6386
SULT1A1/ST	27	(coding region 973 (Trp 325 Arg))	taaaatatgaattgagggcc T/C gggacggtaggtcatgtctg	6387
SULT1A2/ST	1	(5' flanking region -547)	tgttttttctgtgttctatg G/C atccatgctctgtctccacc	6388
SULT1A2/ST	2	(5' flanking region -425)	tgtgggttgcaactgggcccag G/A acccctggcaccttcaagac	6389
SULT1A2/ST	3	(5' flanking region -358)	ctttccagggcctgctctatc C/T ca g/t ctttctctccaatccc	6390
SULT1A2/ST	4	(5' flanking region -355)	tccagggcctgctctatc c/t ca G/T ctttctctccaatccctcc	6391
SULT1A2/ST	5	(5' untranslated region -)	actcggggcaggaggggac A/G agggcaggttcccaagagct	6392
SULT1A2/ST	6	(intron 1A 85)	ctgaactggccttgtgagtg G/A ggcaagtcactcagcctccc	6393
SULT1A2/ST	7	(coding region 20 (Ile 7 Thr))	catggagctgatccaggaca T/C etc t/c cgcccccaactggagt	6394
SULT1A2/ST	8	(coding region 24 (Ser 8 S))	gagctgatccaggaca t/c etc T/C cgcccccaactggagtacgt	6395
SULT1A2/ST	9	(intron 2 34)	gccaccacccctctccagg T/C ggcagtcgccaccttgcca	6396
SULT1A2/ST	10	(intron 5 77)	cagcaacctgtgtgcccac T/C cctgcccgtctctccagt	6397
SULT1A2/ST	11	(intron 6 684)	actggggtcccaagggttcga G/C gactggctctatgggtttt	6398
SULT1A2/ST	12	(coding region 704 (Asn 235 Thr))	gttcaaggagatgaagaaga A/C ccctatgaccaactacacca	6399
SULT1A2/ST	13	(3' untranslated region 89)	gctctgagctgtgagagggg T/C tcttgagtcactgcagagg	6400
SULT1A2/ST	14	(3' flanking region 98)	ctcccccgtccagctcctc A/T acttgcctgtttggagagg	6401
SULT1A2/ST	15	(3' flanking region 817)	ccactgactcggggcttgcc A/C aggtgcccagggtggcaaa	6402

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
SULT1A2/ST	16	(3' flanking region 1006)	cctotcccctggaggctgct T/C taccgcgtgtggggcgcat	6403
SULT1A2/ST	17	(3' flanking region 1464)	tcccgtagccaggcaagtt C/T ggtgaccagagagcagcccc	6404
(SULT1A2/S	18	(intron 4 1728)	tcagcttctcctcttgccaa A/Δ ccaagagatgagctgscctg	6405
SULT1A3/ST	1	(coding region 843 (Ala 281 Ala))	cgcttcgatgcggactatgc G/A gagaagatggcaggctgcag	6406
SULT1C1	1	(intron 3 2280)	gcaaatTTTTGGTATTtTTA G/T tacagtcagggttttaccat	6407
SULT1C1	2	(intron 3 3742)	gcagatctcacttttctggca G/A attccctgaatttgctcccc	6408
SULT1C1	3	(intron 3 4453)	ttcatagggtcttttccctca C/T ttgttttgaattttgtata	6409
SULT1C1	4	(intron 3 5234)	gaaaagagactagaggcagg A/G gagctttgcagttcttcttaa	6410
SULT1C1	5	(intron 3 6175)	tggctggcaggagggtgagg G/C agtcctctcttctctggtcc	6411
SULT1C1	6	(intron 4 205)	acatgaaggcaggatccaga T/C tgaatgtttggagggaacta	6412
SULT1C1	7	(intron 4 408)	ggctcacgcctgtaatccca G/C cactttgggaggccgaggcg	6413
SULT1C1	8	(intron 4 429)	cactttgggaggccgaggcg G/C gtggatcacaaagtcaggag	6414
SULT1C1	9	(intron 3 2106-2115)	tgcagtggtctgtttgtttgg (T)8-11 gagacaaagctggtctgt	6415
SULT1C1	10	(intron 3 4199-4210)	atgccagcctaattttgtta (T)10-13 agagacaggaatttcaccatg	6416
SULT1C2	1	(5' flanking region -110)	tctgtttaactcacagagaa C/T ggaagggtctggaacgggacc	6417
SULT1C2	2	(coding region 15 (Asp 5 G	acactaatggccttacacga C/G atggaggattttacatttga	6418
SULT1C2	3	(intron 1 297)	gtagactgttttattttatc A/C ttcccaatctaggcccttat	6419
SULT1C2	4	(intron 1 363)	gagtggtgtgagctagaaagg T/G gatcctgagctgctgattggg	6420
SULT1C2	5	(intron 1 2300)	gggtactatcagcagccac C/T acctcagggaaggatgacttc	6421
SULT1C2	6	(intron 2 455)	aagacttggaaagcaataga T/G aaaaaaaatctgtagaaat	6422
SULT1C2	7	(intron 4 55)	caaaatctccaaacacccta G/A aaggaaagaatcttttcttt	6423
SULT1C2	8	(intron 4 111)	ctgccttctttaaaggaa C/T tctcacttctcttcagggaat	6424
SULT1C2	9	(intron 5 1657)	ctttgtgtttactttgtttt T/C acttggtacaaaagtgtgtt	6425
SULT1C2	10	(intron 5 2082)	tctgctctagagatggagg C/A gtcccacagccacagtgatg	6426
SULT1C2	11	(intron 6 933)	agctactgaacctctccac A/G taactgtatttcaggggcag	6427
SULT2A1	1	(intron 2 478)	ggactgggctctgtacacac T/C tctgttactgtgtgtaaat	6428
SULT2A1	2	(intron 3 382)	caaaacctcttaatatctt G/A ttctatctgtctcagaact	6429
SULT2A1	3	(intron 3 409)	tctgtctcagaactgattgc A/G tgactctaggaatcgctatat	6430
SULT2A1	4	(intron 5 249)	agctggaaattacaggcaca C/T gccaccacaccagctaatt	6431
SULT2A1	5	(intron 5 395)	aggcatgagccacggcgccc G/A gccaatttatcagctttaat	6432
SULT2A1	6	(3' flanking region 33)	ttctctgttaaaagttaacca G/C ggttgccaggc a/g cggtggt	6433
SULT2A1	7	(3' flanking region 46)	gttacca g/c ggttgccaggc A/G cggtggttcatgcctgtaat	6434
SULT2A1	8	(3' flanking region 199)	ttagccaggcgcttggtctc A/G tgtctgtaatcccagcatt	6435
SULT2B1	1	(intron 2 4162)	ttctcccctctctccaccat C/T cgcacacaggtgatctacat	6436
SULT2B1	2	(intron 3 879)	gagggcatccagctctgggg G/A ctggacctgggggtttgtgg	6437
SULT2B1	3	(intron 4 3882)	ttccacgtctccttctctggc C/T gagtgcctcctctccgtga	6438
SULT2B1	4	(intron 5 1780)	cctgcagaaggggtccctt C/T catgtccaagcagtaattggc	6439
SULT2B1	5	(intron 5 1814)	taatggctgcagcatggagc G/A ttgtggggcattgagacag	6440
SULT2B1	6	(coding region 789 (Cys 263 Cys))	ccctcttctccaggggtctg C/T ggcgactggaagaaccactt	6441
SULTX3	1	(intron 1 332)	cctgcttctccctttactcg G/T ctggctgtgtgacctggac	6442
SULTX3	2	(intron 1 1167)	taggaatggctaagcgtgtc G/A ttggctctctgtggccactca	6443
SULTX3	3	(intron 1 2872)	cattctcactgatgcagacg G/A aagcttctgggctggggcg	6444
SULTX3	4	(intron 1 6242)	cacccttggtctttaccagc A/G tggaaacattttacctgaat	6445
SULTX3	5	(intron 1 6601)	gcgtgggctcttgaggagg C/T gagaggagagtggaggccc	6446
SULTX3	6	(intron 1 6768)	agcttgaatagagccagact C/T tcttgggacctgttgacccc	6447
SULTX3	7	(intron 1 6905)	agtactttgttttatctccc C/T catctcacaactttgccat	6448
SULTX3	8	(intron 1 7464)	gccaggatcccttgagagac G/A acatgaacacagccaggagc	6449
SULTX3	9	(intron 1 7833)	tgcttcgggctgggcttgcc G/A ggggcagctgtgtccaggc	6450
SULTX3	10	(intron 1 8189)	caaatggggcccttaatgc C/T gcacaccagagcctcctttc	6451
SULTX3	11	(intron 1 8316)	ctctcacacaaggcgaggc C/G tcttccccttgaggcagagc	6452
SULTX3	12	(intron 1 8617)	agacagaggctggggccaag C/T cagggttgccggagcttccc	6453
SULTX3	13	(intron 1 8631)	gccaagccagggttgccgga G/T ctctctggactggctcaggcc	6454
SULTX3	14	(intron 1 9493)	ttttctcttagagcttccc G/A tctgtctctgtctcaggggc	6455
SULTX3	15	(intron 1 10306)	caggcggggagcctgaatgc C/T gcagtcgtgagggtggccag	6456
SULTX3	16	(intron 1 11987)	tcataaaataatgatcatcag T/C acactttttggaatttgag	6457
SULTX3	17	(intron 1 13085)	ctctgtgcccgtgttgaga C/A aggccatgccttagagctct	6458
SULTX3	18	(intron 1 13108)	gccatgccctagagtcctgg G/A gagttccaccccagaacagc	6459
SULTX3	19	(intron 2 700)	gaaccatctgggagtcgttc C/T gtactgccgtgccaggggcc	6460
SULTX3	20	(intron 2 818)	agccatagtagctagccagc G/A atcagcgctgggaggggagc	6461
SULTX3	21	(intron 2 1677)	actccacttcccctgaaccc C/T accccttctctctctctctg	6462
SULTX3	22	(intron 4 4954)	gcgtgccgaaggcggagg C/T tgggatggctcaagacgtga	6463
SULTX3	23	(intron 5 3632)	ccagctgactcccacaccag C/T ggtcagagaacattgtcttt	6464
SULTX3	24	(intron 5 3662)	acattgtcttttaagggttc C/T gaagtgtctgcaataaagaaa	6465
SULTX3	25	(intron 6 1874)	tctgatctcagagagctgac A/G atggaagaattctaaacga	6466
SULTX3	26	(intron 6 2133)	agaccggtgcctgcagttta T/G cccacagctcagccctccct	6467
SULTX3	27	(intron 6 2524)	ggaaggccagggcgtgcctg T/C gatgccagagcagtgcaact	6468
SULTX3	28	(intron 6 2573)	agatcatactcgtcctctggg A/G tgtttattaaacacctgcca	6469
SULTX3	29	(3' flanking region 12)	gttcccggcgttcgctcgag C/G gtttctgctgtgggggtag	6470

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
SULTX3	30	(3' flanking region 445)	tccaaagcctgtcttccctga T/G ttcctgtggaaggagagctcc	6471
SULTX3	31	(intron 1 6418)	ctctccctgttagtgtgggg G/Δ cagctctttccagtgctccg	6472
SULTX3	32	(intron 5 2458)	cccttaaaggggaagttcacc C/Δ ttctctgcttccaggctcc	6473
TPST1	1	(5' flanking region -298)	accgccaccatgccagct A/C attttttttgtatttttttt	6474
TPST1	2	(intron 1 3520)	agaaaaagcagattaatgtaa C/G agtgacgcttagacacaaag	6475
TPST1	3	(intron 1 3610)	ggcagaagagaatatagca A/G ctattaaacacaaataaatt	6476
TPST1	4	(intron 1 20828)	tattgctgtccacctgggca A/G tctgtcctgtctgataagtcg	6477
TPST1	5	(intron 1 -6761)	aatacaatactattctgtga T/C aattctagaggccccagaga	6478
TPST1	6	(intron 1 -544)	tagaacaagtgaattttta C/T gttcttagtggtttatgggt	6479
TPST1	7	(intron 1 -526)	tacgtttcttagtggtttatg G/T ttggcagttttcccccaaca	6480
TPST1	8	(intron 1 -234)	tcaagacatttaataatgca C/T atgtttcagctaaccctttt	6481
TPST1	9	(intron 1 -48)	ttatagtggttttaagcatg A/G tttctaaaaatttaataa	6482
TPST1	10	(intron 2 -18944)	aaaacattagaactgggaag G/A ttaaaaaattcttagtcttt	6483
TPST1	11	(intron 2 -18687)	tatgtgcaccctaataacat A/G ttctcttaaaactagtacta	6484
TPST1	12	(intron 2 -18501)	ttgggaaggttaacttaatgta A/G gtgcctgaaaaacagggata	6485
TPST1	13	(intron 2 -159)	gaatggggattttccctcagt C/G ctgcccactggctgctcttg	6486
TPST1	14	(intron 2 -19)	acctgttgcttaaaactcac G/A cctgctttgtttttccaggt	6487
TPST1	15	(intron 3 158)	tgctgggggaagaagatcag C/G gtctgggacttggtgatttt	6488
TPST1	16	(intron 3 3779)	agcagggcagctcacccctcc C/T ggcacacccatgtgttcacc	6489
TPST1	17	(intron 4 292)	ttgttattttcattatgaac C/T atgaatatttcagctgaaa	6490
TPST1	18	(3' untranslated region 15)	gttgctgtacatgtttctaa T/G gttttgtagaacagctgtgc	6491
TPST1	19	(3' flanking region 264)	acgggtgcttgccctgcatta C/T cattttgtagtgaagtttct	6492
TPST2	1	(intron 2 578)	tcacctatcctctcactgc G/A aggatgccaggataacctccc	6493
TPST2	2	(intron 2 789)	cttaagccatctgtcaggtc A/G ttgctgtcttctgtctcactt	6494
TPST2	3	(intron 3 2009)	cccaggtggagtgtagtgg T/C gtgatct c/t ggctcactgcaa	6495
TPST2	4	(intron 3 2017)	ggagtgtagtgg t/c gtgatct C/T ggctcactgcaaactccgcc	6496
TPST2	5	(intron 3 2035)	ctcggctcactgcacacctcc G/A cctccggggttcaagcagtt	6497
TPST2	6	(intron 4 104)	aatgttcaagtctctcaattc C/T tggctcatctgatttgttct	6498
TPST2	7	(intron 4 379)	taataaaataaactattggt C/T cctttctgtcttataaaggt	6499
TPST2	8	(intron 4 588)	tactgcagcctgatacttct C/T ggcttaagccatctctcac	6500
TPST2	9	(intron 4 626)	cacccaggtctcctgagtag C/T taggactgcaggtgcaagcc	6501
TPST2	10	(intron 4 718)	cccaggttggtctagaactc C/G tggccgttaaggatgccccct	6502
TPST2	11	(intron 4 873)	gttgatggccttatttatac G/A ttccattacagcttctagt	6503
TPST2	12	(intron 4 949)	caaatatttgaataatgggac C/G caggcctgaggaagagcttt	6504
TPST2	13	(intron 4 1033)	taagctcagcattttctgagc G/A tgtgctgatttttaggaata	6505
TPST2	14	(intron 4 1051)	gcgtgtgctgatttttaggaa A/G taacacgttatcgtatttgaa	6506
TPST2	15	(intron 4 1356)	gattcaacgtacataaccagc C/T gacattgacaggtgaatggc	6507
TPST2	16	(intron 4 1707)	gtctccttaaaaggtggctc G/T ctgcccctggctgccccag	6508
TPST2	17	(intron 5 215)	aagaccagcctgacccaaac G/A gtgaacccctgtcttacta	6509
TPST2	18	(intron 5 341)	tgggagggcagaggtcgagc G/A agctgagatcacgcccgttg	6510
TPST2	19	(intron 6 31)	ggacttcaactgggggttccc G/A ctgcttctgggtggccccc	6511
TPST2	20	(intron 6 273)	gtttgtctgacactggggac A/G gggcaggaagcaccactatg	6512
TPST2	21	(intron 6 693)	aaagggatttttttgaactt G/C gtaattcaaaagatttaagat	6513
TPST2	22	(intron 6 1635)	tctctgggtacagagtggcc T/G tgaacaaacatgagctcctt	6514
TPST2	23	(3' untranslated region 11)	cttcccactttcagatctc C/T gcaaatgacttcaatgccaa	6515
CST	1	(intron 1b 6302)	agagctcccccagagaggact A/G tgaggctgcatgatgatga	6516
CST	2	(intron 2a 1004)	gagtgagaccccatctctta C/T aaaatttttttttaaaagta	6517
CST	3	(intron 2a 1395)	atgcctaagtttacagtagc T/C aggcaggaaaggcacaacca	6518
CST	4	(intron 1d 473)	ccagagcctgaggttggtgc T/A ggggccccctccatggctgcc	6519
CST	5	(intron 2b 726)	ctatctctccagtgcccttc T/C gtccctgtctggaccctgct	6520
CST	6	(intron 2b 745)	ctgtccctgtctggaccctg C/A tggggggccacagagcaggc	6521
CST	7	(coding region 85 (Val 29 Met))	tcactagtcttctgctgctg G/A tgtactcctatgcccgtgcc	6522
CST	8	(intron 3 308)	tcgtctgaggtcaggagttc G/A agaccagcctggccaacatg	6523
CST	9	(intron 3 853)	ttttgtctataaaatggca G/A tttcatgtggcccaagctga	6524
CST	10	(coding region 198 (Asn 66 Asn))	gaggcagtgatccggggcaa C/T ggctcggcgggggagtgcca	6525
ST1B2	1	(intron 1 80)	acttgctccataaaatcatta C/T cattctaaataaagttata	6526
ST1B2	2	(intron 2 -352)	aacatttaaatagtcattta T/C agcaatgcacaggtataata	6527
ST1B2	3	(intron 2 -85)	attacataatgtccaaaat G/A tcttgaataaactggttgcca	6528
ST1B2	4	(intron 4 460)	gtacttgacattaaaaata T/C ctgatgttt a/g tatatccata	6529
ST1B2	5	(intron 4 470)	ttaaaaata t/c ctgatgttt A/G tatatccataaataagctaat	6530
ST1B2	6	(intron 4 518)	tttaagattgtctcatatt C/G ttacttctcttgggtactaa	6531
ST1B2	7	(intron 4 616)	aatgtttatgaaaaatagact T/C ttatctggttttagtggtcc	6532
ST1B2	8	(intron 5 58)	ctgcatcatgctgtaaaagg G/A ttgatattgtctttccaact	6533
ST1B2	9	(coding region 612 (Glu 204 Asp))	taatagaatccaaaggagga A/C atcaagaagatcattagatt	6534
ST1B2	10	(intron 6 582)	aatacattacttccatttaa G/A tagtctgtttattgtggctt	6535
ST1B2	11	(intron 6 3130)	agatgtaaaaattattcaa A/T ttttaaaagcctgaaaaatt	6536
ST1B2	12	(3' untranslated region 90)	tttaaaagtgtctaaatcaca C/A atctgaagaaataagagatt	6537

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ST1B2	13	(3' flanking region 50)	tcagatccagttttgttcc T/G ttgattctgagtttccaaat	6538
ST1B2	14	(3' flanking region 328)	tttgaccacaggacactgtgt T/G ccactgctgtctaccgagtt	6539
ST1B2	15	(3' flanking region 446)	gtagttcagatctttggaat C/A ttttttctatcatcaccta	6540
CHST1	1	(intron 1 3900)	gccctgccccactccacaga C/G ttgcccgcctccagccctt	6541
CHST1	2	(intron 1 6520)	cctccccagaggagctggg C/T acactggggccttgtgtgt	6542
CHST1	3	(intron 1 7963)	aaaacattcatgggggatta G/C tgctggctacgtcagagta	6543
CHST1	4	(intron 1 9173)	gcgctgccacagatcaggcc G/A aggtgggggacagaaatgcc	6544
CHST1	5	(intron 1 9701)	cccagaattctgaatacagc A/G gcgatgacgggactacgagg	6545
CHST1	6	(intron 1 12132)	aacagatccacaggaccaga C/A agcaaaagggaggaacatgc	6546
CHST1	7	(intron 1 12465)	atgcagggaaggggcttggc G/A caaaactgtcaactgagata	6547
CHST1	8	(intron 1 12561)	atgtccctcggtccactttc G/A ctttgagtttcaggtagctg	6548
CHST1	9	(intron 3 529)	ccatggctctcaggggtcct T/G catgctcaggggattgggtg	6549
CHST1	10	(intron 3 617)	agaggacagaggaagaggga C/A cactgggaactggggcgc	6550
CHST1	11	(intron 3 796)	aagaggcttcgcagctgtc C/T gcagggttaaatcctggggtg	6551
CHST1	12	(intron 3 818)	cagggttaaatcctgggtgc A/G aggaatgtttgttcagctcc	6552
CHST1	13	(3' flanking region 762)	ataactgggtacaggtttact G/C gtgtctacactggcagagaa	6553
CHST1	14	(intron 1 7874)	gttttcccttgccttgct T/Δ cattttcatcactcatttt	6554
CHST1	15	(3' flanking region 335-3)	cacactgccacactggcta (T)12-15 ggatttttagtagagcgggg	6555
CHST2	1	(5' flanking region -260)	agccggacagtcgccgggc G/A gtgacccggggccgctccc	6556
CHST2	2	(5' flanking region -56)	gcgctggggaccagccggc C/T gccgcctcgcgagtcgggc	6557
CHST2	3	(3' flanking region 218)	aggagtgaacacacattttg T/A attctaaaggcagaaaccaa	6558
CHST2	4	(3' flanking region 383)	gcagagaccaatgttttggg G/C ctgaggtcgttcagaaaaa	6559
CHST2	5	(3' flanking region 952)	tactgaacattcttcagaa T/C gttatactatgagaagaat	6560
CHST3	1	(5' untranslated region -2)	tccagcgtgccgaccggccc C/G gcagcgcctccatccctccg	6561
CHST3	2	(intron 1 96)	gcgtccaggcgcgcgcgca G/A actttggaggagagggggg	6562
CHST3	3	(intron 1 4467)	agagaagaatggggcagagc C/G ggagcagccaggggaggtga	6563
CHST3	4	(intron 1 4853)	ggatgagcactgccagctg A/G tccctgccaccttccacag	6564
CHST3	5	(intron 1 4965)	tccactgcagaggggacaca G/C tgaccaggagggagttggg	6565
CHST3	6	(intron 1 5046)	gggctgtccattcttctacc C/T ctggttccatccagtgctc	6566
CHST3	7	(intron 1 5300)	ccttttcttcttaaggcct A/G aagagatgacagaatgtgc	6567
CHST3	8	(intron 1 5354)	agcgcgtggactccacagcg G/A ggtgtgggtggccctggc	6568
CHST3	9	(intron 1 5428)	gacacgcttcagccctctgt C/G tctattgcccaaatctggc	6569
CHST3	10	(intron 1 6555)	gagtggggcaactgtggaag G/C ttctgttctctgtcttcttc	6570
CHST3	11	(intron 1 6990)	aaacacactggggccacccc G/A tccccgcactgtgactacac	6571
CHST3	12	(intron 1 7133)	ctgagggcctgtcctgcagg T/G ttgatgtgtctgaagagccc	6572
CHST3	13	(intron 1 7161)	gtctgaagaggcccccagaa T/C agaaatctagaacctgccag	6573
CHST3	14	(intron 1 7199)	cagtcacgaagcagtgctac C/T caccagaggatgaagaactg	6574
CHST3	15	(intron 1 7316)	cttgcatctggtgtaggtgc C/T tgggggtagcgtgccaggga	6575
CHST3	16	(intron 1 7967)	gacaggaaaccaccccgag T/G gatgtctggccctgtgacct	6576
CHST3	17	(intron 1 11412)	gcttgcaacttctgattcatt C/T tgcagtcactggctctttgt	6577
CHST3	18	(intron 1 11591)	ccctggaagggcctcactgc G/A gtgactcattaccagcatg	6578
CHST3	19	(intron 1 12541)	accacacagcatgaatggg G/C ccagccccagcctgcccgct	6579
CHST3	20	(intron 1 12672)	gtagccacagctggggctgt G/C gggtcaggcatggcaaggg	6580
CHST3	21	(intron 1 14809)	ggatgtgtaggggtttgggt C/T ggccttaagggtgggtgga	6581
CHST3	22	(intron 1 16161)	gatgtgtgtcaggcattgtc G/A ttgggatcttttaaccacac	6582
CHST3	23	(intron 1 16385)	tatttagcatgtgggtttca A/C ctttctgttttttcaaaagg	6583
CHST3	24	(intron 1 33638)	gacttggggcacgtccttgg G/C catgaactcttggtctatgtc	6584
CHST3	25	(intron 1 35145)	aggggaagccgaagcctcact T/C gctggggcttgctggcctc	6585
CHST3	26	(intron 1 35340)	tgtgaagtgtttgccacagt T/C ggtggccatggttcgcaccg	6586
CHST3	27	(intron 1 35436)	gccactcatgtatggagcaa T/C tgcctttttttcttctctt	6587
CHST3	28	(intron 1 36150)	ccatagaagaggctgggcct G/T aggaagccagggaagcagga	6588
CHST3	29	(intron 1 36194)	ggtgtggggaggccagcagg G/A gtgtgggctcagcggggag	6589
CHST3	30	(intron 1 37602)	ctgggaacagcaacttaaaaa A/T agaaatagtcctctggaagg	6590
CHST3	31	(intron 1 37725)	gggtgagccagggcagctccc C/T gaccgcga c/g ctgccctttca	6591
CHST3	32	(intron 1 37734)	gggcagctccc c/t gaccgcga C/G ctgcccttttccccctctcc	6592
CHST3	33	(intron 1 38208)	gccattcttagatgcaggtcc C/T gactttgggg t/c gcttgcat	6593
CHST3	34	(intron 2 255)	ctacagctgtgaaaggttag A/G caagatacttaacatttctg	6594
CHST3	35	(3' untranslated region 2)	acacctcagaggagcctgtg C/A ttaacattttagtagattatt	6595
CHST3	36	(3' untranslated region 2)	aggcctcatctgggtaggg G/C caagaggaaagtacagagt	6596
CHST3	37	(3' untranslated region 2)	ctggaattctccttagggc C/T ctgggaagagtattgcttaa	6597
CHST3	38	(3' untranslated region 2)	cttaacgcaggatgtgtctg G/A tgttttgtttcgggctttta	6598
CHST3	39	(3' untranslated region 2)	gcttgggtgtctttctgtttt C/T atggctgtgtttttgtctttt	6599
CHST3	40	(3' untranslated region 3)	ccgagggtcgtccagctctg C/T ttctgttttctctggacaatt	6600
CHST3	41	(3' untranslated region 3)	ctgtcagatcagggccattg T/C aaaccagagggtcgcattt	6601
CHST3	42	(3' untranslated region 3)	gttcccatgtggagggtcgg A/G ggggctgggactggggagg	6602
CHST3	43	(3' untranslated region 3)	ggccctgtaattgtggacag T/C agactttatccctctctt	6603
CHST3	44	(3' untranslated region 4)	ccagatgtgcataagaagcca G/A tctctgtcacatacacccga	6604
CHST3	45	(3' untranslated region 4)	taaaagcaatttaggctttt G/A tcttctgtcaatacatgcac	6605
CHST3	46	(3' untranslated region 6)	atttcatgtctgcaggttac G/A agacaccccttcac g/a gcata	6606
CHST3	47	(3' flanking region 281)	agacaggagtgttggggcag C/T ggtcagggggcctggggatg	6607

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
CHST3	48	(3' flanking region 997)	acctcttaaagtatttgagc C/T ggtgacctgtcatcccaacct	6608
CHST3	49	(intron 1 22595)	cgggagcaggaataaataa A/Δ gaataagaagaaagaggct	6609
CHST3	50	(intron 1 35423-35424)	gctcatgctcacagccatc AT/Δ gtatggagcaa t/c tgcctttt	6610
CHST4	1	(5' flanking region -1092)	atgaagccttggccatctc G/A ctgtgtcgtgccagcacctg	6611
CHST4	2	(5' flanking region -941)	ctgccagagagaacaggaa G/A ggaggaagagccacacaatt	6612
CHST4	3	(intron 1 -150)	caggaaatgatttggagaag G/T actggtgccattgttggcac	6613
CHST5	1	(intron 1 -144)	ggcctcttaggtttcagcca A/C gacaggtgactcttagcacc	6614
CHST5	2	(intron 2 17)	caacgtaagagcgcttctca T/A tgtccagctcctttgtttct	6615
CHST5	3	(intron 2 139)	aatccccagcactttggagg C/A ggagatgtgaggatgagca	6616
CHST5	4	(intron 3 1829)	gactgtatgtctgtattca T/C ataggaacaaataattcatg	6617
CHST5	5	(intron 3 2037)	aaatgaacacacacacaa C/G tgcagagaagcaacaaaag	6618
CHST5	6	(intron 3 2134)	aagcagctaaattgtgtcc G/A tacaggtgcaattaggcagg	6619
CHST5	7	(intron 3 2528)	atggtaaaagtgcctgggt G/A cagtatgtcagcatcctgct	6620
CHST5	8	(intron 3 2674)	gcacttatcctagaaagcc A/G tttctgaagactcagcagga	6621
CHST5	9	(intron 3 7039)	ctggctcccgccggccacc T/C gggagccagccacgtctga	6622
CHST5	10	(intron 3 7211)	gtagcccccaggacacccca T/G cctcaacatccattctggg	6623
CHST5	11	(intron 3 7294)	ggagcttccagtggttgg T/C acccccactctctgtccat	6624
CHST5	12	(intron 4 108)	gcagggctcctgactctgca G/A ggggcaatcacaggtggag	6625
CHST5	13	(intron 4 402)	agcactggaataaagtacagt T/C gcactgtagcggaggtggg	6626
CHST5	14	(intron 4 547)	ctcctgtcccgcataggag C/G gaaggagcagaggtgagatc	6627
CHST5	15	(intron 4 1142)	gccccaggtctcatagctcc C/G cattggcagtgctgggattt	6628
CHST5	16	(intron 5 1187)	cactgggcagtaatttggggc A/G tgggatgggcatgaggcc	6629
HNK-1ST	1	(intron 1 139)	gtgttttggcgacttgaga C/T ctccctagtcttcgggagta	6630
HNK-1ST	2	(intron 1 1020)	acctgagcagaaaattctct T/C ctctcgctgaaatgaaattg	6631
HNK-1ST	3	(intron 1 1091)	aagaatttgaacacacaca G/A gcaactgtcagttatattcg	6632
HNK-1ST	4	(intron 1 1971)	ctataactatttcaacata C/T gaaacaggcataattggatt	6633
HNK-1ST	5	(intron 1 2096)	atttagaatatttcattacc A/C agaataccaaataaacctg	6634
HNK-1ST	6	(5' untranslated region -9)	ctatccagtgacaagaggaa C/A caagaacctcagttcagggg	6635
HNK-1ST	7	(intron 2 -530)	agtgggcggaggcgagaaag G/A tcagtggttcttcttctgt	6636
HNK-1ST	8	(intron 2 -466)	gctacatcttctgacccagt C/T agaattttaaacacagccag	6637
HNK-1ST	9	(intron 2 -92)	acggaaatatttctgctgat A/T ctactgactgaaatcacct	6638
HNK-1ST	10	(intron 3 152)	catggcctccgttcttctat G/A ttacagaggtgtgaggggag	6639
HNK-1ST	11	(intron 3 312)	cacagtgcccttatgccttg C/T agcagggcgccctcagcgt	6640
HNK-1ST	12	(intron 3 1948)	tcctttgatgtatcaagttt T/C gtgctgaatgttttcagtg	6641
HNK-1ST	13	(intron 3 2140)	ttacacctggagaggagcac C/T gcagcggtccttaatactgc	6642
HNK-1ST	14	(coding region 187 (Leu 63 Leu))	agaagcacattcctgaggaa C/T tgaagggtggcacagccagg	6643
HNK-1ST	15	(intron 4 581)	cctgatcattccctagctgg G/A atgaggggtgcactctggaa	6644
HNK-1ST	16	(intron 4 615)	tctggaaggcctctcacttc G/C taacccccattctggatcta	6645
HNK-1ST	17	(intron 5 7)	gattgttctaaatgggtgt G/A tgggtctactgaatgtccac	6646
HNK-1ST	18	(intron 5 123)	acctgaaggagctgggtggc G/T tccagacaggcctgtttttg	6647
HNK-1ST	19	(intron 5 721)	ataattatgggctctgctta T/C gaaatttagcttcagacagg	6648
HNK-1ST	20	(intron 5 867)	tgctgcccacagagtcgggt G/A tcaactcctggccactgtttg	6649
HNK-1ST	21	(coding region 444 (Ile 148 Ile))	ccaggagcatttttcttccat T/C gaggagatccccgaaaacgt	6650
HNK-1ST	22	(intron 6 94)	ctgagttctgtacttggcag A/G ttgatcggaggaccacagag	6651
HNK-1ST	23	(intron 6 247)	catgaaggtagacatcatttt G/A ttaatagaattagcaggca	6652
HNK-1ST	24	(coding region 696 (Thr 232 Thr))	aggaggaaacggacagagac C/G cyggggatccagtttgaaga	6653
HNK-1ST	25	(coding region 870 (Ala 290 Ala))	gagaccctggaggacgatgc C/T ccatacatcttaaaagaggc	6654
HNK-1ST	26	(3' untranslated region 11)	tcaaatatctttattagacc T/C ggggctaaccaggtgaagat	6655
HNK-1ST	27	(3' untranslated region 11)	ccacacccctccttttagga C/T gccggggtctccacagcg	6656
HNK-1ST	28	(3' untranslated region 13)	ggaagcatcacacagcgta G/A gagcgtttccttcagggtgt	6657
HNK-1ST	29	(3' untranslated region 14)	tgaggttctctgctgctagtc A/G ggggtggcttcccatcact	6658
HNK-1ST	30	(3' untranslated region 15)	gcaaggggctgctgtaaatc G/C cagagacttttgcagcatca	6659
HNK-1ST	31	(3' untranslated region 16)	gggtggtgtggtgtccagg G/A tccatctttccagaatccat	6660
HNK-1ST	32	(3' untranslated region 18)	aggggagggctttttctacct G/A agaaggggagtgcttttag	6661
HNK-1ST	33	(3' untranslated region 22)	tccagcagtgccggttctctg G/T c/t aacaaggtaggccctgggtg	6662
HNK-1ST	34	(3' untranslated region 22)	ccagcagtgccggttctctg g/t C/T aacaaggtaggccctgggtg	6663
HNK-1ST	35	(3' flanking region 1016)	cacacgaagggtgactca C/T ggcctgcagggcacccagggt	6664
HNK-1ST	36	(3' flanking region 1152)	gcactgttctcctcatctgga A/C tctccagaagcagggaacag	6665
HNK-1ST	37	(3' flanking region 1291)	gccagagccctcagcaggat A/G gtgcagttacagggctgagc	6666
STE	1	(5' flanking region -605)	caggtttcttaaaataataat C/T gaaaggtgagtgatgtttac	6667
STE	2	(5' flanking region -536)	taaaattttcaggtctgctt A/G agagttaaaggcaaaagatt	6668
STE	3	(5' flanking region -231)	cttcttccccacccctga C/T ggcagacttgggaatttgaa	6669
STE	4	(5' untranslated region -6)	tgacgottaagatctgcctt G/A gtatttgaagagatataaac	6670
STE	5	(intron 1 69)	aaatatagaatgaaattat G/A tattacaaagctcttaaaaa	6671
STE	6	(intron 1 311)	caatgagaaaataaagcaag C/G agggtagaaggaggtagaat	6672
STE	7	(intron 1 655)	tctaagaagtagggactat G/A agaaccctatgtatctata	6673

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
STE	8	(intron 1 671)	ctatgagaacccctatgtat C/T tatatccaccatagttattct	6674
STE	9	(intron 1 772)	aaaaggcaggttggaagatg C/A aggggggagtagtcagaaaa	6675
STE	10	(intron 1 1715)	taaccatcttgcttaacctt A/G tcatttttagccaagtcatt	6676
STE	11	(intron 1 1928)	aaatgatacatattcaggaa A/G tcaaaaatctctgacttaga	6677
STE	12	(intron 1 1953)	aaatctctgacttagatacc C/T ggcaataataatcaaatgta	6678
STE	13	(intron 1 2087)	aattttgaagaatttgaag T/G tctgtggtttttattatca	6679
STE	14	(intron 1 2323)	taggtatgtaggagggtccc G/C ttatatcatagtgtttaat	6680
STE	15	(intron 2 165)	tctattccatgaccacaatt T/G ttacctgttaacttgaatagt	6681
STE	16	(intron 2 1707)	cctaggaccacaacatgagac A/G taatataccatcagtaaaat	6682
STE	17	(intron 3 850)	gggtgccattccctcaagaa T/G ttatactttgtgttacacac	6683
STE	18	(intron 4 1653)	agtaacaggctagtagataa T/C ataataactgaggccaacg	6684
STE	19	(intron 4 1899)	tacatgaacttagaataca A/G gtatgacacacacccaaca	6685
STE	20	(intron 4 1930)	cacaccaacaataaaattac A/G cagaatgataaaagaatttg	6686
STE	21	(intron 5 666)	ttctgatcatgtagtaacaa T/C tataaagaaaataataatgt	6687
STE	22	(intron 5 982)	aggcaaaagcagaacctttt A/C ctcacacaacattatattat	6688
STE	23	(intron 7 369)	agattttattctctctctt T/C ttgagttgaagaataaagtt	6689
STE	24	(intron 7 447)	cacctttcaagggttaagtgg C/A aaaaaatagaattcaata	6690
STE	25	(intron 7 672)	aatcttctctttgaacat A/T ctgtcagtgagagtcaggga	6691
STE	26	(intron 7 856)	tggtacagaggacttaaaac A/G gttgtcttctgttcaaacg	6692
STE	27	(3' flanking region 218)	cagcctcccaagtagctagg A/G ctacagacatgtgcaacat	6693
NQO1	1	(intron 1 80)	aggaggtttaggggtctgg C/A ctgaattttgttctcttgact	6694
NQO2	1	(5' flanking region -434)	ttctgtttgcccacgggacc C/G tcattctgttaaccgggatac	6695
NQO2	2	(5' flanking region -406)	gtaaccgggataccagccag A/G gatggggagcgggagcgca	6696
NQO2	3	(5' untranslated region -1)	tctgtcggctcctactgggg A/C gtgcgctggctggaagtgta	6697
NQO2	4	(intron 1 1919)	tcactcaaatagagctgagt T/C agtcaactcagctcttgacc	6698
NQO2	5	(intron 1 2004)	acaaactcacatgccaccag C/G catatgatgtaaacatgtaa	6699
NQO2	6	(intron 1 3391)	aaagcagagggctgtgcagg C/T gccctgtcccttaggctagg	6700
NQO2	7	(intron 1 3456)	caaaggcctcactcctcagg C/A ggccaactctctgttttag	6701
NQO2	8	(intron 1 3595)	actgccagcttttaggttca T/C tcttgaagtgttctgtgtgt	6702
NQO2	9	(intron 1 3596)	ctgccagcttttaggttcat T/C cttgtaagtgttctgtgtgt	6703
NQO2	10	(intron 1 3598)	gccagcttttaggttcatc T/C tgttaagtgttctgtgtgtca	6704
NQO2	11	(intron 1 3651)	ccctgcgcttttgaagggtg A/G atgtgacctctcccaatcc	6705
NQO2	12	(intron 1 6036)	tggtgtggcggttcaactgat C/T cccagcctcttctgctgac	6706
NQO2	13	(intron 2 14)	atggcaggttaattgattcact A/G ttgtggagtaagactttttt	6707
NQO2	14	(intron 2 192)	gccacgtggaagtgtataaa C/T tatctggaaattatctgttt	6708
NQO2	15	(intron 2 635)	caccctgttttagcacctagc A/C ccattccctggcctctgccc	6709
NQO2	16	(intron 2 685)	agtagcacccctccccacc G/A gctgtgacaaacaaaatgt	6710
NQO2	17	(coding region 139 (Phe 47 Leu))	ctgatttgtatgccatgaac T/C ttgagccgagggccacagac	6711
NQO2	18	(intron 3 36)	aatgctctatttataaaaaa C/T atctttatgtttttacttt	6712
NQO2	19	(intron 3 728)	aacgtgggataaaaccacca T/C ctagtgcacaaaagcaggtg	6713
NQO2	20	(intron 4 1577)	tgccctctgcacaccccttcc C/T gacaccagcccttctttac	6714
NQO2	21	(intron 4 1832)	tcggccggccacgtggagcc C/T gcttctcctctcgacccac	6715
NQO2	22	(intron 4 2583)	tggtgttacgcacagctcct C/T gtccccctcctgctgccc	6716
NQO2	23	(coding region 330 (Pro 110 Pro))	ctgtactggttcagcgtgcc A/G gccatcctgaagggtggat	6717
NQO2	24	(coding region 405 (Ser 135 Ser))	atcccaggatttctacgattc C/T gggtttgctccaggtatgtgc	6718
NQO2	25	(intron 5 21)	gtatgtgctcttgataagg A/T tcactatggatagttggagg	6719
NQO2	26	(intron 5 253)	atggcaaacaggaggtggg T/C caggtgtcaggtgacggggg	6720
NQO2	27	(intron 6 2435)	cccccttaaatcatttaac T/C gaattggtatgtaacaggtgt	6721
PIG3	1	(5' flanking region -47)	gggaaggaggaaaggaaga G/A ggggaggtgtgttctgctta	6722
PIG3	2	(intron 2 243)	taaacccggagcccgagcag A/C agtcccagctttcttagaatc	6723
PIG3	3	(3' flanking region 282)	agcaggccccagccctgcc G/A ctactcactgggccccacc	6724
PIG3	4	(5' untranslated region -9)	tccgcgagatacagcgccc (CCTGY) 16 cagacaatatgttagccgt	6725
PIG3	5	(3' flanking region 625-62)	ctcctcaggccccgccctt (T) ccattactcacttgggtccc	6726
PIG3	6	(3' flanking region 770)	tcacctgggtcccgccctac C/Δ tgtcataacctgtctcaagc	6727
NDUFA1	1	(5' flanking region -1437)	agggtcaaaaatcctgatta T/A acctaccttgaagcttttaa	6728
NDUFA1	2	(intron 2 3071)	aataaaagtacatggcatat C/A tttagtgggaacagacttgt	6729
NDUFA1	3	(3' flanking region 1218)	aactccatgtgtataaagca A/G caccacagatgacacttcca	6730
NDUFA1	4	(3' flanking region 1411)	ggattgtgccatcccttgat C/T ggcaatgaccttttactttt	6731
NDUFA1	5	(3' flanking region 1411)	ggattgtgccatcccttgat C/G ggcaatgaccttttactttt	6732
NDUFA2	1	(intron 2 1087)	aacatacaaaaattagccgg A/G t a/g tgggtggcgggacactgta	6733
NDUFA2	2	(intron 2 1089)	catcaaaaaattagccgg a/g t A/G tgggtggcgggacactgta	6734
NDUFA2	3	(intron 2 1356)	tccctgaacaaacacattg T/C ggccatccagaaatcagccaa	6735
NDUFA2	4	(3' flanking region 467)	cacagcctcatgggtcagcc C/T actccagaggtgtcattccc	6736
NDUFA2	5	(3' flanking region 744)	ggaagcaggggcccctggcca C/T agccgctggcagtaagcagg	6737
NDUFA2	6	(3' flanking region 838-83)	tatagttctacaagaatgaa (ACAC) aaagatcataacaatagcta	6738
NDUFA2	6	(3' flanking region 838-83)	tatagttctacaagaatgaa aaagatcataacaatgaa	6739

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
NDUFA3	1	(intron 2 2656)	tccttgcctgccctccctgc G/A cactttatcttccctttgcc	6741
NDUFA3	2	(coding region 241 (Leu 81	agggcccccagcctggagtg C/G tgaagaaactgtgagcacct	6742
NDUFA3	3	(3' flanking region 1019)	tccttaactgcactggcacc A/G gctctggagcccccagtcct	6743
NDUFA5	1	(intron 3 2155)	agactcttagctgttacctg G/C aacataaggtttcccttagaaa	6744
NDUFA5	2	(intron 3 2493)	ggcatattgctagtctttctc G/T gtctcaatttcacatctat	6745
NDUFA5	3	(intron 3 2712)	acaaattttgaactgttcac C/T taacacaggctttttctgaa	6746
NDUFA5	4	(3' flanking region 1296)	aggtatctaaaaggtattgc A/C atttggtcattgtgtctttc	6747
NDUFA5	5	(intron 3 30-31)	aagtcaagttttgtgtcttg (GATTGTGGTATCCAG)	6748
NDUFA5	5	(intron 3 30-31)	tgtaacatttaacaaaaaa	6749
NDUFA5	6	(intron 3 427-428)	attagtagcagttataaaa AG/Δ tctagactgctgattcatab	6750
NDUFA5	7	(intron 3 4733-4734)	tataggaatttttaaaatata TA/Δ ggatattgaaacattcagtt	6751
NDUFA6	1	(5' flanking region -1148)	tttataatttatatatgtta C/T gtgctttctttttagtagct	6752
NDUFA6	2	(5' flanking region -363)	actaccaaggagcgcgccg G/A cagccggatgacgagcgct	6753
NDUFA6	3	(coding region 26 (Ala 9 V	ggggagcggcgctccgccag C/T tacttctaccgcccagcacct	6754
NDUFA6	4	(intron 1 1318)	attcagcagtttgaaaacat A/G atgtttgctctggcagaatac	6755
NDUFA6	5	(intron 2 562)	agttaaaagatctgaaaagt G/C tcagaaatgattaccctga	6756
NDUFA6	6	(5' flanking region -861)	ctgtaaaatggggatgctga (T) ggtacctacctgacctatga	6757
NDUFA6	6	(5' flanking region -861)	ctgtaaaatggggatgctga ggtacctacctgacctatga	6758
NDUFA6	7	(intron 1 1251-1278)	tgtggggagtgactgtagca (GT) 12-14 ttoggggtgtgtgattcaaa	6759
NDUFA7	1	(5' flanking region -731)	accaaccsaaggtctatcaa A/G ggggtgtctctctttgcaccc	6760
NDUFA7	2	(5' flanking region -434)	aaagggaaaccatcagaaccc C/T gtgatgaaatgagaatcgcc	6761
NDUFA7	3	(5' flanking region -395)	gctcccgattccggctggc A/G ggggttagggcagggtagag	6762
NDUFA7	4	(5' flanking region -100)	agaggagtcacgtgcttcgg G/A gagagcctttataggacgtt	6763
NDUFA7	5	(intron 1 92)	tcacctccctcctaagccgg G/A acccttcgctctccccgaat	6764
NDUFA7	6	(intron 1 133)	ctccctgggaacccccagct A/C gt c/g accccttcagccccgga	6765
NDUFA7	7	(intron 1 136)	cctgggaacccccagct a/c gt C/G accccttcagccccggaacc	6766
NDUFA7	8	(intron 2 89)	tccttttagaccctgaaacg G/C agggctgacatcctgccacc	6767
NDUFA7	9	(coding region 196 (Pro 66 Ala))	gccgcccgggaatctgtgccc C/G cttccatcatcatgtcgtcg	6768
NDUFA7	10	(intron 3 4203)	gctccacccctggggcgccc T/G cctccatcacccccctcc	6769
NDUFA7	11	(intron 3 4604)	gggccttggtgtacgctggag A/G ccaaaagtgggaaggagga	6770
NDUFA7	12	(5' flanking region (-1353)-(-1360))	aggggtccagggtccctgct CAGAGGCT/Δ aacactggccgaagagaa	6771
NDUFA7	13	(5' flanking region (-1233)-(-1234))	agccctgatccaccactct CT/Δ gaaacttctttgctaataaa	6772
NDUFA7	14	(intron 2 4142-4143)	cattttgtgactgaggtgac AG/Δ gggcccaacagcgggccatg	6773
NDUFA8	1	(intron 1 -75)	tttgtgtctctctattctgac C/T cgcataaggtaaagctgaga	6774
NDUFA8	2	(intron 2 790)	caaacctagacaaagtgtgc C/T cttatccagaagttagcag	6775
NDUFA8	3	(intron 2 900)	ttcaggagataaaaagctct G/A attgctcaggcctgagatgg	6776
NDUFA8	4	(intron 2 3837)	gaagttgtctgtgaagttag A/G taagaatagtactcacata	6777
NDUFA8	5	(intron 2 3942)	tcattgttttgcaaaagat G/T cccctaaccagcttctttt	6778
NDUFA8	6	(intron 3 -66)	gaggagacaccaggaggcg A/G ttgatggttacagattcctc	6779
NDUFA8	7	(3' untranslated region 52	tttattcttggaacaaagtaa A/G gatgggtcgtggcccacac	6780
NDUFA8	8	(3' flanking region 367)	gtcatcaaggaggagcctcc A/G ggatagaagtgcagaaact	6781
NDUFA8	9	(3' flanking region 777)	attcttttttctactactagg C/T tgtttctctccacatctgact	6782
NDUFA8	10	(3' flanking region 1053)	aaagaaaaagcactgtgtga T/A ctgcatgcccgcctctctga	6783
NDUFA8	11	(3' flanking region 1190)	gattctctaatgaaaaataa G/T acttttttttgcattttttt	6784
NDUFA8	12	(intron 2 449-453)	tcattgtgcatgatacttaa GTAAA/Δ aaaaaactaagctgtgtaat	6785
NDUFA8	13	(intron 2 455-459)	tgcataacttaagtaaaa AAAA/Δ ctaagctgtgtaattgtagg	6786
NDUFA8	14	(intron 2 707-708)	tcatttttgaaagactctca (A) ccttgctgtacaaaaatgg	6787
NDUFA8	14	(intron 2 707-708)	tcatttttgaaagactctca ccttgctgtacaaaaatgg	6788
NDUFA9	1	(5' flanking region -807)	gatggctctttgtagaacaa T/G gcagattctcaaaagtgacc	6789
NDUFA9	2	(5' flanking region -769)	accacagttaaagaaaaaat T/C acaagccattgcgctagaga	6790
NDUFA9	3	(5' flanking region -353)	cacaccctattttggtttct C/G ttctccacttttccctcgt	6791
NDUFA9	4	(5' flanking region -322)	ttccctctgtttctgtctccc C/T cttttctctctcctgggcc	6792
NDUFA9	5	(intron 1 447)	attcatatgagcacaatgga A/G atgataatattacaatacca	6793
NDUFA9	6	(intron 1 1039)	ggcttgatgttcagcctgag G/A caagaattaggagtggttag	6794
NDUFA9	7	(intron 1 4010)	aatgtatccaaaagagattc T/G cattcctgccatgaagaa	6795
NDUFA9	8	(intron 3 49)	gacaaatataaattactaag G/A tcatttttaggagtgatagg	6796
NDUFA9	9	(intron 3 107)	aattttctccagaatggac C/T aaaggcatcctctgttccca	6797
NDUFA9	10	(intron 3 1183)	attctctggtaattatctac A/G gattatttgaatcccttta	6798
NDUFA9	11	(intron 3 1395)	attcctagttctttgtccct C/T aagttttgtgttcacctgt	6799
NDUFA9	12	(intron 3 2363)	agaaaatagtcgatgaatggc C/T ccaactaacactagtcttta	6800
NDUFA9	13	(intron 3 2608)	gtcatttgattacctgagta A/C agtgactgttacctgtttg	6801
NDUFA9	14	(intron 4 561)	attttataaattctttgatg A/C cttgggggtcttattcaact	6802
NDUFA9	15	(intron 4 860)	attgtgtagagtaagtacag C/T agagctgtcaacttttttaa	6803
NDUFA9	16	(intron 4 879)	gcagagctgtcaactttttt A/T aaaaaataatttttagcttaa	6804
NDUFA9	17	(intron 4 893)	tttttttaaaaaataattttt A/G gcttaaaaaataaaaaatt	6805

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
NDUFA9	18	(intron 4 1090)	atcattgctgttttaaagtt T/C aagtagtgtaatttcagta	6806
NDUFA9	19	(intron 4 1188)	aaccaatcctttttttttt A/T tcttccagaaactttgattt	6807
NDUFA9	20	(intron 5 161)	gggtgtgtgtgatgttttga C/T gttttgattgattgcttct	6808
NDUFA9	21	(intron 5 373)	ctttctcacccttgcaactg C/T agtgggttttgtgccactctt	6809
NDUFA9	22	(intron 5 457)	gccagggaagatgcctattc A/C cacagtgttatgtctccttt	6810
NDUFA9	23	(intron 5 3113)	gattttttctccttcttcaat G/A taagcttcccttaaaataaa	6811
NDUFA9	24	(intron 5 3339)	tctaaactcaaaacaggttt G/A tttggttattgtttaggctg	6812
NDUFA9	25	(intron 6 414)	tatagttttgccttttccag G/C atattacatatatggttaga	6813
NDUFA9	26	(intron 6 518)	ctttcattttctttcatagc T/C tgatagctcatttctttata	6814
NDUFA9	27	(intron 7 974)	ggattatgcgtacttggaaa A/G tactttggatagcgggtgatta	6815
NDUFA9	28	(intron 8 368)	acattaattttgatggagta T/G cacaatgcctccagaggctg	6816
NDUFA9	29	(intron 8 954)	gcatgcaatcagttatatag T/C ctatagataagaattacaattc	6817
NDUFA9	30	(intron 8 1253)	tcctcttgaattgttagata G/T gtatctacacatttctcatc	6818
NDUFA9	31	(intron 8 11608)	gaaaagatagatgtataaat G/A accaaaaattcgtgaagaaa	6819
NDUFA9	32	(intron 8 11930)	ctacaaatatattctaaatg C/T gtaatcattggataagtacaa	6820
NDUFA9	33	(intron 9 1998)	tgtttttcaagcctttaaac G/A gctgtggaaccctgtgctca	6821
NDUFA9	34	(intron 9 2238)	ccagctacttggaggctga A/G gttggaggatcacttgagcc	6822
NDUFA9	35	(intron 9 2885)	acagcgtctgtcttctctgc A/G gttctcataggctagcttac	6823
NDUFA9	36	(intron 10 801)	tacactaaagtgtctcttac G/A tttatacttgagaagtgttt	6824
NDUFA9	37	(intron 10 910)	tgcagactttcaggtgggta G/C gatgagggttgctgctgct	6825
NDUFA9	38	(intron 10 1180)	aaaactgagtcagaacgccc G/A tgctcagaaaacaggggcgt	6826
NDUFA9	39	(3' flanking region 554)	gtgccagcacttaggaatta T/G gaccttctaatagaagtcttt	6827
NDUFA9	40	(5' flanking region (-1129) - (-1128))	taaacagtaggggcaagata (TC) gagtggaaacagccaagatt	6828
NDUFA9	40	(5' flanking region (-1129) - (-1128))	taaacagtaggggcaagata gagtggaaacagccaagatt	6829
NDUFA9	41	(5' flanking region -341)	tggtttct c/g ttctccacttt T/Δ ccctctgttcttctgcccc c/	6830
NDUFA9	42	(intron 4 594)	attcaactttttatcccccc T/Δ aatgattaaacatagtgtatt	6831
NDUFA9	43	(intron 10 356-375)	taacttctctctaactgtctt GAAGAACTGTTGACAGTT/Δ	6832
NDUFA9	44	(intron 10 379-381)	cttctctttttctttaacct	6833
NDUFA9	44	(intron 10 379-381)	gaaactgttgacagtttctt CCT/Δ tctttctttaacctactcca	6833
NDUFA9	45	(intron 10 384-387)	tggtgacagttttcttctctt TTTCT/Δ ttaacctactccagtcagg	6834
NDUFA9	46	(intron 10 436-437)	ccattttctccctataaattg (TCTTTTAAATG) ctcttttcaaggt	6835
NDUFA9	46	(intron 10 436-437)	ccattttctccctataaattg ctcttttcaaggt	6836
NDUFA9	47	(intron 10 495-496)	gccacatccaatggtcagtt (TTCAGGCCCTT) ctacagacctatgtca	6837
NDUFA9	47	(intron 10 495-496)	gccacatccaatggtcagtt ctacagacctatgtca	6838
NDUFA9	48	(intron 10 519-520)	gacctcatgtcatgtgctg (GGCCTG) tgcatttgcttctaggagg	6839
NDUFA9	48	(intron 10 519-520)	gacctcatgtcatgtgctg tgcatttgcttctaggagg	6840
NDUFA9	49	(intron 10 558-559)	gatgcataataataataaaaa (A) tactataccaataccacatc	6841
NDUFA9	49	(intron 10 558-559)	gatgcataataataataaaaa tactataccaataccacatc	6842
NDUFA10	1	(5' flanking region -1734)	tgcaccttgaactgtttact T/C tctgttaaccatttaccctt	6843
NDUFA10	2	(5' flanking region -1492)	aaaacatccacgcaaacagg T/C tgtgagaagttacgtctg	6844
NDUFA10	3	(intron 3 370)	aagactgtgcatgtgccaatg C/A agacagagatgtggatgcca	6845
NDUFA10	4	(intron 3 2485)	ttgttattttcttttctctg G/A aatgcagtgatcagttgaca	6846
NDUFA10	5	(intron 4 236)	ctgtgaaagcagattggagc C/T ctggacctcaaacacacgca	6847
NDUFA10	6	(intron 4 1742)	tgctggcatctgctgtagt C/T tgctgaagtctgaggactgg	6848
NDUFA10	7	(intron 4 2090)	ggctgggggaaagcagatca T/C gttggctaaaggacaggtgg	6849
NDUFA10	8	(intron 4 3054)	cagctgattatactactgaa A/C cgggataaatg c/t agcttgat	6850
NDUFA10	9	(intron 4 3066)	ctactgaa a/c cgggataaatg C/T agcttgatgattttcagctg	6851
NDUFA10	10	(intron 4 3377)	gtcacagtttaaatgctgct G/A ttttactctgtgtaagtagc	6852
NDUFA10	11	(intron 5 46)	aagcatctctattttgaatg T/C agatcagcactaaaagccct	6853
NDUFA10	12	(intron 8 1465)	gcaacgcccagtttctggtta C/T aggcctcatatccagcgtgc	6854
NDUFA10	13	(intron 8 1809)	cctggaggcacaaggtggc C/A ggggcactcaacttccctct	6855
NDUFA10	14	(intron 8 11226)	gttggtgactgtgtggggc A/G tctcacctctcgggctgag	6856
NDUFA10	15	(intron 8 11319)	atcttgcccttccctctgccc G/A tctgttccaggcttgaacct	6857
NDUFA10	16	(intron 8 11386)	ccataatcctagcttgaacc C/T tcttttttccctgctgaccc	6858
NDUFA10	17	(intron 8 13361)	ccaggccactgattgttttc G/A cattttctagcattttctta	6859
NDUFA10	18	(intron 9 183)	ttctgtgtggaagctgat G/A aagtcctcagatgacagccc	6860
NDUFA10	19	(intron 9 8028)	gaggacattccacagaactg G/A tgactattagagcagaaggt	6861
NDUFA10	20	(intron 9 10742)	ctggaggagaggggtggagc C/G agttcagccagcactggggt	6862
NDUFA10	21	(intron 9 13908)	cacattgttatgtaaccaag C/T ct g/t gaattgcagtgtaaga	6863
NDUFA10	22	(intron 9 13911)	attgttatgtaaccaag c/t ct G/T gaattgcagtgtaagaact	6864
NDUFA10	23	(intron 9 14064)	tcttgactattagaacctt A/G tcagataaaatttttaaacag	6865
NDUFA10	24	(intron 9 14184)	tggttttggttgggaacagc G/A agagatacagaaccgacggt	6866
NDUFA10	25	(intron 9 16487)	cttgaagctgatcgctccct C/A cttgaagctgatcgctccct	6867
NDUFA10	26	(intron 9 16779)	gccagacgtgactgcttttag G/A ttctctatgacattcagacc	6868
NDUFA10	27	(intron 9 17663)	ttccaaatcaccacagaact T/G tgcatgattttgaagctcct	6869
NDUFA10	28	(5' flanking region (-1668) - (-1659))	gtaaaattgttttaactaga (C) 9-11 ttcttaaccaaggtataaa	6870

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
NDUFA10	29	(5' flanking region (-1355) ~ (-1334))	ctgtatccatttgggaaggcac (A)15-21 tgcaaggaaacaaggcaaa	6871
NDUFA10	30	(intron 1 46-61)	tggcgggggtggcagggtggc GGGGTGGCGGGTGGG/Δ gacgattcc	6872
NDUFA10	31	(intron 4 2486)	ctcactggaacttttttttt T/Δ aatttaatttttaaaatttt	6873
NDUFA10	32	(intron 7 1600-1601)	cacttccattctgactgtta (A) cgggtgtgattcttctcgcca	6874
NDUFA10	32	(intron 7 1600-1601)	cacttccattctgactgtta cgggtgtgattcttctcgcca	6875
NDUFA10	33	(intron 9 1054)	ggcggtgctgttttccctt A/Δ tctgtcctgtacacgtgtg	6876
NDUFA10	34	(intron 9 8161-8172)	tttctcgcttttctgggagac (T)10-12 aatgttgaaaatatgtgttt	6877
NDUFA10	35	(intron 9 8646-8647)	aattccccattgtcttctct (TT) ctgtagacattttaaacctta	6878
NDUFA10	35	(intron 9 8646-8647)	aattccccattgtcttctct ctgtagacattttaaacctta	6879
NDUFA10	36	(intron 9 16503-16523)	ccct c/a ctggaagctgatcgt TCCTCTCTGAAGCTGATCGT/Δ gtccaagatagttgctagga	6880
NDUFA10	37	(intron 9 17905-17936)	caaatatagtatacatgta (CA)12-18 tccttcatgaaaactctttc	6881
NDUFAB1	1	(intron 1 8451)	cagcacccctgtagaggcctc G/A ggatgctgaagatgccatga	6882
NDUFAB1	2	(intron 1 8495)	gacacagggcattctgcagac G/A ctgagacaattttatggcgag	6883
NDUFB3	1	(5' flanking region -1439)	ttaaaagtgtacttttttct G/A cc g/a ggcacggtggctcacgc	6884
NDUFB3	2	(5' flanking region -1436)	aaagtgtacttttttct g/a cc G/A ggcacggtggctcacgcctg	6885
NDUFB5	1	(5' flanking region -213)	ggcggtgaaactctctctac A/C aagaaggcgcaaacggccg	6886
NDUFB5	2	(intron 1 6288)	ggggatgttgattacctagg T/C cagtaaaagtaagaaggcat	6887
NDUFB5	3	(intron 1 -1581)	cttctggggcactgtatcct A/G tttctttcccttctgtaccct	6888
NDUFB5	4	(intron 1 -1487)	ccctcttagacgctatatag T/G tctagcataggtatctgcaca	6889
NDUFB5	5	(intron 2 556)	ttgtctggacctctgccac G/A gtatataaagctctgaaatca	6890
NDUFB5	6	(intron 3 467)	ggcgccatcgcaactccagcc C/T gggcaacagagtgcactct	6891
NDUFB5	7	(intron 3 497)	agtgcactctgtccccccc C/G caaaaaaaactataatcct	6892
NDUFB5	8	(coding region 397 (Tyr 133 His))	atgatagtcctgaaaagata T/C atgaagaacaatggccgtc	6893
NDUFB5	9	(intron 1 213-215)	attagcattttctaaaacgtt GTT/Δ attcaccatcccaattaatg	6894
NDUFB7	1	(intron 1 68)	cctgaacacctggcaccacca G/A ggctggcaccacagggtctg	6895
NDUFB7	2	(intron 2 266)	gggctctcttaggggctgtt T/C gatggggacagggcaggtg	6896
NDUFB7	3	(intron 1 4480-4481)	agttctgaggctgagagaga (GA) ggccacgcgcggccagtg	6897
NDUFB7	3	(intron 1 4480-4481)	agttctgaggctgagagaga ggccacgcgcggccagtg	6898
NDUFS1	1	(5' flanking region -3)	tcttagggggtctgtctgtgt C/G cagacagtttagcagaacag	6899
NDUFS1	2	(intron 1 445)	gtgttagcaatggctcacgc T/C tctgtttgtgtctctgttt	6900
NDUFS1	3	(intron 1 470)	tttgtgtctctgtttgttt G/T gtccattgaccacgttggac	6901
NDUFS1	4	(intron 1 502)	acgtttggacagcattttttt A/G ttcctttaactaacgggaaa	6902
NDUFS1	5	(intron 1 557)	ttttgaaaagttagccagg A/G ttgcattgcaataacaaaa	6903
NDUFS1	6	(intron 1 5218)	tatctcagaatatctcagga A/G catttagtagacagctatgc	6904
NDUFS1	7	(intron 3 1371)	aagccctaaaatagatagtg T/G caatgggaatgaaaacaaga	6905
NDUFS1	8	(intron 5 414)	ttttgaaacgaggtctcact A/G tgtgtccaggctgggcttg	6906
NDUFS1	9	(intron 10 812)	gagtgcggtggcgcgatctc G/A atctcggtgcactgcagcct	6907
NDUFS1	10	(intron 11 233)	ggaggcccaaggcaggcagat C/T gcctaagtgcaggagtttga	6908
NDUFS1	11	(intron 11 283)	ggccaacatggcgaaacccc G/A tctctactaaaaatacaaaa	6909
NDUFS1	12	(intron 11 585)	ctgtatgtcttaatttttaa G/T taaatttgcattttatatat	6910
NDUFS1	13	(coding region 1251 (Arg 417 Arg))	gcaccactgtttaatgctag A/G attcgaagaggttggtaat	6911
NDUFS1	14	(intron 13 5159)	attacttttagaaaacgtgt T/C tttagctgatactcaggcata	6912
NDUFS1	15	(intron 14 250)	aaaaattgttatattagttta C/T accttggttcaaaaattgca	6913
NDUFS1	16	(intron 14 550)	gataaagtctcactatgttg C/T ccagggtgactctcaaaactcc	6914
NDUFS1	17	(intron 14 2429)	ctgaaaatacaaaaattagc C/T ggggtgtgtggcagtgctct	6915
NDUFS1	18	(intron 14 2530)	ttacagttagcgagatcac G/T ccactgcgctccagcctggg	6916
NDUFS1	19	(intron 14 2659)	acacatttaattttttacat T/C gaaaatactgcagttatggt	6917
NDUFS1	20	(intron 16 150)	agaaaactgtattcagaaa C/T aggaattcaaggttacagtg	6918
NDUFS1	21	(intron 18 279)	cactgtgtagcaatttatgg T/C gaattttccaaagtggcaaa	6919
NDUFS1	22	(3' flanking region 182)	tctaggataaattataataa T/A aataatcatagtaacaatgg	6920
NDUFS1	23	(intron 12 3226)	aaatgtattgtctgtgcttt T/Δ aacattttgtaaatagtaaat	6921
NDUFS3	1	(5' flanking region -194)	tctgccacaaggagctagga C/T cagctcacctcacgatttc	6922
NDUFS3	2	(intron 1 46)	cggggtcaggcgacgagcg T/C gccagtgacagagctcct	6923
NDUFS3	3	(intron 6 -439)	aaagctgtgtcaaatgtact G/A ctttagatctggactgtgaa	6924
NDUFS3	4	(intron 6 -280)	gggtgggtgagcagtcagttc G/A gagctcctgatgtgggagt	6925
NDUFS4	1	(5' flanking region -439)	aactgaatacagccctgtcc T/A gagggttgcaaaagtgaatc	6926
NDUFS4	2	(intron 1 1829)	gaaaaaaaatcttaatgccca G/T ggaagacgttttttaaatc	6927
NDUFS4	3	(intron 1 2057)	attaatgggaaaaatctacat C/G taaaattcattttattgtaa	6928
NDUFS4	4	(intron 1 -521)	ttcattttaactaattttat T/G tctccattttgtgtaaggg	6929
NDUFS4	5	(intron 3 -1259)	ataaaaattatgatattatta G/A tactaatatagccagccata	6930
NDUFS4	6	(intron 3 -1174)	aatatatataattataggaa T/C ctacagtagtcaaacctggt	6931
NDUFS4	7	(intron 4 10682)	cacaatataggcacaacatt A/C ctaccaagcactaacaagt	6932
NDUFS4	8	(intron 4 12299)	tttactatatagatatatgg A/T atagactatagagtatctct	6933
NDUFS4	9	(intron 4 12560)	accaaatgaagttattatgca G/A gctcatctttttatataaga	6934
NDUFS4	10	(intron 4 18801)	ggaagactgtctttgccag T/C gtatccgaaacctctgttat	6935
NDUFS4	11	(intron 4 19888)	tgcacagctgagaagagca A/G ggggctgtttttcagttacc	6936

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
NDUFS4	12	(intron 4 20178)	agaaaagatgagtataattc G/A tctaacttaccattctttaa	6937
NDUFS4	13	(intron 4 23016)	ctactctgtgaaagtaagg T/A atgttgacaagtaaat	6938
NDUFS4	14	(intron 4 23124)	actttcttggagatggagt T/A ccagcagttgggaatgta	6939
NDUFS4	15	(intron 1 766)	tgtgatgatttttttttt T/Δ ggctgtattaaccttccatt	6940
NDUFS4	16	(intron 1 1261)	tttcttctcttttttttt T/Δ gagatacttctcactctga	6941
NDUFS4	17	(intron 4 19744-19745)	ctcatcatttaggtgctggt (T) agttgggtttgtggcaaatc	6942
NDUFS4	17	(intron 4 19744-19745)	ctcatcatttaggtgctggt agttgggtttgtggcaaatc	6943
NDUFS5	1	(intron 1 388)	ccaaacatagccagcacttc C/T ggctgtaactccgggctggt	6944
NDUFS5	2	(intron 1 -13082)	agtgaagcagagattgcacca G/A tgcattccagcctgggcaac	6945
NDUFS5	3	(intron 1 -12905)	gttttcaacaaggactcca G/T agtagtagagaagtcttctgt	6946
NDUFS5	4	(intron 1 -12564)	attttcatcacacctcaact T/G aaggtataacagccttaaga	6947
NDUFS5	5	(intron 1 -12561)	ttcatcacacctcaactaa G/A gtataacagccttaagaatg	6948
NDUFS5	6	(intron 1 -10561)	aaacaatgtggtatagtgagg C/G ggggtgtgagcaggtgtcat	6949
NDUFS5	7	(intron 1 -9065)	cctgatgctcctggctccag G/A gttagaccttttccctttaga	6950
NDUFS5	8	(intron 1 -8871)	tcacacagctgtctgtatga T/C agggccgagaccttcgctt	6951
NDUFS5	9	(intron 1 -7312)	aaatccctggcttctagaa G/T ggtcactgtggtatataat	6952
NDUFS5	10	(intron 1 -6827)	aaactctgcttccccgattc A/G cgccattctctctgctcagc	6953
NDUFS5	11	(intron 1 -6725)	agtagagacgggttttcc G/A tgttagccagcatggtctcg	6954
NDUFS5	12	(intron 1 -6631)	aggcgtgagccactgcgcgc G/A gcctagaccttctcttata	6955
NDUFS5	13	(intron 1 -6531)	cccaacagctcccaatgtaa A/G acagatcttataatattctg	6956
NDUFS5	14	(intron 1 -6346)	gcaacagatcttgacctata T/C cccataggggtacagctgagg	6957
NDUFS5	15	(intron 1 -6327)	atcccataggggtacagctga G/C gactttaacagaaaggag	6958
NDUFS5	16	(intron 1 -6122)	tagccttgcttttactctac T/C gttcctcccaatcacaccc	6959
NDUFS5	17	(intron 1 -2512)	acaaactcttaatgcgaatt T/C tgcagatcaaagtgggctta	6960
NDUFS5	18	(intron 1 -1945)	tttaactctctttaaatttc G/A caatttcacacactagggtta	6961
NDUFS5	19	(intron 2 75)	ttttttttttttttttttgagac G/A aagtctcactcttgcctcc	6962
NDUFS5	20	(intron 2 148)	ctgtagcctctgctcctccag G/A ttcaggcgattcgcgtacct	6963
NDUFS5	21	(3' flanking region 150)	cagattcaagtggtttctcct G/C cctcagcctcccaagtagct	6964
NDUFS5	22	(intron 1 (-10682)~(-10681)	attataaacactaaacaaac AT/Δ gtgtggtctcttttagagggg	6965
NDUFS5	23	(intron 1 -10267)	caagtgtactacctgaaaaa A/Δ gaagagatgaacaaatcac	6966
NDUFS5	24	(intron 1 -2069)	accagacagagtttccctta C/Δ ttgttttctgtggcaaga	6967
NDUFS6	1	(intron 1 26)	ggccgctgggtacaggatgc A/C ccttctccagccgacacct	6968
NDUFS6	2	(intron 2 1076)	ggatcatggtggtggagagg G/A gcttgtgtctggtgggtttg	6969
NDUFS6	3	(intron 2 1260)	cagttgtcagagtaagtggtg T/C atagggtaagtgtctttct	6970
NDUFS6	4	(intron 2 1413)	caaaggagctcatggcattg C/T gaatgggacatttcttccgt	6971
NDUFS6	5	(intron 2 1568)	tggagaaggggagggtttctc T/C tagtgtggtatggtgtggt	6972
NDUFS6	6	(intron 2 1692)	gaccgtggtgacggagggtt C/T ctgggcatcgatgggtggt	6973
NDUFS6	7	(intron 2 6488)	tagcttaataatattatggc A/G ttcagtgttcagaatgcctga	6974
NDUFS6	8	(intron 2 6563)	tttaaaccttttattttaa G/A tccatgaatggggtcggtat	6975
NDUFS6	9	(intron 2 6740)	aaagatttaaacctacatat C/T tttatgcccacatttggat	6976
NDUFS6	10	(intron 2 6832)	gcgagggactcattttacag A/T ggttggaacttctactgtgt	6977
NDUFS6	11	(intron 2 7054)	ttcactgcccagagcttggcc G/A tgtgaacccggagccgggt	6978
NDUFS6	12	(intron 2 7186)	ggtcagggtcacccttgagc T/C gcgcacactaaatgacggga	6979
NDUFS6	13	(intron 2 7225)	gagggacatcccgctcagtc G/A ccagtgtcgaggcgtcagca	6980
NDUFS6	14	(intron 2 7810)	cttccactctggggcgggga C/T gctgtagaaggagcacaag	6981
NDUFS6	15	(intron 2 11080)	gtactgttccagtgctttct C/T ctttggatttcatgtaaatc	6982
NDUFS6	16	(intron 2 11657)	gggacagaaacgatgtgttg G/A gagaagagggcgtggcagag	6983
NDUFS6	17	(intron 3 208)	cgaaaacccctttcaactg T/C gaagtgtggggcgcatgtt	6984
NDUFS6	18	(intron 3 1031)	ctagagtgggactgggcacc C/T ggcagtgcctctctggggt	6985
NDUFS6	19	(3' flanking region 270)	gcttcagagagccaaggtgg G/C tcttgaggtgcagtgaag	6986
NDUFS8	1	(5' untranslated region -4	agtgtagcctcgcctcccg A/C ttgactggcctgcttggcaa	6987
NDUFS8	2	(intron 1 163)	aggtgcagcggggagccggc T/C ctcagggcgcagtcgccc	6988
NDUFS8	3	(intron 3 123)	tctctgagcctgtttccact T/C ttaaaatgattatggtgatg	6989
NDUFS8	4	(intron 5 -505)	aggcaaggcaggccgggac G/A gtggctcacgcttgtaatcc	6990
NDUFS8	5	(3' flanking region 491)	ggccctgagctggcctcgct C/A cagccacatcctcttccctg	6991
NDUFS8	6	(3' flanking region 693)	ttcacttcatgttcagtgag G/A aaaccagctccgagaggtga	6992
NDUFS8	7	(3' flanking region 1267)	ttttccagacgttaaccgc G/A tcagagcgtggcattggagcc	6993
NDUFS8	8	(3' flanking region 1362)	cgctgggttctttcccttac C/T gtgtgtctccaggaacttac	6994
NDUFS8	9	(3' flanking region 1449)	tgtcagaacaggcctatggc G/A ccaaccacaagtccccaa	6995
NDUFS8	10	(3' flanking region 1572)	cagccccacaggcctgtgct C/A gctgtgtgggcttagggat	6996
NDUFS8	11	(3' flanking region 783-78	cagagaccttgacccccccc (C) atctaccatcatttccaaaa	6997
NDUFS8	11	(3' flanking region 783-78	cagagaccttgacccccccc atctaccatcatttccaaaa	6998
NDUFV1	1	(intron 3 670)	ctgggtggagtggtggca T/C ggagttgaagaccagtcct	6999
NDUFV1	2	(intron 6 160)	tgtgcccggccagccctga C/G catgcattcccttggggacc	7000
NDUFV1	3	(intron 9 27)	accacccctctcgtagcac G/A gagggtgggtggcatcaagg	7001
NDUFV1	4	(3' flanking region 1111)	tgtaggctgaggtcagcccc A/C atccagtcacaaagccaccc	7002
NDUFV1	5	(3' flanking region 1658)	gaatgcggaagtgtctgtg G/A gcaccacatgtctccgggc	7003
NDUFV1	6	(3' flanking region 1713)	gatctggggcgagggtaca C/T ggggctggcgtgggtgaag	7004
NDUFV1	7	(intron 4 214)	tgggtgtaatttttttttt T/Δ gcttcaaaaatagatattt	7005
NDUFV1	8	(3' flanking region 772-7	tgaactcggggttcagggtc TTC/Δ ctgtgaacactggtttttaa	7006

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
NDUFV2	1	(intron 1 526)	ggaaatgctggcctaataaa C/T ggtatcaaaactaactctgaa	7007
NDUFV2	2	(intron 1 6689)	tcgttggatggtagtattgt T/G tgaacaacagaagaattca	7008
NDUFV2	3	(intron 1 14767)	ccaaatgcatgccagcagag C/T gtggcaggaaggtacacaag	7009
NDUFV2	4	(coding region (Ala29Val))	aaggaatttgcataagacag T/Ctatgcacaaatggagctggag	7010
NDUFV2	5	(intron 2 -289)	cagaagatcttactctctaa T/G gaagctggataaacacttttt	7011
NDUFV2	6	(intron 2 -168)	tttacttttggttaactact T/C atcaaatgtgtgttagaca	7012
NDUFV2	7	(intron 4 677)	aaaccacatactatttgatt C/A tgatgagaatcacataacca	7013
NDUFV2	8	(intron 4 2295)	tatgattcaactttcaaaag A/T gtattgtgatatgaaataga	7014
NDUFV2	9	(intron 5 102)	caacttctgccatcttattg G/A atctgtacttacctagtaat	7015
NDUFV2	10	(intron 7 5466)	tggttaagaggctttaagata A/C caaatgctcagctttcagga	7016
NDUFV2	11	(intron 1 13562-13563)	tactcttaaaattaatcctt (CTT) ttattataagtatacagct	7017
NDUFV2	11	(intron 1 13562-13563)	tactcttaaaattaatcctt ttattataagtatacagct	7018
NDUFV3	1	(5' flanking region -222)	cgccgcgcccccgccacagc G/A cccaggcgccccgagggcac	7019
NDUFV3	2	(5' flanking region -111)	tgcccccgaaggaggcactt A/G gcctactggggatgcgcgc	7020
NDUFV3	3	(intron 1 137)	ttgggcccgtgaccccgctc C/T ctgggcccagagctgaccgc	7021
NDUFV3	4	(intron 2 152)	tatacaagacacaagatcta T/C aacagatttttagaccaaca	7022
NDUFV3	5	(intron 2 6304)	ttcacagatgaagggttcc G/A aaattttgtcaagaagac	7023
NDUFV3	6	(intron 2 6433)	tcgcctctgcttcttctctc T/G tccagctcctctgattctga	7024
NDUFV3	7	(intron 2 6563)	cccttgaaacacagagccccc C/T gaggtaagatcatgcaaaa	7025
NDUFV3	8	(intron 2 9619)	actatcttctgtgctcatgc G/A cagagccacacctgcagagc	7026
NDUFV3	9	(intron 2 9858)	aggatgcagcgtctttaaag G/A agacatcgtttttgcctaac	7027
NDUFV3	10	(intron 2 11673)	cttggttagtgaagcgcctgt A/G tgtgagcccaagtcattcata	7028
GGT1	1	intron 1 + 85	ttatccagtaaggtggtcc G/A tcacctcttttctcgtggg	7029
GGT1	2	exon 3 + 68	gacggccaggtccggatggt G/T gtgggagctgctgggggcac	7030
TGM1	1	exon 2 + 179	tgccgaatgcggcagatga C/T gactggggactgaaccctc	7031
TGM1	2	intron 9 + 1594	acttaccactctgtctctc C/T tgccaggcctcttctctga	7032
TGM1	3	intron 9 + 1933	ccgcacatctgtacctgcc C/G ccactctccagcagagcagc	7033
TGM1	4	intron 10 + 54	tcagtcagtggtttctctggt C/T ccaacttccagcgtgactga	7034
TGM1	5	intron 10 + 420	aggaggccgggagtcagccc A/G ccctcagaccctctggctca	7035
TGM1	6	intron 12 + 101	gggagtcctctgggggaagcc T/G catgtagggaagcagggcctc	7036
TGM1	7	intron 13 + 72	ggataaggacatcagaggtg G/A gcgctaagccagcagcagcc	7037
TGM1	8	intron 14 + 1671	atctcttaccacaccccaca C/G catggtggggaggttctca	7038
TGM1	9	intron 14 + 1691	ccatgggtgggaggttctctc G/A tcctaagggtatccgcagagc	7039
TGM1	10	intron 14 + 2983	tcctgtcctcctctctctcag G/A gagctcagaaacacctcaa	7040
TGM1	11	intron 14 + 3158	ggaaacccctcagaaccagg T/C tccaagccaaatgcttggcc	7041
TGM1	12	intron 14 + 3816	cagaatacaaaagtgggatg G/C gaggcaaggagtcccgtag	7042
TGM1	13	exon 15 + 233	ctcgaggtggagcttagccc T/C gtgccaggagcaatgggact	7043
TGM1	14	exon 15 + 369	ggagtcagcttctcacttgca C/A tgggggaacagatgtaata	7044
CYP1A1	1	5'flanking - 1061	cgcccccagactccctccccc C/G tcgcgtgactgcgagccccc	7045
CYP1A1	2	5'flanking - 1035	tgactgcgagcccccgccc G/A gggccggggaatgggtcggt	7046
CYP1A1	3	5'flanking - 1020	gcgcggggccggggaatggg T/G cggctgggtgggtgcgcggg	7047
CYP1A1	4	5'flanking - 947	cgccctcgcggccaggtgg G/A gcggggagcggccgcgctgac	7048
CYP1A1	5	intron 1 + (1326-1334)	cattcattgagaattgagcc (A)8-9 ccttggcctggatttctctg	7049
CYP1A1	6	intron 1 + 1357	ctggcctggatttctctgac T/C aaagagctcaatctagctg	7050
CYP1A1	7	intron 1 + 1590	ccactcttcaaaaggagta C/T atgtgacagcagctggaaat	7051
CYP1A1	8	exon 2 + 160	gaatccaccagggccatggg G/A ctggcctctgatttgggaca	7052
CYP1A1	9	3'flanking + (710-720)	caccgcgagatttccaggtc (T)10-12 gagacggagtctcactgtgt	7053
CYP1A1	10	3'flanking + 834	gcctcagcctcccaagtagc C/T gggactacaggcgcctgccca	7054
CYP1A2	1	intron 1 + 103	gcctgggctaggtgtagggg T/G cctgagttccgggctttgtct	7055
CYP1A2	2	intron 2 + 371	cttccctgtgttccactaa C/T ctttccctcttcttgaattg	7056
CYP1A2	3	intron 4 + 44	atagccaggagaagccttga G/A acccaggtgtttgttcagt	7057
CYP1A2	4	intron 4 + 206	aagagtgcacatggggtataa G/C aggggataattctatgggca	7058
CYP1A2	5	intron 5 + (623-648)	tgccccaggtgcctgctgc (T)22-25 catagaaaatagaaaaacat	7059
CYP1A2	6	intron 6 + 81	tcctctgctaggaactgttta T/C ataataaggaggggacct	7060
CYP1A2	7	exon 7 + 181	ctggccactctgtacagca A/T ctggagttcagcgtgccgc	7061
CYP1A2	8	exon 7 + 295	cggtgcgcttctccatcaa C/T tgaagaagacaccaccattc	7062
CYP1B1	1	5'flanking - 3669	tgatcctgtgaagcatcac G/A gttatccttctctgcacatg	7063
CYP1B1	2	5'flanking - 3149	tgacagcacttaccaccta G/C ttctctgtattttttagatca	7064
CYP1B1	3	5'flanking - 1222	gggggaagccaccccgccc G/A agcgctccggcttccctta	7065
CYP1B1	4	5'flanking - 376	ttccgggaagcaagctcaag T/C cgcggagagggaaggagggt	7066
CYP1B1	5	5'flanking - 265	ctggggacaccgtgcggcct C/T gattggaggtggtgtgatg	7067
CYP1B1	6	intron 1 + 129	tgcccgacagctgtgcccga G/A attgcaggaaacggttaacgcg	7068
CYP1B1	7	intron 1 + 379	tgagtgtcacgcttctctct C/T tctgtccccagcatgggac	7069
CYP1B1	8	exon 3 + (799-800)	agcttctgtggagattttttt (T) gagtcaaaagacttaaggggc	7070
CYP1B1	8	exon 3 + (799-800)	agcttctgtggagattttttt gagtcaaaagacttaaggggc	7071
CYP1B1	9	exon 3 + 1284	agtatagtggttttccatga G/T ttatcatgaatttttaagta	7072
CYP1B1	10	exon 3 + 1398	tcagcaaaagaaaaaaataa A/Δ gccagccaaagctttaaatta	7073
CYP1B1	11	exon 3 + 1468	tctcataggttaaaaaaaata A/Δ gtcaccaaagtagtgtgaaat	7074
CYP1B1	12	exon 3 + 1564	ttgaataatatatgccttgt G/A taattattgaaaattgaaaag	7075
CYP1B1	13	exon 3 + 1762	ctgaaattctatttataata C/Δ agaattctgttttgaaaata	7076

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
CYP1B1	14	3' flanking + (2216-2226)	agccagcctcttcttcttctt (T) 10-12 aaaatttattcctatttctt	7077
CYP1B1	15	3' flanking + 2230	tttttctttttttttttttaa A/Δ tttattcctatttcttcttaca	7078
CYP3A4	1	intron 2 + (754-763)	cacaaaatgagttgtgtggg (T) 9-11 acacaaaggcggaatcacat	7079
CYP3A4	2	intron 7 + 258	accactaatcaactttctgc C/T tctatggatttgctattct	7080
CYP3A4	3	intron 7 + 894	tgctgatctcactgctgtag C/T ggtgctccttatgcatagac	7081
CYP3A4	4	exon 9 + (32-33)	ttccttcagctgatgattga (A) ctctcagaattcaaaagaaa	7082
CYP3A4	4	exon 9 + (32-33)	ttccttcagctgatgattga ctctcagaattcaaaagaaa	7083
CYP3A4	5	intron 10 + 12	cccaataaggtgagtggtg G/A tacatggagaaggaggagg	7084
CYP3A4	6	intron 10 + 459	agacatgtgactttttttt T/Δ gaaaggttaacaatcactttc	7085
CYP3A4	7	intron 10 + 608	agccgtctcgaatgtctccc C/T acttcataactcctccacac	7086
CYP3A4	8	intron 12 + 2467	ttttttgcccattactccat A/G gagatcagaatatcactctg	7087
CYP3A5	1	exon 1 + 69	ggaagactcacagaacacag T/C tgaagaaggaaagtggcgat	7088
CYP3A5	2	intron 1 + (955-956)	tgtgggtagtgagggtcca (A) cctgtcccattaaacttctac	7089
CYP3A5	2	intron 1 + (955-956)	tgtgggtagtgagggtcca cctgtcccattaaacttctac	7090
CYP3A5	3	intron 1 + 1126	acatttttaaatgaattgat A/G tggtttaaatcttattcattt	7091
CYP3A5	4	intron 1 + 1145	tatggtttaaatcttattcat T/G tttaaaccagaatttttgg	7092
CYP3A5	5	intron 1 + 1543	ttcatgggtcctggccccc C/A gtggagggtcactcaaaagggc	7093
CYP3A5	6	intron 1 + 2366	cttatcttatatgcccatact G/A caccatttgctatcaacagg	7094
CYP3A5	7	intron 4 + 1813	tggttcttaattttactcttc G/A tgttctctatccttgaaat	7095
CYP3A5	8	intron 4 + 1887	aatgacatgaacaaggtgtg A/T ttgtgaagcaagggatattt	7096
CYP3A5	9	intron 4 + 3384	gagtgtctcgctatttgct C/T aacaagaaaagtctattgt	7097
CYP3A5	10	intron 4 + 3415	agtcatttgctccacttttca T/C tgaacaactcttcttctatcc	7098
CYP3A5	11	intron 4 + 3760	aagataacacactggaagtc G/A cacaccaccataaaaactgaa	7099
CYP3A5	12	intron 4 + 3885	acaattcacttccagtgcca C/T tgaatagcgtctctctgct	7100
CYP3A5	13	intron 4 + 5061	tacctacttttcaaaaaaaa A/Δ tcaccacatcatggcatccc	7101
CYP3A5	14	intron 4 + 5316	ccagatggctgggtctctccc A/T ctcccaccccgcccccacat	7102
CYP3A5	15	intron 9 + 77	gttctgaaaaatgtgcaggaa G/T tattccagggaagatgagaat	7103
CYP3A5	16	intron 9 + 1791	aaattttttatgggaaaaag C/T ctaccccatatttacttaca	7104
CYP3A5	17	intron 12 + 1408	atttaataaaaaaa A/Δ cagagtcacacaagaatttg	7105
CYP3A5	18	3' flanking + 542	tggagaaaatattcatagtt T/C cattctgcctctcttgaaga	7106
CYP3A5	19	3' flanking + 737	atgaacactgaataaaaaat T/G gtcaattctgctagttgattg	7107
CYP3A5	20	3' flanking + 804	ttttctcttttttattcttttc A/C ttttctctctcttttctgaat	7108
CYP3A7	1	5' flanking - 1680	cccaagggaacatgtgctcc C/A ggcacatactggcacaaca	7109
CYP3A7	2	5' flanking - 1191	tagaaaaatcctccactgttc A/C aaaagggaagccatttgcttt	7110
CYP3A7	3	intron 1 + 1173	ccccattttcaaatcacact G/A cttagcaggttatctctaaac	7111
CYP3A7	4	intron 1 + 1597	ttttctgtttagcctcttcca T/C tghtaaccaaaagcagcatta	7112
CYP3A7	5	intron 3 + 762	tccagtgtctgctattctcc C/T tcttcttttttcttctccctt	7113
CYP3A7	6	intron 7 + (1060 - 1069)	atggtttctgttttctgttg (T) 9-10 ctacagaagtcttctccattc	7114
CYP3A7	7	intron 11 + (592 - 594)	taagacaaggtagggaggag AAG/Δ gaggagaattgaaaaacaa	7115
CYP3A7	8	intron 12 + 911	ccccctccattaaacatct C/T tctcattttattccatttaa	7116
CYP3A7	9	intron 12 + 1137	gtctgtctgcagggaata T/Δ attcatgctcttttgaataat	7117
CYP3A7	10	intron 12 + 2147	tattgtcagtaatttttttt T/Δ actttgatgctatactttct	7118
CYP3A7	11	exon 13 + 218	ttcatccaatgtgtgcata A/C ataatacagggtattctgtacg	7119
CYP3A43	1	intron 1 + 3579	tcattgtcactttttttttt T/Δ ctcaaaatgatcagtcacac	7120
CYP3A43	2	intron 2 + 2427	tagaggaatcttttttttt T/Δ cctttttttctgctgccag	7121
CYP3A43	3	intron 3 + 3034	tttttatatagctagggaga T/C tghtaataacaagtcttct	7122
CYP3A43	4	intron 3 + 3433	agtcagaataactttttttt T/Δ cataaaggaccacagtatgt	7123
CYP3A43	5	intron 3 + 3504	catgactcagtttccaacca T/C aacttttctattttggcatag	7124
CYP3A43	6	intron 4 + 2767	tagtgacttttgaaaaaaaa A/Δ tagtaataagcaaaagact	7125
CYP3A43	7	exon 5 + 22	aaaacttaaggcacttttca G/A aaatcccattggacctaaag	7126
CYP3A43	8	intron 12 + (1585-1584)	tactttgagccctcattctc (A) ccaagtcacttcagtgctag	7127
CYP3A43	8	intron 12 + (1585-1584)	tactttgagccctcattctc ccaagtcacttcagtgctag	7128
CYP4B1	1	5' flanking - 333	gaaacattcacagtgcttgt A/T tgagaagacagtggttatta	7129
CYP4B1	2	5' flanking - 18	gagcagctgaaggcaggtca G/T atgaaggctaggtgctgga	7130
CYP4B1	3	intron 1 + 341	tccaaaacctctggatagta C/T atagaagtaggcaatccatt	7131
CYP4B1	4	intron 1 + 542	cctatgggtggtcaggagc C/T gtgacaccttccagggttca	7132
CYP4B1	5	intron 1 + 2856	gaggactttgcacatagtag G/A tgetcagctatattgttggc	7133
CYP4B1	6	intron 1 + (2923-2938)	caacaaattggtgtgtgtg (GT) 7-8 agaatgccagctcccagatc	7134
CYP4B1	7	intron 1 + 6086	tttggaaatcaagactggg G/T cagcatgctagtgtgtgtgac	7135
CYP4B1	8	intron 1 + 6598	ttttggggtgtgggagagg G/A cccatagtagggagacagct	7136
CYP4B1	9	intron 1 + 6660	acctaaagggtgtccactctg A/G aggagagcagtcctaggggg	7137
CYP4B1	10	intron 1 + 7242	ccctgggtctcccttaactca T/C gctggactgttcccttgggt	7138
CYP4B1	11	intron 2 + 107	gcctgtgtactaagctctgc C/G agctgaggttccaccctac	7139
CYP4B1	12	intron 3 + 361	atggtgtgtgtgttaggacca C/T ggctgggtcaccagaggtgt	7140
CYP4B1	13	intron 4 - 492	aaaggctttcacatctaaaa C/A gtgtctctctcattttctgtc	7141
CYP4B1	14	intron 4 - 315	ggattacttacatatacacc A/G tgggggggagctcaccacct	7142
CYP4B1	15	intron 4 - 157	ctaccacacctatcctgata T/C tccagcaggatggaggcgag	7143
CYP4B1	16	exon 5 + 22	acaagtgggaagagaagct C/T gggagggtaagctccttgac	7144
CYP4B1	17	intron 5 + 125	cccaggagaccttagcttgc G/A gggagacaggacctgctcat	7145
CYP4B1	18	intron 5 + (287-289)	tgtctaaagccaatccctctc CCT/Δ accctctgctttagcagggac	7146

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
CYP4B1	19	intron 6 + 54	gcttgggttctctctctctg C/T cctctatgccccctcccat	7147
CYP4B1	20	intron 7 + (99-100)	agctcttaagcatttcccc (TC) tttctcagcaaatataacc	7148
CYP4B1	20	intron 7 + (99-100)	agctcttaagcatttcccc tttctcagcaaatataacc	7149
CYP4B1	21	exon 8 + 114	tcttgggttctctactgcat G/A gccctgtaccctgagcacca	7150
CYP4B1	22	exon 8 + 139	tgtacctgagcaccagcat C/T gttgtagagaggaggtccgc	7151
CYP4B1	23	intron 8 + 247	agaaagtgtcaacaagagg C/T tgatatgttgtgtgctaact	7152
CYP4B1	24	intron 8 + 366	tgtgggggtgaacagagctg A/G gacagctgggagagccagtt	7153
CYP4B1	25	intron 8 + 650	cccttgcctgtgtgtcagaca C/A cctgcctttctctctgggct	7154
CYP4B1	26	intron 8 + 844	tcatatgtgagaatcccc C/A ccacggggtatccagacaca	7155
CYP4B1	27	intron 8 + 1767	tcacattccaagaatgttct G/T gttgtgtgtgtggcaggat	7156
CYP4B1	28	exon 9 + 53	tgtgcacgaaggagagcttc C/T gccctaccacacgtgccc	7157
CYP4B1	29	intron 9 + 652	agtcggatgtgtcatgaac G/T ctctgtcactggcagtggtc	7158
CYP4B1	30	intron 9 + 774	cctgggtcaccaacctctgtt C/T tgcccacaggaagcctgac	7159
CYP4B1	31	intron 10 + 33	tgggctgggagatcagacag G/T gtgggggactgggaggtca	7160
CYP4B1	32	exon 12 + 224	ccagatggctcaggctgtga C/A ctcctcgggaccacccctcc	7161
CYP4B1	33	exon 12 + 270	ctgggtgtggaggagttggg G/A cccctgccttcaggaggt	7162
CYP4B1	34	3'flanking + 129	ctgtgtctccacagtcacgt G/A gtgctccaggcattcagggt	7163
CYP4F2	1	intron 1 + (145-146)	ccaagccctgtggcaacctca CA/Δ gtgattcaggctgggcttt	7164
CYP4F2	2	intron 1 + 193	tttaatcagctctctctct C/T tttccattcttaagtgtta	7165
CYP4F2	3	intron 1 + 324	ccctgctctacactccggcac T/C gccctcctcctcctctccac	7166
CYP4F2	4	intron 1 + 367	tccttggagggtccctgggccc G/C tctctcgggctcaggatct	7167
CYP4F2	5	intron 1 + 402	ggatctccaccgtccatcccg T/C ctgcccctcaggatgtccca	7168
CYP4F2	6	exon 2 + 35	gcctgtcctggctgggccc T/G gggcagtgccagcatccct	7169
CYP4F2	7	exon 2 + 166	cggtgttttccacaccccc A/G agacggaaactggttttgggg	7170
CYP4F2	8	intron 2 + 125	ggcagagaagcagagaggc A/G tcttactcattcctctgctt	7171
CYP4F2	9	intron 2 + 440	gggcccgtctccactctccac T/C acaccgaaggcacctttct	7172
CYP4F2	10	exon 3 + 48	gttctgactcagctgtgtggc C/T acctaccccgagggtttaa	7173
CYP4F2	11	intron 3 + 701	agactccacccacagcttggg T/A cctttccttgaccctgtg	7174
CYP4F2	12	intron 3 + 742	cttcccatcgttggaggggc G/A aggtcagcaggggggaatgg	7175
CYP4F2	13	intron 3 + 1020	gccttagcttttccatgtc G/A cttttccatcaagggtggcc	7176
CYP4F2	14	intron 3 + 1039	cgcttttccatcaagggtgg C/A cttttccatcatgtgtcaac	7177
CYP4F2	15	intron 3 + 1040	gccttttccatcaagggtggc C/G ttttccatcatgtgtcaacg	7178
CYP4F2	16	intron 3 + 1920	ccacctgtctaacctctgtt G/C ctgtttgtctatgtctgggg	7179
CYP4F2	17	intron 3 + 1945	ttgtctcatgtctggggcgtg T/A ctctacaatggctgttatat	7180
CYP4F2	18	intron 3 + 2621	agcattctgtagaatgtga G/A ctgtgctcaggggttgcgga	7181
CYP4F2	19	intron 3 + 2665	tgttgatcgtgtaggaggc A/G tgtcaaggcatgctggaacc	7182
CYP4F2	20	intron 6 + 194	gggtttgaactggtgggtgt G/T gtcagagctctgtaggggac	7183
CYP4F2	21	intron 7 + 67	tgtgaaatgtcagatgaaag G/A atttgaactgtattaaagg	7184
CYP4F2	22	intron 7 + 2811	ttccaaggggaattgccatt T/G aattctcctgttaactcaggt	7185
CYP4F2	23	intron 7 + (3096-3097)	gggggtgggggttggggggg (G) ttactgccttctctccagga	7186
CYP4F2	23	intron 7 + (3096-3097)	gggggtgggggttggggggg ttactgccttctctccagga	7187
CYP4F2	24	intron 8 + 145	gggtcgtctacactctgggt G/A ctgaagcagccagagaccc	7188
CYP4F2	25	exon 9 + 44	ctctcctgggtcctgtacca C/T cttgcaagcaccacagaata	7189
CYP4F2	26	exon 11 + 48	gaaccatcacacccagct G/A tgtggccggaccctgaggtg	7190
CYP4F2	27	intron 12 + 108	tgttccaagttccagctctc C/T ttcctcactcctctctggag	7191
CYP4F2	28	intron 12 + 285	gcgatggggtccaggcacgg A/T taccctctctctattctctc	7192
CYP4F2	29	exon 13 + 238	aagtgaagcctagaattacc C/A taagacctgttccacagtc	7193
CYP4F2	30	exon 13 + 342	tgtgcgtgaatgttcatggc G/A gccctattccagtagccaa	7194
CYP4F2	31	exon 13 + 563	tagtgtactgtctctttata T/C gaaatttccagacagggcca	7195
CYP4F2	32	exon 13 + 707	aaatgttccggacccatagata G/C tgacgaaggtagcacgacac	7196
CYP4F3	1	intron 2 + 258	cattaatgcacctctcgggg G/T cttctgggcagggggttggg	7197
CYP4F3	2	intron 2 + 916	ttaggacatgtcctgagtc C/T acactgctccccacaaacct	7198
CYP4F3	3	intron 2 + 3417	atccagggtctcacacagtg C/T acttctctcttggcttttag	7199
CYP4F3	4	intron 2 + 4090	gagagcatgaattgggtcct G/A tgtctttctctccagattca	7200
CYP4F3	5	intron 3 + 89	tgtgtgcctccagcgggtc G/A cgtgcccatgtgcagacagg	7201
CYP4F3	6	intron 3 + 243	tcaagtctgtctgacggcta C/T gtcttgcacctgtatattt	7202
CYP4F3	7	intron 3 + 502	aggtctgggacccagggtcc G/C taagtgaactgtctgagaca	7203
CYP4F3	8	intron 3 + 755	ttttgtggccatgtcaggac A/T tgtgaacacatgtcagtgte	7204
CYP4F3	9	intron 3 + 855	gggacagacaggggtgtcta G/A gtccctgtgaaggcattctg	7205
CYP4F3	10	intron 3 + 970	cctgacatagctcctacgtg C/T catgttaggcagtgctcattg	7206
CYP4F3	11	intron 6 + 122	gaggagttgttatacctgat C/T gttgaaggactggtatgaat	7207
CYP4F3	12	exon 7 + 159	gggtcacgacttcacagatg C/A cgtcatccaggagcggcgcc	7208
CYP4F3	13	intron 7 + 2107	caggttgccagtgatttttt T/Δ ctcagaagtgtttcatcaag	7209
CYP4F3	14	intron 7 + 2255	gaccaagaagggtctaggag T/A gcaagatgggcttgggtttc	7210
CYP4F3	15	intron 8 + 132	cctcaatgcaaggtgtctgt A/C caccctcgggtgctgaagca	7211
CYP4F3	16	exon 9 + 59	taccaccttgaagacaccc G/A gaataccaggagcgtgtcg	7212
CYP4F3	17	intron 9 + 13	attgaatggtgagtgagggt G/A ctgggtccctgttctcagc	7213
CYP4F3	18	intron 9 + 36	gggtccctgttctgagcct G/C tctcattggctctgttcccc	7214
CYP4F3	19	intron 9 + 167	acccatcctgactgtctggg C/G aaaggttataggcccttagg	7215
CYP4F3	20	intron 9 + 369	tcctaatctcaccctcc G/A tccagtcacagggtattataa	7216

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
CYP4F3	21	intron 9 + 458	tcattcatccatccagtcct T/C gttcagcaaaactctcata	7217
CYP4F3	22	intron 10 + 46	ctcctgggttaggaagagggg A/C ccctcaggcagggagcattg	7218
CYP4F3	23	intron 10 + 63	gggccccctcaggcaggagc C/A ttgtcctgactgcccccttc	7219
CYP4F3	24	intron 11 + 14	ccctcagggtgcgggcccccc C/G tctctgtttttgtccattcc	7220
CYP4F3	25	intron 11 + 84	gatcaggagaatccaacatc G/A cctccctccaagacacacac	7221
CYP4F3	26	intron 11 + 113	caagacacacaccactgtct T/C tccaaggctggcgactggg	7222
CYP4F3	27	intron 11 + 164	cggcaaccctctctgtgtctc T/G cctccaggctctatgacctc	7223
CYP4F3	28	intron 11 + 165	ggcaacccttctgtgtctcg T/C ctcagggtctatgacctct	7224
CYP4F3	29	intron 12 + 156	gaaaaggccccacagtagg G/A ttgggtgtgtctctagaagga	7225
CYP4F3	30	intron 12 + 253	gagctcgggtaggctcgag T/G atatgcaagccacatgggg	7226
CYP4F3	31	intron 12 + 346	tgggtgtcccaggccagggtt A/C ccggcttgatggggccagga	7227
CYP4F8	1	5'flanking - 61	accatgtttacccatcatg G/T tcttgagctccccagcccc	7228
CYP4F8	2	exon 1 + 67	gtggcagcatccccgtggct G/T cctctgtgtgtgtgtgggg	7229
CYP4F8	3	intron 1 + 707	tacgcagcaggtagttaccca T/G tatttccacattatccactg	7230
CYP4F8	4	intron 1 + 857	acacccccctaccctcacatc G/A tgacacagctggggcagaag	7231
CYP4F8	5	intron 1 + 907	tgccatctccaccctcccc G/A tgcaggggcatcttctttat	7232
CYP4F8	6	intron 2 + 668	tgtggcacttccaccatag T/C tcatgtccctctgtgtccag	7233
CYP4F8	7	intron 2 + 818	gccacagagacatgtgtcca G/A gccccaaaaatgtgagtgc	7234
CYP4F8	8	intron 2 + 1079	tatgtctgggtgtgtgcagaa C/T atgttgaccatgtaggagc	7235
CYP4F8	9	intron 2 + 1194	ccggctccccctttatgcccc C/A accctcccttcttctctgtc	7236
CYP4F8	10	intron 5 + 45	aacatggggtggagtggggg G/T gtgggtgtggggagcaaa	7237
CYP4F8	11	exon 8 + (19-20)	ggccatgacaccacggccag (GCCAG) tggcctctcctgggtcttgt	7238
CYP4F8	11	exon 8 + (19-20)	ggccatgacaccacggccag tggcctctcctgggtcttgt	7239
CYP4F8	12	intron 8 + 222	tttatttccccactaacttg C/G tatgcaagcttagtaaaate	7240
CYP4F8	13	intron 8 + 334	cttgagaattaaacggcaaa A/T accgcaatgacttttgacc	7241
CYP4F8	14	intron 8 + 1999	ttctaagtacattattctc T/C tgccttttagctatgatctag	7242
CYP4F8	15	intron 8 + 4184	caggagggccgtgtatgtctc C/T ctggataattgttgggtgtt	7243
CYP4F8	16	exon 9 + 119	acgtgggtgctccagacagc C/T gagtcatcccaagggtgcc	7244
CYP4F8	17	intron 11 + 282	gggttgggggttccgggccc G/C gtctctggcgagtggggcc	7245
CYP4F8	18	intron 11 + 340	tcagctcagacccctccacct C/T gggcccccaggaaactgcacg	7246
CYP4F8	19	3'flanking + 35	atcacctaccccttgcaccaa T/C taccctttcagatttccggt	7247
CYP4F8	20	3'flanking + 83	ctgtgtgtggccctgtgccc G/C agtcccgcgagtgggcagta	7248
CYP4F8	21	3'flanking + 90	ggcccccgtgcccctcagtcce A/G cggatggccagtagggggcg	7249
CYP27A1	1	intron 1 + 295	aggagggagctgtcttggga A/G gagagtggcagagggcaaatg	7250
CYP27A1	2	intron 1 + 17503	cagtgcataaagccctctgat C/T ctccttagagaaggaggagc	7251
CYP27B1	1	intron 6 + 173	cagccccctagcctcatcttg C/T tgcctccattttgtgctttg	7252
CYP27B1	2	intron 8 + 113	atataagacctggtagaatg A/C atcttctgaaatagataag	7253
CYP27B1	3	3'flanking + 1081	taccctggaaatcagtgatga G/C aattctgccccatccgtactc	7254
AADAC	1	exon 1 + 29	attaaagtacactattccagg C/T atatcatgtaggtttacttt	7255
AADAC	2	intron 1 + 138	gctgtggcctttgacaatgt G/A ttacttagaaatgtgtgttg	7256
AADAC	3	intron 1 + 142	tggccttttgacaatgtgtta C/T ttgaaatgtgtttgtttt	7257
AADAC	4	intron 1 + 1033	ttccagcagagacacaca A/G gtaaaacaccccagctaca	7258
AADAC	5	intron 1 + 1253	tttttttccctcatatttgc T/C gtctgtgctacaaatgtga	7259
AADAC	6	intron 1 + 1366	ctctggtagccttttaatta A/G ttaattcattcatttaetta	7260
AADAC	7	intron 1 + 1369	tgttagccttttaattaatt A/C attcattcatttaattacat	7261
AADAC	8	intron 1 + 2501	ggttacagaaagatggtag C/A ttggccaaaaaatgatagg	7262
AADAC	9	intron 2 + 46	tgtcactgaggtagttcgca A/G acattttactaaagtcttcag	7263
AADAC	10	intron 2 + 1971	aaatgagagttaagtaggag A/C attttcttttattttttgtgc	7264
AADAC	11	intron 2 + 1988	gagaattttcttttattttt A/G tgcaggagaaataataacaa	7265
AADAC	12	intron 2 + 2341	agggtgccttttctattgtcc C/T atgcagacttaggtgaccc	7266
AADAC	13	intron 2 + 2546	gtctgacacagaaggatcaa T/A ggcaaaatgtgcaagacaaa	7267
AADAC	14	intron 2 + 2609	taggaggttccactgggaaac T/C tgaattccactgagtcatga	7268
AADAC	15	intron 2 + 2663	tataaatcacagtgttaaat T/C gtctctcgtatttttaaggta	7269
AADAC	16	intron 4 + 605	tgtgtcagtaaaatattata T/C taagttaggtgaatgagatca	7270
AADAC	17	intron 4 + 621	tatattaagttagtgaaatga G/T atcatgtaattgtgagacta	7271
AADAC	18	intron 4 + 679	ttagagattcagacgaattc A/G tataatcttcgatgggtgat	7272
AADAC	19	intron 4 + 1680	gttaaaatgtggataaaatc C/T acaatttgcataaattttgg	7273
AADAC	20	intron 4 + 1748	atttagaagttctatcacatc T/C tttatagtatattacacact	7274
AADAC	21	intron 4 + 1771	tatagtatattacacacttc G/A aaaaacacaaattattttt	7275
AADAC	22	exon 5 + 238	caagctcatctctcaaaattt A/G ttaattggagttccctgtctc	7276
AADAC	23	exon 5 + 678	ttagaatttggctctttctta A/G aatggctcagtttaagttcca	7277
AADAC	24	3'flanking + 208	aatgctaaaaaataaaaaaa A/Δ tcaactgtgttactttgggga	7278
CES1	1	5'flanking - 983	tatttctcttagccagcgta T/C cacagtgtgttttagtgatt	7279
CES1	2	5'flanking - 814	tcacattgctcttgacatcac A/C cctactgctctccacccta	7280
CES1	3	5'flanking - 248	agtccctgcaaggggtgacacc G/Δ ttatgccacaagcagttggg	7281
CES1	4	intron 1 + 22	tgtgtcctctggaagtcaaa T/Δ atgcggggcactttttgaaa	7282
CES1	5	intron 1 + 30	tctgaagtcaaatatgcggg G/T cactttttgaaatcctgttt	7283
CES1	6	intron 1 + 1662	aagggaatccctgagctgag C/A atgaccagcccagtggtttc	7284
CES1	7	intron 1 + 1726	cctccctgaagtcctcagca A/C tcttagctgggttccctgccc	7285
CES1	8	intron 1 + 2716	tgcttccaaggaagttccatc T/G cagtattattttgtaattagc	7286

Year	Age	Sex	Height (cm)	Weight (kg)	Body Mass Index (kg/m ²)	Waist Circumference (cm)	Hip Circumference (cm)	Waist-Hip Ratio	Trunk Fat (%)	Visceral Fat (cm ³)	Subcutaneous Fat (cm ³)	Visceral Fat Index (cm ³ /m ²)	Subcutaneous Fat Index (cm ³ /m ²)	Visceral Fat to Subcutaneous Fat Ratio
2002	25	M	175	75	24.5	95	105	0.90	15	150	100	1.50	1.00	1.50
2003	26	F	165	65	23.9	85	95	0.89	12	120	80	1.50	0.80	1.88
2004	27	M	180	80	25.9	100	110	0.91	18	180	120	1.50	1.20	1.25
2005	28	F	170	70	24.4	90	100	0.90	14	140	100	1.40	1.00	1.40
2006	29	M	185	85	26.0	105	115	0.91	20	200	130	1.50	1.30	1.15
2007	30	F	175	75	24.5	95	105	0.90	16	160	110	1.60	1.10	1.45
2008	31	M	190	90	25.5	110	120	0.92	22	220	140	1.55	1.40	1.11
2009	32	F	180	80	24.7	100	110	0.91	18	180	120	1.80	1.20	1.50
2010	33	M	195	95	25.4	115	125	0.92	24	240	150	1.60	1.50	1.07
2011	34	F	185	85	24.9	105	115	0.91	20	200	130	1.90	1.30	1.46
2012	35	M	200	100	25.0	120	130	0.93	26	260	160	1.65	1.60	1.03
2013	36	F	190	90	25.0	110	120	0.92	22	220	140	2.20	1.40	1.57
2014	37	M	205	105	25.4	125	135	0.93	28	280	170	1.70	1.70	1.00
2015	38	F	195	95	24.7	115	125	0.92	24	240	150	2.40	1.50	1.60
2016	39	M	210	110	25.0	130	140	0.93	30	300	180	1.80	1.80	1.00
2017	40	F	200	100	25.0	120	130	0.92	26	260	160	2.60	1.60	1.63
2018	41	M	215	115	25.0	135	145	0.93	32	320	190	1.90	1.90	1.00
2019	42	F	205	105	25.4	125	135	0.93	28	280	170	2.80	1.70	1.65
2020	43	M	220	120	25.0	140	150	0.93	34	340	200	2.00	2.00	1.00
2021	44	F	210	110	24.7	130	140	0.93	30	300	180	3.00	1.80	1.67
2022	45	M	225	125	24.9	145	155	0.93	36	360	210	2.10	2.10	1.00
2023	46	F	215	115	24.9	135	145	0.93	32	320	190	3.20	1.90	1.68
2024	47	M	230	130	24.8	150	160	0.94	38	380	220	2.20	2.20	1.00
2025	48	F	220	120	24.5	140	150	0.93	34	340	200	3.40	2.00	1.70
2026	49	M	235	135	24.5	155	165	0.94	40	400	230	2.30	2.30	1.00
2027	50	F	225	125	24.5	145	155	0.93	36	360	210	3.60	2.10	1.71
2028	51	M	240	140	25.0	160	170	0.94	42	420	240	2.40	2.40	1.00
2029	5													

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Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ESD	4	intron 1 + 1864	gctttcatgcaggattgac G/C tagtgggatgtattaggaag	7357
ESD	5	intron 1 + 2389	ttttgggaacacctgtctag G/A ttgttaagagccagtggaat	7358
ESD	6	intron 2 + 22	taaaactgttttattgttta T/C atgttactctgaacattgaa	7359
ESD	7	intron 2 + 589	taaaattagtagtctctctct G/A taagtctcattatttaagata	7360
ESD	8	intron 2 + 1499	tagaaaaatgtgtatcacac C/T gtaagtgttcagtaattgtta	7361
ESD	9	intron 3 + 92	ctttatctagatattatagt C/A cctcatcttactttttaaact	7362
ESD	10	intron 3 + 422	gtaaaagagattaacacaca C/T gcacacatacatataccat	7363
ESD	11	intron 3 + 581	agaaaaacctgagaaatgaca C/T aatttattttaaagccatagt	7364
ESD	12	intron 3 + 2270	gccagtaattacatgtagcc G/A tttacatcaaattagctaat	7365
ESD	13	intron 3 + 2951	taatgaaagtaaatgtttca A/G cttccctaacaaaagttgaa	7366
ESD	14	intron 3 + 3003	aaatgtcagaaaattttttgt G/A ccgtcagtcacacaagaa	7367
ESD	15	intron 3 + 3097	aaggagcatcacagaaaactt G/C ccatgatggggcctttgtgg	7368
ESD	16	intron 4 + 2616	tctaagtgtccagctatta A/G tgggtgcacatcttcagtcc	7369
ESD	17	intron 5 + 392	tcttttttctctctctgttaa C/T atcaaccatacagttaaaca	7370
ESD	18	intron 7 + 107	ttagtattggaactaaactt T/C tctagtgttgagaactttgg	7371
ESD	19	intron 8 + 1091	aaattcttaactaattaaagg G/T ttcactcttttagtaactaga	7372
ESD	20	intron 8 + 1652	tataaagtgtgtgtaataga A/G tatatatgaataagaatatt	7373
ESD	21	intron 8 + 2048	agaaggaaaaagccactttt G/C ttaagaatccctgagatag	7374
ESD	22	intron 9 + (1523-1526)	ctgccacacaaagtctgaaaa (TC)2-3 aagtttgttataaaaaacagc	7375
ESD	23	intron 9 + 2468	atagaaggagaggtctatact A/G cctccttaagtctcaggacc	7376
ESD	24	intron 9 + 3362	actaaggataaaaatattggc A/G tactcagtcacattggaact	7377
ESD	25	intron 9 + 5292	aggccttaattgacataattt C/T cctcacaataaagatacaaca	7378
ESD	26	intron 9 + 5298	taatgacatatttccocctca A/C ataaagatacaacatgcttt	7379
ESD	27	3'flanking + 798	tatggtaactgaagaaaaatg A/G cattaagtctcctaaagtatt	7380
CEL	1	5'flanking - (611-617)	tggatcaaggcaataaattt (A)6-7 ggaattatttgaagaaaa	7381
CEL	2	intron 1 + 20098	atctctaccaaggtaccaat T/G ccttaagggaagtgttaatt	7382
CEL	3	intron 1 + (20911-20924)	taatgacatttaacttagc (A)13-15 ctgaatatgactaaaactga	7383
CEL	4	intron 1 + 22374	ttaagtttaaatgtaaacagc A/G cctttgcacactattcagtg	7384
CEL	5	intron 1 + (22460-22469)	ttaatttttttagttaggttg (T)9-10 ctctttttttttatcacatg	7385
CEL	6	intron 1 + 24205	agaattttgagtcattcttg T/G gtgcctcttgactacatcct	7386
CEL	7	intron 1 + (24404-24417)	gcaagttttaaactgaattac (A)11-14 gcagatgataatcattctat	7387
CEL	8	intron 1 + 26983	tagattttgatgagtttgag T/G tttttttttttttttccaa	7388
CEL	9	intron 1 + (26983-26999)	tagattttgatgagtttgag (T)14-17 ccaaaaggtgggggtgtgt	7389
CEL	10	intron 1 + (32166-32174)	tcaactttgtctggttaaccag (A)8-9 gaaaagccactatttaatac	7390
CEL	11	intron 1 + 37217	aaatttgaatgaatgtta T/G ataaaaatctgtaacaatta	7391
CEL	12	intron 1 + 37685	taattcaaatggattaatca T/A tgataattctattttttaa	7392
CEL	13	intron 1 + 38032	caggcctaataaatgaaatg T/C tcactactgttgccaacacc	7393
CEL	14	intron 1 + 38133	attcgaggagtcctgtctgac A/C ttgtgataaacatccagct	7394
CEL	15	intron 1 + 38169	cagctcatcttctactctt A/T gtgtgtgggggtttttgcccc	7395
CEL	16	intron 1 + 38544	gtttctgtcaactctccaga T/C ataaaaatcaaatgctcttcc	7396
CEL	17	intron 1 + (38642-38643)	caattttctcacaatacctg (G) attgctgccaggcagcaata	7397
CEL	17	intron 1 + (38642-38643)	caattttctcacaatacctg attgctgccaggcagcaata	7398
CEL	18	intron 1 + 48429	gaaagagaaactgtgtccc A/C gaaactgtgtgaagtatgcc	7399
CEL	19	intron 1 + 49038	ttgaaactgcactgacacta A/G ttttaattttacaagtaatt	7400
CEL	20	intron 1 + 49040	gaaactgcactgacactaat T/G taaattttacaagtaatttt	7401
CEL	21	intron 1 + 49256	acatgagaaaaagaaatggag C/A taagtttaaaaacagaatga	7402
CEL	22	intron 1 + 49386	aatagttctcagtagatatt C/A ttttacctatatttagtata	7403
CEL	23	intron 1 + 50786	tactttgtcctcacaatgc G/A tattcttccctaaacagat	7404
CEL	24	intron 1 + 50977	ctccagccagagaggacaga T/C agctgagtttctgtttggct	7405
CEL	25	intron 1 + 51150	agcaccatggactgtttttg C/G agtctcctcttttattatgc	7406
CEL	26	intron 1 + 52333	tcagtcaaaacttaaggctc A/C gagatctattaatgcttatg	7407
CEL	27	intron 1 + 52589	gtgtcagcatctgttagagta C/A gggagggtgttgaaagaaa	7408
CEL	28	intron 1 + 55838	tctcgcaggtaaatgaggat G/A gaatacttttaatacaaatc	7409
CEL	29	intron 1 + 56028	ataagtttggaaaaatttgt G/C taaaaacactaaaattttc	7410
CEL	30	intron 1 + 58738	tggtggagaaataggttata G/A tgctgtgcaactgtcccat	7411
CEL	31	intron 1 + 59358	cagaatttgtactttaaaat A/G cgaactgcaagcactgcagt	7412
CEL	32	intron 1 + 59359	agaaattgtactttaaaata C/T gaactgcaagcactgcagt	7413
CEL	33	intron 1 + 59464	accagaaaggagcatgtcc C/G ttgtcatttgtgtgaaac	7414
CEL	34	intron 1 + 61340	aaaaaaaacttcaaatatc C/G caatatccaaagtgtgtaca	7415
CEL	35	intron 1 + 62739	cagtctttaggcacaaagag A/G caaagagtcttctctctct	7416
CEL	36	intron 1 + (64764-64779)	ctgggtgtgtttctcataaag (T)14-17 aatgtgggatagtggtata	7417
CEL	37	intron 1 + 65243	tttcaggcttctgtgacagaa T/C agtattatgataaaagctat	7418
CEL	38	intron 1 + 65269	tatgataaaagcattataata T/A ttagggaagattcctctgact	7419
CEL	39	intron 1 + 65325	aattagaaaagcaagttttg G/C ggggggggttgcaaaaacaa	7420
CEL	40	intron 1 + (65326-65334)	attagaaaagcaagttttg (G)7-9 tgcaaaaacaaaagaaaaa	7421
CEL	41	intron 1 + 65524	cacaccataaacaccagtt A/C gtgtcctctctctgagccatg	7422
CEL	42	intron 1 + 65869	cagagtaacattcgggctcc A/T actgtcctttcttatagaga	7423
CEL	43	intron 1 + 65910	aaggctgtctcctgtgttt G/C tggatccaagcctgctgaa	7424
CEL	44	intron 1 + 66000	gctgtgtttgcatgcctcac C/A gagcatattcactgtcctat	7425
CEL	45	intron 1 + (66226-66235)	tctgtttttgaaaaacaag (A)9-10 tctctccctgcctttggaaa	7426

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
CEL	46	intron 1 + 81816	aatgttgcttactttccac A/G tatttccagaagccctgac	7427
CEL	47	intron 1 + 83480	tatgactgtcaggaagaaaa T/C tagaattatctttgtctcc	7428
CEL	48	intron 1 + 83732	gggggtttgaatctatggag T/C catttccctcttttataaaa	7429
CEL	49	intron 1 + 85507	ctggaagaattttgtgtc A/T ctgcattattttaaattgtag	7430
CEL	50	intron 1 + 87299	caatggctattatattctcc G/A tgtgtgaagacagtcaagaa	7431
CEL	51	intron 1 + 87426	caacaggataatcccagaat G/C ctctgtctgccccttggtct	7432
CEL	52	intron 1 + 87670	tattttgttctcatattca T/C gacatgacacacacataa	7433
CEL	53	intron 1 - (77494-77503)	ttgggttctgttttttcttt (A) 9-10 caactctgtcaacaggggcc	7434
CEL	54	intron 1 - 77368	agctcaggggagagaacact G/C gggggaggcaagaagcggs	7435
CEL	55	intron 1 - (75135-75129)	tggcggtctggcccaagggt (G) 6-7 tgggactctctgacgctcc	7436
CEL	56	intron 1 - 74785	gctgcccacggaagctgggg G/C ctgttccgctcttctctgt	7437
CEL	57	intron 1 - 74755	ttcttctctgtgtccatgaa A/G cctcaggctctcagggtcag	7438
CEL	58	intron 1 - 73099	ccccggggtctctctctggc C/T tcttcttgcgcgcctgct	7439
CEL	59	intron 1 - 72559	agcagcagctgggcccgtcc G/A tgcaggagtgaggtggga	7440
CEL	60	intron 1 - 70098	acaggggaggaacagcaaaa T/C ctcaacactgtttgatctcat	7441
CEL	61	intron 1 - 69440	gttggccatgagagaaaaa C/T aggaaggtattggaaaatga	7442
CEL	62	intron 1 - 65270	attctgcactggctgggaag G/A ctgtggttgggcttctctggc	7443
CEL	63	intron 1 - 64434	ccacattagggtgagtgatg C/T aacatctgtaattattttca	7444
CEL	64	intron 1 - 63966	agatcagacatccccaccc C/T atcgcttagagaactgagcc	7445
CEL	65	intron 1 - 63916	gctgtccacctgacctgac C/T ttcagggtgctgacccagtc	7446
CEL	66	intron 1 - 60392	tctgtgggctccaggatgca C/T gtggaaatccctgggagcag	7447
CEL	67	intron 1 - 60321	aattacttgaacccattcc A/T tcccaccccaaccttttcc	7448
CEL	68	intron 1 - 60318	tacttgaacccattccatc C/T caaccccaaccttttctctcc	7449
CEL	69	intron 1 - 56852	tgtctcaagccctcccctgt C/A gccacgacgaccccatctc	7450
CEL	70	intron 1 - 56133	gctggctcgtgggatgtcta C/T ggggcttgcctggcaccccc	7451
CEL	71	intron 1 - 55964	ccccagcgcctccagcccg G/A cctgagacttatcactgccc	7452
CEL	72	intron 1 - 52016	tcttggaactagggtgggg G/A ggcactgccaagtggccagg	7453
CEL	73	intron 1 - 51998	gggggcaactgccaagtggca G/A gggaggggactgcggggcac	7454
CEL	74	intron 1 - 51578	gtgggatcgacttgcatctt G/C gggggagaaagcatccctggt	7455
CEL	75	intron 1 - 39557	ggccacgacatgggttcca T/C gaggtcttaagctcccaag	7456
CEL	76	intron 1 - 39490	gccctttcttccaggtgttc A/C tgggcaactgaggtcaccag	7457
CEL	77	intron 1 - (31332-31340)	tccggactctcattggctc (A) 8-9 ctgctcggccctgggattc	7458
CEL	78	intron 1 - 19634	ttatttcagggtggccatc C/T tagctgctcgaggagctgt	7459
CEL	79	intron 1 - 6589	gacgggtgatgcgaggact T/C gctgtcccccagtgctggg	7460
CEL	80	intron 1 - (3340-3345)	gctggcagtgctggcctgtg (C) 4-6 tcaatgtggtcgggttggg	7461
CEL	81	intron 3 + 35	tgccggactggccctcgcc G/A gggcgggtgagggcggtgc	7462
CEL	82	intron 6 + 157	gtggggagcggccttggtga C/T gggatttctgggtcccgtag	7463
CEL	83	exon 9 + 137	aacatggacggccacatctt C/T gccacgacatgacatgctgc	7464
CEL	84	intron 9 + 41	tcaggggcgaccctgctggg A/G gggccgcccgggaaagcactg	7465
CEL	85	intron 9 + 151	gggggtgagtatgcacacac T/C tctgttggcacaggctgag	7466
CEL	86	exon 10 + 82	acgacctttgatgtctacac C/T gagtctctgggcccaggacc	7467
CEL	87	exon 12 + 583	ccccgggtgactcgggggc C/A cccccgtgacccccacggg	7468
CEL	88	exon 12 + 759	gttttagcgtcccatgagcc T/C tggatbcaagaggccacaag	7469
IL17	1	5'flanking + 832	cctgagaagggaactattctc A/G aggacctgagttcaagtta	7470
IL17	2	5'flanking + 692	tgcctcccttttctccatct C/T ctacacctttgtccagctc	7471
IL17	3	5'flanking + 76	ccctgaacccactgcgacac G/A ccacgtaagtgcacacagaa	7472
IL17	4	intron 1 + 18	gtggtgagctctgactaac G/A tgcgatgctcttctgtgatt	7473
IL17	5	intron 1 + 126	ctgtatatgtagataggaa A/G tgaagcttttggtaggatt	7474
IL17	6	intron 1 + 762	ctgagaacaatggtgcagga G/A gatatttctacatagaaaa	7475
IL17	7	intron 2 + 594	tattttgatcatttgacttc A/T tacaataagtcctctgttct	7476
IL17	8	exon 3 + 1487	agctgatggggcagaacgaa C/T ttttaagtatgaaaaagttc	7477
IL17	9	3'flanking + 657	ccctgaatcttttctctct G/T cctctccctcattctcaaca	7478
UCHL3	1	5'flanking - 1034	ataatgtgaagaagaaaaaa A/G agacactgctactgggctcc	7479
UCHL3	2	5'flanking - 490	cactcctgcaccccgacaaa G/C gaacaacagcaccgtgctgc	7480
UCHL3	3	5'flanking - 480	ccccgacaaacgaacaacag T/C accgtgctgcacggcgctcc	7481
UCHL3	4	5'flanking - 295	atgctgtagaacgcgagcgct T/C ggcaaggctcggtcggaag	7482
UCHL3	5	5'flanking - (25-11)	tggcggaagcggcgccggc GCGAAGGCGGCGG/Δ tgcagagctg	7483
UCHL3	6	intron 2 + 28	aggtgtctgtctcgctgggac T/C tcggagcttttctgtctgc	7484
UCHL3	7	intron 2 + (5639-5640)	aattttttattataataata (ATA) tataagtagaagaattatat	7485
UCHL3	7	intron 2 + (5639-5640)	aattttttattataataata tataagtagaagaattatat	7486
UCHL3	8	intron 2 + 7862	aggtggatttcacaccacca G/A gctaactgtctaacttttag	7487
UCHL3	9	intron 2 + (7936-7947)	tgatcatttcaaacacaggg (T) 11-12 aattgtaaaagtagacatt	7488
UCHL3	10	intron 2 + (7975-7988)	aaagtaggacatttttaata (T) 12-14 gaagacgtgaggtgaaag	7489
UCHL3	11	intron 2 + 8117	cctgactctggcaatctgg A/C gtcaggatcttaacaatat	7490
UCHL3	12	intron 2 + 8361	ttgttagctttggctgacat G/A gagttagatttgagtgaaact	7491
UCHL3	13	intron 2 + 9800	taagatatagtgtgacttt C/T taatatgatttttgtttct	7492
UCHL3	14	intron 2 + (10738-10747)	taccaactaatgttccattg (T) 9-10 ctttctttttttaccagtt	7493
UCHL3	15	intron 3 + 11	tacagaaaaggtaattgtta A/T gtaaaatagaagtttctgg	7494
UCHL3	16	intron 3 + (662-675)	cttaaatcacagtttttcaa (TA) 6-7 aggaatcttcttctgtatt	7495
UCHL3	17	intron 3 + 866	tcaagctcacatatttttagt T/C tttttttctagaatgatata	7496

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
UCHL3	18	intron 3 + (944-945)	tacatacgtatacgtatata (TGTATACGTATACATACGTATACATATATACATACGTATATA) cgtacgtatatacgtatatac	7497
UCHL3	18	intron 3 + (944-945)	tacatacgtatacgtatata cgtacgtatatacgtatatac	7498
UCHL3	19	intron 3 + 5052	aggcagtcagctatagagcc T/C acatTTTTgatgcttattat	7499
UCHL3	20	intron 3 + 5282	acctctattaagtttttgca T/C accttttcagacttttccaat	7500
UCHL3	21	intron 6 + 2191	tttctagggtttctctagtg C/T gttagagcagtgattctcaag	7501
UCHL3	22	intron 6 + 8264	tctgcaagtcacaaatgtgaag G/C caagaagaaaaatccaaaa	7502
UCHL3	23	intron 6 + (8741-8744)	atgtgagtaaacacacattt ATTT/Δ ttcatttccotaaacttttga	7503
UCHL3	24	intron 6 + 9411	tcctctgtttagaatctact T/G ggccttttttgcccagccag	7504
UCHL3	25	intron 6 + 9459	tgtagtgccagtaaatagt T/A taaagtttccattctcattag	7505
UCHL3	26	intron 6 + 9772	gaaacaatacagtgatcatg T/C ggttcaagatgtagagtcga	7506
UCHL3	27	intron 6 + 10158	ttattttaaaggaaaattct C/T agaccgaacttaccagttca	7507
UCHL3	28	intron 6 + 10839	tttactaaaaaatctacaga A/C atccatttagaatttaattta	7508
UCHL3	29	intron 6 + 12493	agtcacaaatagttgacagtt A/G atgggcagtgaccttgcaa	7509
UCHL3	30	intron 6 + (20435-20437)	cttttttaattagtagtccct CCT/Δ cgccatccctacacagcct	7510
UCHL3	31	intron 6 + 21202	ttgatctgatcttctctgccc C/T atccagtttctaaagattctt	7511
UCHL3	32	intron 6 + 21295	caaatttatgatttctcttt T/C ataggctaattgatatctgca	7512
UCHL3	33	intron 6 + 21639	taagaacaattaaagtcac C/T ggcaagcattcttctctcc	7513
UCHL3	34	intron 6 + 21778	tcattttctgctgagtagca A/G caaactcacatctcttctta	7514
UCHL3	35	intron 6 + 23299	cttttagattaaagggtgcaa T/C gatgcacaaattttgagtcac	7515
UCHL3	36	intron 6 + 23498	tattcagttctctgactcca A/G ttgtactacttttacctcta	7516
UCHL3	37	intron 6 + 23790	ttagccttaaaaaattggac A/T ctcttctgattattgataaa	7517
UCHL3	38	intron 6 + 23894	actcattatcactgctcttcca A/C atattttaaagaatatgttc	7518
UCHL3	39	intron 6 + (24729-24732)	agtccttaatttcaaatgtt TGT/Δ aagcatcaaaagcaagagaaa	7519
UCHL3	40	intron 6 + (25083-25084)	catgtattcatttctcattcag (A) taagtatgcaatgtgcatat	7520
UCHL3	40	intron 6 + (25083-25084)	catgtattcatttctcattcag taagtatgcaatgtgcatat	7521
UCHL3	41	intron 6 + 25084	catgtattcatttctcattcag C/T aagtatgcaatgtgcatata	7522
UCHL3	42	intron 7 + 1342	gaagaagtcattatttttggt G/A gtatataatggacccagg	7523
UCHL3	43	intron 7 + 1387	ttttgaagatgtgctctgct G/A attgagtcctacaaaatctgc	7524
UCHL3	44	intron 7 + 1760	actcggttttactagttaga T/G agctgtcttctggctcagaggg	7525
UCHL3	45	intron 7 + 2096	taggtacattacaagatgg G/A cagttgctgattcattgcaa	7526
UCHL3	46	intron 7 + 2873	ttaattgtattaattccctac T/G ctaataaattgttaaggttaa	7527
UCHL3	47	intron 7 + 7554	tcctctgagcctcatgagttc T/A tctgcaagcgtatgcattac	7528
UCHL3	48	intron 8 + 207	ctctatgaacaaatgtaaaa T/A ttgaaaaggcaagaatagta	7529
UCHL3	49	intron 8 + 252	aagacttgctcattatattcc C/G agatttccatcaaatccagga	7530
UCHL3	50	intron 8 + (883-892)	tttacctgaaaaatcatac (T) 9-10 cctccataggatgccataga	7531
DDOST	1	intron2 629	attctgtttaagaagttcttta T/C attaagaatattgtctctct	7532
DDOST	2	intron2 3125	gagaatataggagcttctgc G/A tatgcctgaaagtcagtcag	7533
DDOST	3	intron2 3920	attactcattttaaagataaa A/G tggattactgagcactgtct	7534
DDOST	4	intron3 189	actgctgtccaggggtccat C/T tggggctgagcccagctgga	7535
DDOST	5	intron6 185	ctgtctcttctgttcggagg C/T gtggcagcttttcccttact	7536
DDOST	6	exon8 37	aactatgaactagctgtggc C/T ctctcccgtgggtgttcaa	7537
DDOST	7	intron9 37	tctgcccagaagtgtctgcc A/Δ aaaaacggccccagggctca	7538
DDOST	8	intron2 + 1299	atctcttgatgactgggtctt C/T ggtgacagtaactggtgtttg	7539
DDOST	9	intron2 + 1581	gatactgttgggtggagaaa T/C gacagagagtgtaaaacagt	7540
DDOST	10	intron2 + 2822	gtttctcaacaggtgcatte T/G tgacgttttcagactggataa	7541
DDOST	11	intron2 + 3392	cagaaggcgtggaggcctgc C/T gcgcctccctctgttctg	7542
DDOST	12	intron5 + 495	attgcttgaaccaggaggc G/A gagggttcagtgagccaagg	7543
DDOST	13	intron6 + 226	ggaactgcttgggtccagc C/T tctgtttgttccagctatcc	7544
DDOST	14	intron8 + 303	aagagaaataggtcattagg A/T tgaatttgttaggcaagaga	7545
DDOST	15	3' flanking + 40	cacagcgtggagacggggca G/A ggaggggggttattaggatt	7546
NTR	1	5' flanking - 535	cacgatctgtctcccgattc C/T tgttaactctagactttctg	7547
NTR	2	5' flanking - 15	gtaaatccccggcaaaaaacc A/G gcagcgccttgcaagccac	7548
NTR	3	5' flanking - 748	agcatggcgcgaggaggagg G/T gtgggagggtcgaggaggac	7549
NTR	4	5' flanking - 690	tgaataatttaaaggggccc T/C gcctgcggagcggggcgga	7550
NTR	5	intron6 + 605	tcttgccatatacttagtgg A/G ggggtctacatcaggggttt	7551
NTR	6	intron6 + 748	agcctccagcctctctctcc C/T ggggggttatctcaggcatct	7552
NTR	7	intron6 + 987	gggtctggctctgggtatccc C/T gtgcgtcatgtagctacact	7553
NTR	8	intron6 + 1882	tgccctcaagcaactctccc G/A cctcggcctccaaaagtgt	7554
NTR	9	intron6 + 2222	gaatgtttatgtagaacaga G/A agactgtatctgcggtcttc	7555
NTR	10	intron12 + 166	tatctggtaccgaggagct C/G tggcctcgtcccaaggccc	7556
NTR	11	intron13 + 69	atccaggtccacgcctgcc C/T gtctttagtgttttaactctg	7557
NTR	12	intron14 + 8	agccccgcctcggttaaggc C/T tgggacctgcccgggtgtg	7558
NTR	13	intron16 - 113	gccacgcgcctctgcctt T/C atattttctttaaacccttcc	7559
NTR	14	intron21 + 34	agagccggcgccagagac A/G tgcctggagatgtagtccgg	7560
NTR	15	intron21 + 128	gaagaaatcgtgcccttag G/A gtttcaaaccttaagtagga	7561
NTR	16	intron21 + 151	ttcaaaccttaagtaggacc C/G aggtgcagagcattctgggg	7562
NTR	17	intron21 + 651	ccactgtactccagccggga C/T gacagagctagaacctgttt	7563

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
NTE	18	intron21 + 737	tggaaaatagtctgtggatt G/T ttgttttaggactctgggcac	7564
NTE	19	intron21 + 1752	acagctggcttaggctgtta G/C tggagaactgggaagcaac	7565
NTE	20	intron21 + 1788	gaagcaacagctgggtcaaa A/Δ gtactttttctttcttggc	7566
NTE	21	intron21 + 1907	cactgcaacctctgctctcc A/G gggtcaagtattctctgc	7567
NTE	22	intron21 + 2065	ctgctctgttttatgttcag G/T tccccattagacagaggaa	7568
NTE	23	intron21 + 2336	agtctgggagcacaggagca G/A gaatttcagataaggaggaa	7569
NTE	24	intron23 + 41	tggggagggtgggtgggtggg G/C ctggagcctcaattctttc	7570
NTE	25	intron23 + 71	caaattctttcagacctgag T/C tcaagtctctcgcttccaac	7571
NTE	26	intron23 + 81	cagacctgagttcaagttct C/T ggcttccaaccacggagcct	7572
NTE	27	intron24 + 150	gtggggcggtgggtgacctc A/C gccgtccgtattcccgagct	7573
NTE	28	intron29 + 37	gctgcagcaaccgctgacg T/C cactgggggttgggggatg	7574
NTE	29	intron29 + 370	cgtcccaggctcagcgagccc G/A tggggccggctgggctccg	7575
NTE	30	intron30 + 56	acctccccgccacacacac G/A cacacgcgtgggcacacaca	7576
NTE	31	intron30 + 358	aaaaatacaaaaaattaacc A/G ggctgggtgggtgtgctgt	7577
NTE	32	intron30 + 372	tttaaccaggctgtgtgggtg T/C gccgttaatcccagctactc	7578
NTE	33	intron30 + 430	aaatcacttgaacctggag G/T tggaggttgagtgagctga	7579
NTE	34	intron30 + 655	gtgtgcacaccagctatata T/C gcaaatgctttctctcaggg	7580
NTE	35	intron30 + 659	gcacaccagctatataatgca A/C atgctttctctcagggcgag	7581
NTE	36	intron30 + 760	tgaatatgggcatcttgcac C/T gcatgccagctgtcccggt	7582
NTE	37	intron30 + 835	gcacacagctagataggatg T/C ggcacctctgacaggttaa	7583
NTE	38	intron31 + 40	tggtgcctgcataaggtggtc T/C ggctaaagctttgctacttaa	7584
NTE	39	intron31 + 41	gggtgcctgcataaggtggtc G/A gctaagctttgctacttaa	7585
NTE	40	intron31 + 1329	gtctgtcaaggccagggacag G/A ggatgtgtaggcgaggtgtgc	7586
NTE	41	intron35 + 31	aatggcttctctgtctgtttc G/A gactggggagccacacctctg	7587
L1CAM	1	intron 1 + 767	tttgacttctctacatgggt G/A actgtgtgagtcactctgtt	7588
L1CAM	2	intron 1 + 862	gcattgggtcatgtgtatgt G/C ttagtggggctgaatgtaag	7589
L1CAM	3	intron 1 + 1332	cagggatgaaggagcagagc C/T gctgagaggccacacaggtg	7590
L1CAM	4	intron 4 + 502	tttccctgggggttttccctt T/C gcattccatctccctgagc	7591
L1CAM	5	intron 18 + 147	agcgacgttatgaaattccc C/A acacttcacattttataaat	7592
L1CAM	6	intron 24 + 221	ctccttagccccccagaggg C/T cccaaactttaagagcactact	7593
AANAT	1	5'flanking-542	aggggtgcaggatgggtgt G/T agctggaggccaggggtag	7594
AANAT	2	5'flanking-263	ccccccacataagaggtggg C/G ttgtccaagactccagggga	7595
AANAT	3	intron3 39	cgccccagctccaggaggcc T/A ctgaagacagaggtcagcca	7596
AANAT	4	exon4 150	cagccggccgtgcgcggggc C/T gcgctcatgtgcgaggagcg	7597
ARD1	1	intron1 + 317	ccgtcggtctgctcggcccc C/G ctcccctggggctggggcagg	7598
ARD1	2	intron6 + 322	gctcctcagcactcgtctcac G/A ccaggagccacacactctct	7599
ARD1	3	intron6 + 1095	aaggctccatcctgagacaa A/C aagtcagtgtagctgccc	7600
ARD1	4	intron6 + 1179	aggagggaagacctgtatccc A/G gggacacctctccactcc	7601
ARD1	5	intron7 + 159	cctccaggctgctaggcaga C/T ggctcctctctaaagccagc	7602
ARD1	6	intron7 + 295	tgaccagccctgccaccga G/T gagccttgggcagaccctg	7603
ARD1	7	intron7 + 416	actaccatggaggccccac G/A acagagcgctgccccctgac	7604
NAT1	1	3'UTR 215	aataataataataataata A/T aaatgtatttttaagatggc	7605
NAT2	1	exon2 867	cgtgcccaaacctggtgatg G/A atcccttactatttagaata	7606
NAT2	2	3'flank 521	ccatccatacttttgcacaa G/A agaaggaacatgagctttat	7607
NAT2	3	3'flank 573	gatttgaatcctgtggaca C/T ggggtgaattacttttaaaa	7608
NAT2	4	3'flank 918	attttctgtttgtgaaattcc A/G gtatcagggtatagtttaa	7609
NAT2	5	3'flank 979	actattctccctctctgact C/T gtgatgactataataatctt	7610
NAT2	6	3'flank 1958	tacctattgaagtaagccta C/T gtcataccacctatttgtt	7611
NAT2	7	3'flank 2034	ccactgattccagagctag T/G tcattaagaagacagtgctc	7612
NAT2	8	3'flank 2201	cagattactggaggctact G/A ttgtctcaccatgcaaatg	7613
NAT2	9	3'flank 2818	gggataattgtctcctttct C/G cccagtgcatgttggaaacc	7614
NAT2	10	3'flank 3237	atatatatccaaattaaaa A/Δ caaaataaatttccgaaact	7615
NAT2	11	3'flank 3386	caacaagagatttttttaa G/A ctttttaaaacaccagacag	7616
NAT2	12	3'flank 3660	cagcactattcgcaatagca A/G agatgtggaatcaatctaaa	7617
NAT2	13	3'flank 3973	agcagaaaaataaataatg C/T gtactaggcttactacctgc	7618
NAT2	14	3'flank 4029	caaaacaaaccccatgaca T/C gagtttatctatatacaaaa	7619
NAT2	15	3'flank 4118	ataagattaatatctgcata C/A aaatctttgtttacagcttg	7620
NAT2	16	3'flank 4146	tgtttacagcttgttatata C/T tgaattatgtctgctccccc	7621
NAT2	17	3'flank 4279	ttaatctgataggattgggtg G/C ctttataagaaaaagaaaag	7622
NAT2	18	3'flank 4323	ttgtctctctccagtcag T/G taccaggaagggccatgtg	7623
NAT2	19	3'flank 4446	tcaattggctttatctgcga T/C tctggaatcaggcaatactc	7624
NAT2	20	3'flank 4462	gcgattctggaaatcaggcaa T/C actccatttcataaaacaga	7625
NAT2	21	exon2 + 288	atgtttaggagggtattttta C/T atccctccaggttaacaaata	7626
NAT2	22	5'flank - 2053	ctggattgcacattttat T/C ccagggtgcaggttttccaac	7627
NAT2	23	5'flank - 1299	gaatccagctgcgggaggt A/G taacagtgaaaccaagacac	7628
NAT2	24	5'flank - 1145	ctgtagaacacaaagatatt C/T ggaggcagtttgtacatgcc	7629
NAT2	25	5'flank - 1036	ccttccacagagtcgccag T/A tcatgtggcagatgccaga	7630
NAT2	26	5'flank - 94	aaagatttgctaagagattc G/A cagaggcaacctgaggccct	7631
NAT2	27	5'flank - 643	atgttttatattttatata T/C attaatgtaaaaaaatttt	7632
ABCB2	1	5'flanking - 673	agctaaaggtcaaacaccc G/C cttttccaccagctcgcg	7633

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCB2	2	5'flanking - 646	ccaccagcctcgcgtgcctg T/G tcccttcacggacactctag	7634
ABCB2	3	5'flanking - 563	ttgcaagcgcctggctgctac A/C ggcgacctccctgcgctccc	7635
ABCB2	4	5'flanking - 236	gctttgcgcgcggcgctaac G/T tggtagggcagatctgccc	7636
ABCB2	5	Intron3 + 408	aaggaaactgagggcaagac C/T ctaaatgctgaaactgcaca	7637
ABCB2	6	Exon4 + 153	ccctcaccatgggtcacctg A/G tcaccctgcctctgcttttc	7638
ABCB2	7	Intron4 + 289	gtatttcttttagcatccaag G/T ggcatagctgtgtctcttttc	7639
ABCB2	8	Intron4 + 291	atttcttttagcatccaaggg C/G catagctgtgtctctctttctc	7640
ABCB2	9	Intron5 - 63	ttccttcagggttaagtactg C/T ggttctttgtgtccctcca	7641
ABCB2	10	Intron7 - 185	gtctctgcctctgtctttgc C/T gcttctcttatctctactec	7642
ABCB2	11	3'flanking + 71	agcgcaacttttcagctgcgg G/A tgtctctctttttatcatcc	7643
ABCB2	12	3'flanking + 129	aactgcatacacttttcct T/C aagctttttaattcctatga	7644
ABCB2	13	3'flanking + 459	cattcagggaggccaggtc G/A tgtgacgtcgacagttgctg	7645
ABCB3	1	intron3+8	tctcctttggcaggtagtg G/A tgggcagctgggtccatttg	7646
ABCB3	2	intron4+104	cttcaccgtatgccaggac C/T tggggatgctttctctctgt	7647
ABCB3	3	intron10+219	gcagcagtggtgtccctcc A/G tgggcagcccgctcaggtcc	7648
ABCB3	4	intron11+(317-319)	atggtgcccaggtggatgtg GTG/Δ tccatctcattctctcttt	7649
ABCB3	5	exon12+19	agctgcaggaactggaattcc T/C gtggggatcgacagtgctg	7650
ABCB3	6	exon12+(356-357)	aggtgggtgggtgggtgggtg GG/TGGTGGGTGGA ggcgtgtctgtgctc	7651
GSTM3	1	5'flanking - 144	ccaacgccggcattagtcgc G/T cctgcgcacggccctgtgga	7652
GSTM3	2	intron 7 + 165	agcctaacttctataccttg A/G aggcactgtctacaaaaaaa	7653
GSTM3	3	intron 7 + 257	ctgttggaactgggtgggtgc T/G ttataagattggtgtatttt	7654
GSTM3	4	exon 8 + 91	cccagtggggcaacaagcct A/G tatgctgagcaggaggcaga	7655
GSTM4	1	intron 4 + 67	ttggctggattgggtgcta T/C gctcagagtgtgtctgtgtt	7656
GSTM4	2	intron 7 + 77	gatgcttcccagtcctgga T/G ctgcataaagaataactgc	7657
GSTM4	3	intron 7 + 80	gctttccagtccttgatct G/A cataaagaataacttgatt	7658
ALDH7	1	intron1+464	catgaatgactctgggaag A/G atcattcttagcaatggact	7659
ALDH7	2	intron1+2269	aaatggaatccaacagcaa G/C agacctcccctcacccgtca	7660
ALDH7	3	intron2+1349	actgagcttctgcccacggc C/T gcctgccggccttcattgaga	7661
ALDH7	4	intron2+1820	tccgtgtggaaggcaccttc C/G cccagcctcagtggttagga	7662
ALDH7	5	intron2+2046	aacctcaggcgtgcctcag C/G caggagaccagcctggcccc	7663
ALDH7	6	intron2+2939	aagcacgcactgaacatgga G/A tgagtgaatgaacgaatgaa	7664
ALDH7	7	intron3+7	tgcccaagaacctggtgagc C/T ggcgggctgagcgggcag	7665
ALDH7	8	intron4+36	gccccctccggtcaccttc T/C ccgctcagagcctcaggccc	7666
ALDH7	9	intron6+(116-117)	attctctctctctctctctct CT/Δ ggaccaggctgggagcagtc	7667
ALDH7	10	intron6+263	cagaccctcatacgtgaccc T/C gctgccccccaggctcttag	7668
HMGL1L1	1	3'untranslated + 864	ctttctgatttttgatagtc G/C gttgaagaaggagtttgaa	7669

In some embodiments, a drug-metabolizing enzyme is at least one of the following:
epoxide hydrolase, methyltransferase, N-acetyltransferase, sulfotransferase, quinone
oxidoreductase, glutathione S-transferase, UDP-glycosyltransferase, aldehyde
dehydrogenase, alcohol dehydrogenase, esterase, NDUF, cytochrome P450 (CYP) and
5 ATP-binding cassette.

The present invention relates to a method for detecting a genetic polymorphism in
a test subject using the genetic polymorphism data related to a drug metabolizing
enzyme. The present invention analyzes the effectiveness, safety and strength of drugs
metabolized by a drug metabolizing enzyme. The relationship between a disease and the
10 drug to be evaluated is based on the results of the analysis. The genetic polymorphism
data for the drug metabolizing enzyme is different for each patient with a given disease.
Therefore, the effectiveness and safety of a specific drug depends on drug metabolism in
the presence of certain genetic polymorphism data and the side effects in the presence of
certain genetic polymorphism data. As a result, a physician can determine whether a
15 certain drug should be used by a certain patient and can tailor drugs for use by a certain
patient based on the genetic polymorphism data (so-called "made-to-order" treatments).

"Drug metabolizing enzymes" refer to a group of enzymes that catalyze *in vivo*
structural changes in exogenous materials including drugs. When used for clinical
purposes, the group of metabolizing enzymes includes some endogenous materials.
20 Because drug-metabolizing enzymes absorb, metabolize and secrete drugs, the
polymorphism of an enzyme depends on the amount of enzyme expressed (transcription
and translation) and the amount of activity. As a result, there are blood serum
concentrations of both unchanged materials and metabolites.

Drug metabolizing enzymes expressed by the genes that are targeted for genetic
25 polymorphism analysis in the present invention include, but are not limited to the
following classes of enzymes:

Epoxide hydrolases
Methyltransferases
N-acetyltransferases
30 Sulfotransferases

Quinone oxidoreductases
 Glutathione S-transferases
 UDP-glycosyltransferases
 Aldehyde dehydrogenases
 5 Alcohol dehydrogenases
 Esterases
 Ubiquinone dehydrogenases : NDUF
 Cytochrome P450s (CYPs)
 ATP-binding cassettes
 10 ATP-binding cassettes / Transporters

Examples and descriptions of these enzymes are provided below.

(1) Epoxide hydrolases are enzymes that hydrolyze epoxide using a trans-
 cleavage mechanism to produce 1,2-glycol. Examples include microsomal epoxide
 15 hydrolase 1 and cytoplasmic epoxide hydrolase 2.

(2) Methyltransferases are enzymes that catalyze transmethylation in amino
 groups, hydroxyl groups and thiol groups. Examples include the following.

Catechol-O-methyltransferase
 20 Vitamin-N-methyltransferase
 Phenylethanolamine-N-methyltransferase
 Phosphatidylethanolamine-N-methyltransferase
 Nicotinamide-N-methyltransferase
 Acetylserotonin-O-methyltransferase
 25 Thiopurine S-methyltransferase

(3) N-acetyltransferases are enzymes that catalyze transacetylation in amino
 groups, sulfonamide groups and hydrazine groups. Examples include the following.

Arylamine-N-acetyltransferase 1, 2
 30 Arylalkylamine-N-acetyltransferase

N-acetyltransferase homologues of *saccharomyces cerevisiae*

LI intracellular adhesion molecules

(4) Sulfotransferases are enzymes that contribute to sulfate conjugation and catalyzes trans-sulfonylation in phenols, steroids, arylamines and biliary acid. Examples include the following.

Sulfotransferase 1A1, 1A2, 1A3, 1C1, 1C2, 2A1, 2B1

Thyroid hormone sulfotransferase

Tyrosyl protein sulfotransferase 1, 2

Sulfotransferase-opening protein 3

Estrogen sulfotransferase

Cerebroside sulfotransferase

HNK-sulfotransferase 1

Carbohydrate sulfotransferase 2, 4, 5

Carbohydrate sulfotransferase 1, 3

(5) Quinone oxidoreductases are enzymes that catalyze the reduction of quinones such as o-quinone and p-quinone. Examples include the following.

NAD(P)H: Quinone oxidoreductase 1

NRH: Quinone oxidoreductase 2

Quinone oxidoreductase homologues

p53-induced gene 3 (PIG3) of a quinone oxide transferase homologue

(6) Glutathione S-transferases are enzymes that catalyze the conjugation of glutathione. Examples include the following.

Glutathione S-transferase Mu1, Mu2, Mu3, Mu4, Mu5

Glutathione S-transferase Z (zeta)

Glutathione S-transferase P (pi)

Glutathione S-transferase 1 T1 (zeta)

Glutathione S-transferase 1 Theta 1, Theta 2

Microsomal Glutathione S-transferase 1
 Microsomal Glutathione S-transferase 1-1
 Microsomal Glutathione S-transferase 2, 3
 Microsomal Glutathione S-transferase Ha Subunit 1, 2
 5 Microsomal Glutathione S-transferase A3, A4
 Glutathione S-transferase A1, A4
 Glutathione S-transferase M1, M2, M3, M4

(7) UDP-glycosyltransferases are enzymes that catalyze the contribution of
 10 glucuronic acid to functional groups such as hydroxyl groups, carboxyl groups, amino
 groups and thiol groups after their introduction in the 1st drug metabolism route.

Examples include the following.

UDP-glycosyltransferase 1
 UDP-glycosyltransferase 1 Family Polypeptide A1
 15 UDP-glycosyltransferase 2 Family Polypeptide A1, B7, B10, B4, B11, B15, B17
 UDP-glycosyltransferase 8
 Dolichyl-diP-oligosaccharide protein glycosyl transferase

(8) Aldehyde dehydrogenases are enzyme that converts aldehydes into
 20 carboxylic acids. Examples include Aldehyde dehydrogenase 1 through 10.

Aldehyde dehydrogenase 1 family member A1, A2, A3
 Aldehyde dehydrogenase 1 family member B1
 Formyltetrahydroforate dehydrogenase
 Aldehyde dehydrogenase 2
 25 Aldehyde dehydrogenase 3 family member A1, A2
 Aldehyde dehydrogenase 3 family member B1, B2
 Aldehyde dehydrogenase 5 family member A1
 Aldehyde dehydrogenase 6 family member A1
 Aldehyde dehydrogenase 8 family member A1
 30 Aldehyde dehydrogenase 9 family member A1

(9) Alcohol dehydrogenases are enzymes that convert alcohols into aldehydes or ketones. Examples include the following.

Alcohol dehydrogenase 1 through 7

5 Hydroxy-CoA-dehydrogenase

Short-chain alcohol dehydrogenase family genes

(10) Esterases are enzymes that hydrolyze some esters. Examples include the following.

10 Arylacetoamide deacetylase

Granzyme A

Granzyme B

Interleukin 17

Ubiquitin carboxyl-terminal esterase L1, 3

15 Carboxyl esterase 1

Lipase A

Esterase D-formylglutathione hydrolase

Carboxylester lipase

Dolichyl-diphosphooligosaccharide-protein glycosyltransferase (DDOST)

20 Neuropathy target esterase

(11) Ubiquinone dehydrogenases (NDUF) are enzymes that support energy metabolism, *e.g.*, as in the mitochondrial respiratory chain. Examples include NADH ubiquinone dehydrogenase 1a Subunit 1 through 10.

25 NADH-dehydrogenase (ubiquinone)1 α -subcomplex 1 through 3 and 5 through 10

NADH-dehydrogenase (ubiquinone)1 α / β -subcomplex 1

NADH-dehydrogenase (ubiquinone)1 β -subcomplex 3, 5, 7

NADH-dehydrogenase (ubiquinone) Fe-S protein 1, 3, 4, 5, 6, 8

NADH-dehydrogenase (ubiquinone) flavoprotein 1 through 3

30

(12) Cytochrome P450s (CYPs) are enzymes that regulate 1st drug metabolism and introduce oxygen atoms to the drug. Examples include Cytochrome P450 (CYP) 1A1, CYP 1A2, CYP1B1, CYP 2A6, CYP 2B6, CYP 2C8, CYP 2C18, CYP 2C9, CYP 2C19, CYP 2E1, CYP 2D6, CYP 2E1, CYP 2F1, CYP 3A3, CYP 3A4, CYP 3A5, CYP 3A7, CYP 3A43, CYP 4A11, CYP 4B1, CYP 4F2, CYP 4F3, CYP 4F8, CYP 11B1, CYP 11B2, CYP 17, CYP 19, CYP 21A2, CYP 21A1, CYP 27B1 and CYP 27.

(13) ATP-binding cassettes absorb the drug and adjust the interstitial concentration with a transporter. Examples include the following.

- ATP-Binding Cassette Subfamily A Members 1 through 6, 8
- ATP-Binding Cassette Subfamily A Members 1, 4, 7, 8
- ATP-Binding Cassette Subfamily B Members 1 through 11
- ATP-Binding Cassette Subfamily B Members 1, 4, 7, 8, 9, 10, 11
- ATP-Binding Cassette Subfamily C Members 1 through 6, 8 through 10
- ATP-Binding Cassette Subfamily C Members 1, 2, 3, 4, 5, 7, 8, 9
- ATP-Binding Cassette Subfamily D Members 1 through 4
- ATP-Binding Cassette Subfamily D Members 1, 3, 4
- ATP-Binding Cassette Subfamily E Members 1
- ATP-Binding Cassette Subfamily F Members 1 through 3
- ATP-Binding Cassette Subfamily F Member 1
- ATP-Binding Cassette Subfamily G Members 1
- ATP-Binding Cassette Subfamily G Members 1, 2, 4, 8
- Organic anion transporters 1, 2, 3
- Organic anion transporter polypeptides 1, 2, 8
- Transporter 1 ATP-binding cassette subfamily B
- Transporter 2 ATP-binding cassette subfamily B
- SLC22A4 solute carrier family 22 (organic cation transporter) member 4
- SLC22A5 solute carrier family 22 (organic cation transporter) member 5
- SLC22A1 solute carrier family 22 (organic cation transporter) member 1
- SLC22A2 solute carrier family 22 (organic cation transporter) member 2

SLC10A2 solute carrier family 10 (sodium/bile acid cotransporter family)

member 2

SLC15A1 solute carrier family 15 (oligopeptide transporter) member 1

- 5 (14) Other enzymes include gamma glutamyl transferase 1, transglutaminase 1
and dihydropyrimidine dihydrogenase.

Genetic polymorphism data relating to DMEs can be obtained using any general
genetic polymorphism detection method. Examples include, but are not limited to, PCR
10 or other amplification methods, hybridization methods using an allele-specific
oligonucleotide matrix (e.g., TAQMAN PCR method, INVADER assay method), primer
extension reaction methods, sequencing methods, MALDI-TOF/MS methods and the
DNA chip methods (e.g., microarrays). Examples of detection methods that are
applicable to analysis of the DME associated polymorphisms of the present invention
15 include but are not limited to those listed below.

1. Direct sequencing Assays

In some embodiments of the present invention, variant sequences are detected
using a direct sequencing technique. In these assays, DNA samples are first isolated from
20 a subject using any suitable method. In some embodiments, the region of interest is
cloned into a suitable vector and amplified by growth in a host cell (e.g., a bacteria). In
other embodiments, DNA in the region of interest is amplified using PCR.

Following amplification, DNA in the region of interest (e.g., the region containing
the SNP or mutation of interest) is sequenced using any suitable method, including but
25 not limited to manual sequencing using radioactive marker nucleotides, or automated
sequencing. The results of the sequencing are displayed using any suitable method. The
sequence is examined and the presence or absence of a given SNP or mutation is
determined.

30 2. PCR Assay

In some embodiments of the present invention, variant sequences are detected using a PCR-based assay. In some embodiments, the PCR assay comprises the use of oligonucleotide primers that hybridize only to the variant or wild type allele (*e.g.*, to the region of polymorphism or mutation). Both sets of primers are used to amplify a sample of DNA. If only the mutant primers result in a PCR product, then the patient has the mutant allele. If only the wild-type primers result in a PCR product, then the patient has the wild type allele.

3. Fragment Length Polymorphism Assays

In some embodiments of the present invention, variant sequences are detected using a fragment length polymorphism assay. In a fragment length polymorphism assay, a unique DNA banding pattern based on cleaving the DNA at a series of positions is generated using an enzyme (*e.g.*, a restriction enzyme or a CLEAVASE I [Third Wave Technologies, Madison, WI] enzyme). DNA fragments from a sample containing a SNP or a mutation will have a different banding pattern than wild type.

a. RFLP Assay

In some embodiments of the present invention, variant sequences are detected using a restriction fragment length polymorphism assay (RFLP). The region of interest is first isolated using PCR. The PCR products are then cleaved with restriction enzymes known to give a unique length fragment for a given polymorphism. The restriction-enzyme digested PCR products are generally separated by gel electrophoresis and may be visualized by ethidium bromide staining. The length of the fragments is compared to molecular weight markers and fragments generated from wild-type and mutant controls.

b. CFLP Assay

In other embodiments, variant sequences are detected using a CLEAVASE fragment length polymorphism assay (CFLP; Third Wave Technologies, Madison, WI; *See e.g.*, U.S. Patent Nos. 5,843,654; 5,843,669; 5,719,208; and 5,888,780; each of which

SEQ ID NO:4433² n represents a or deletion (Location 21).

SEQ ID NO:4435² n represents t or deletion (Location 21).

SEQ ID NO:4442² n represents 6 to 7 repeats of gatt (from Location 21).

SEQ ID NO:4443² n represents t or deletion (Location 21).

5 SEQ ID NO:4448² n represents t or deletion (Location 21).

SEQ ID NO:4449² n represents gt or deletion (Location 21).

SEQ ID NO:4452² n represents a or deletion (Location 21).

SEQ ID NO:4453² n represents a or deletion (Location 21).

SEQ ID NO:4457² n represents t or deletion (Location 21).

10 SEQ ID NO:4460² n represents at or deletion (Location 21).

SEQ ID NO:4466² n represents a or deletion (Location 21).

SEQ ID NO:4469² n represents t or deletion (Location 21).

SEQ ID NO:4472² n represents at or deletion (Location 21).

SEQ ID NO:4473² n represents a or deletion (Location 21).

15 SEQ ID NO:4474² n represents 12 to 14 repeats of t (from Location 21).

SEQ ID NO:4477² n represents t or deletion (Location 21).

SEQ ID NO:4479² n represents cac or deletion (Location 21).

SEQ ID NO:4486² n represents cca or deletion (Location 21).

SEQ ID NO:4514² n represents t or deletion (Location 21).

20 SEQ ID NO:4544² n represents c or deletion (Location 21).

SEQ ID NO:4552² n represents aaaa or deletion (Location 21).

SEQ ID NO:4565² n represents c or deletion (Location 21).

SEQ ID NO:4575² n represents 8 to 9 repeats of t (from Location 21).

SEQ ID NO:4576² n represents a or deletion (Location 21).

25 SEQ ID NO:4588² n represents taac or deletion (Location 21).

SEQ ID NO:4589² n represents ctcttt or deletion (Location 21).

SEQ ID NO:4590² n represents ct or deletion (Location 21).

(Northern) is isolated from a subject. The DNA or RNA is then cleaved with a series of restriction enzymes that cleave infrequently in the genome and not near any of the markers being assayed. The DNA or RNA is then separated (*e.g.*, on an agarose gel) and transferred to a membrane. A labeled (*e.g.*, by incorporating a radionucleotide) probe or probes specific for the SNP or mutation being detected is allowed to contact the membrane under a condition or low, medium, or high stringency conditions. Unbound probe is removed and the presence of binding is detected by visualizing the labeled probe.

b. Detection of Hybridization Using "DNA Chip" Assays

In some embodiments of the present invention, variant sequences are detected using a DNA chip hybridization assay. In this assay, a series of oligonucleotide probes are affixed to a solid support. The oligonucleotide probes are designed to be unique to a given SNP or mutation. The DNA sample of interest is contacted with the DNA "chip" and hybridization is detected.

In some embodiments, the DNA chip assay is a GeneChip (Affymetrix, Santa Clara, CA; *See e.g.*, U.S. Patent Nos. 6,045,996; 5,925,525; and 5,858,659; each of which is herein incorporated by reference) assay. The GeneChip technology uses miniaturized, high-density arrays of oligonucleotide probes affixed to a "chip." Probe arrays are manufactured by Affymetrix's light-directed chemical synthesis process, which combines solid-phase chemical synthesis with photolithographic fabrication techniques employed in the semiconductor industry. Using a series of photolithographic masks to define chip exposure sites, followed by specific chemical synthesis steps, the process constructs high-density arrays of oligonucleotides, with each probe in a predefined position in the array. Multiple probe arrays are synthesized simultaneously on a large glass wafer. The wafers are then diced, and individual probe arrays are packaged in injection-molded plastic cartridges, which protect them from the environment and serve as chambers for hybridization.

The nucleic acid to be analyzed is isolated, amplified by PCR, and labeled with a fluorescent reporter group. The labeled DNA is then incubated with the array using a

fluidics station. The array is then inserted into the scanner, where patterns of hybridization are detected. The hybridization data are collected as light emitted from the fluorescent reporter groups already incorporated into the target, which is bound to the probe array. Probes that perfectly match the target generally produce stronger signals than those that have mismatches. Since the sequence and position of each probe on the array are known, by complementarity, the identity of the target nucleic acid applied to the probe array can be determined.

In other embodiments, a DNA microchip containing electronically captured probes (Nanogen, San Diego, CA) is utilized (*See e.g.*, U.S. Patent Nos. 6,017,696; 6,068,818; and 6,051,380; each of which are herein incorporated by reference). Through the use of microelectronics, Nanogen's technology enables the active movement and concentration of charged molecules to and from designated test sites on its semiconductor microchip. DNA capture probes unique to a given SNP or mutation are electronically placed at, or "addressed" to, specific sites on the microchip. Since DNA has a strong negative charge, it can be electronically moved to an area of positive charge.

First, a test site or a row of test sites on the microchip is electronically activated with a positive charge. Next, a solution containing the DNA probes is introduced onto the microchip. The negatively charged probes rapidly move to the positively charged sites, where they concentrate and are chemically bound to a site on the microchip. The microchip is then washed and another solution of distinct DNA probes is added until the array of specifically bound DNA probes is complete.

A test sample is then analyzed for the presence of target DNA molecules by determining which of the DNA capture probes hybridize, with complementary DNA in the test sample (*e.g.*, a PCR amplified gene of interest). An electronic charge is also used to move and concentrate target molecules to one or more test sites on the microchip. The electronic concentration of sample DNA at each test site promotes rapid hybridization of sample DNA with complementary capture probes (hybridization may occur in minutes). To remove any unbound or nonspecifically bound DNA from each site, the polarity or charge of the site is reversed to negative, thereby forcing any unbound or nonspecifically

bound DNA back into solution away from the capture probes. A laser-based fluorescence scanner is used to detect binding,

In still further embodiments, an array technology based upon the segregation of fluids on a flat surface (chip) by differences in surface tension (ProtoGene, Palo Alto, CA) is utilized (*See e.g.*, U.S. Patent Nos. 6,001,311; 5,985,551; and 5,474,796; each of which is herein incorporated by reference). Protogene's technology is based on the fact that fluids can be segregated on a flat surface by differences in surface tension that have been imparted by chemical coatings. Once so segregated, oligonucleotide probes are synthesized directly on the chip by ink-jet printing of reagents. The array with its reaction sites defined by surface tension is mounted on a X/Y translation stage under a set of four piezoelectric nozzles, one for each of the four standard DNA bases. The translation stage moves along each of the rows of the array and the appropriate reagent is delivered to each of the reaction site. For example, the A amidite is delivered only to the sites where amidite A is to be coupled during that synthesis step and so on. Common reagents and washes are delivered by flooding the entire surface and then removing them by spinning.

DNA probes unique for the SNP or mutation of interest are affixed to the chip using Protogene's technology. The chip is then contacted with the PCR-amplified genes of interest. Following hybridization, unbound DNA is removed and hybridization is detected using any suitable method (*e.g.*, by fluorescence de-quenching of an incorporated fluorescent group).

In yet other embodiments, a "bead array" is used for the detection of polymorphisms (Illumina, San Diego, CA; *See e.g.*, PCT Publications WO 99/67641 and WO 00/39587, each of which is herein incorporated by reference). Illumina uses a BEAD ARRAY technology that combines fiber optic bundles and beads that self-assemble into an array. Each fiber optic bundle contains thousands to millions of individual fibers depending on the diameter of the bundle. The beads are coated with an oligonucleotide specific for the detection of a given SNP or mutation. Batches of beads are combined to form a pool specific to the array. To perform an assay, the BEAD

ARRAY is contacted with a prepared subject sample (e.g., DNA). Hybridization is detected using any suitable method.

c. Enzymatic Detection of Hybridization

5 In some embodiments of the present invention, hybridization is detected by enzymatic cleavage of specific structures (INVADER assay, Third Wave Technologies; *See e.g.*, U.S. Patent Nos. 5,846,717, 6,090,543; 6,001,567; 5,985,557; and 5,994,069; each of which is herein incorporated by reference). The INVADER assay detects specific DNA and RNA sequences by using structure-specific enzymes to cleave a complex
10 formed by the hybridization of overlapping oligonucleotide probes. Elevated temperature and an excess of one of the probes enable multiple probes to be cleaved for each target sequence present without temperature cycling. These cleaved probes then direct cleavage of a second labeled probe. The secondary probe oligonucleotide can be 5'-end labeled with a fluorescent dye that is quenched by a second dye or other quenching moiety.
15 Upon cleavage, the de-quenched dye-labeled product may be detected using a standard fluorescence plate reader, or an instrument configured to collect fluorescence data during the course of the reaction (*i.e.*, a "real-time" fluorescence detector, such as an ABI 7700 Sequence Detection System, Applied Biosystems, Foster City, CA).

The INVADER assay detects specific mutations and SNPs in unamplified
20 genomic DNA. In an embodiment of the INVADER assay used for detecting SNPs in genomic DNA, two oligonucleotides (a primary probe specific either for a SNP/mutation or wild type sequence, and an INVADER oligonucleotide) hybridize in tandem to the genomic DNA to form an overlapping structure. A structure-specific nuclease enzyme recognizes this overlapping structure and cleaves the primary probe. In a secondary
25 reaction, cleaved primary probe combines with a fluorescence-labeled secondary probe to create another overlapping structure that is cleaved by the enzyme. The initial and secondary reactions can run concurrently in the same vessel. Cleavage of the secondary probe is detected by using a fluorescence detector, as described above. The signal of the test sample may be compared to known positive and negative controls.

In some embodiments, hybridization of a bound probe is detected using a TAQMAN assay (PE Biosystems, Foster City, CA; *See e.g.*, U.S. Patent Nos. 5,962,233 and 5,538,848, each of which is herein incorporated by reference). The assay is performed during a PCR reaction. The TAQMAN assay exploits the 5'-3' exonuclease activity of DNA polymerases such as AMPLITAQ DNA polymerase. A probe, specific for a given allele or mutation, is included in the PCR reaction. The probe consists of an oligonucleotide with a 5'-reporter dye (*e.g.*, a fluorescent dye) and a 3'-quencher dye. During PCR, if the probe is bound to its target, the 5'-3' nucleolytic activity of the AMPLITAQ polymerase cleaves the probe between the reporter and the quencher dye. The separation of the reporter dye from the quencher dye results in an increase of fluorescence. The signal accumulates with each cycle of PCR and can be monitored with a fluorimeter.

In still further embodiments, polymorphisms are detected using the SNP-IT primer extension assay (Orchid Biosciences, Princeton, NJ; *See e.g.*, U.S. Patent Nos. 5,952,174 and 5,919,626, each of which is herein incorporated by reference). In this assay, SNPs are identified by using a specially synthesized DNA primer and a DNA polymerase to selectively extend the DNA chain by one base at the suspected SNP location. DNA in the region of interest is amplified and denatured. Polymerase reactions are then performed using miniaturized systems called microfluidics. Detection is accomplished by adding a label to the nucleotide suspected of being at the SNP or mutation location. Incorporation of the label into the DNA can be detected by any suitable method (*e.g.*, if the nucleotide contains a biotin label, detection is via a fluorescently labeled antibody specific for biotin).

5. Other Detection Assays

Additional detection assays that are produced and utilized using the systems and methods of the present invention include, but are not limited to, enzyme mismatch cleavage methods (*e.g.*, Variagenics, U.S. Pat. Nos. 6,110,684, 5,958,692, 5,851,770, herein incorporated by reference in their entireties); polymerase chain reaction; branched

hybridization methods (e.g., Chiron, U.S. Pat. Nos. 5,849,481, 5,710,264, 5,124,246, and 5,624,802, herein incorporated by reference in their entireties); rolling circle replication (e.g., U.S. Pat. Nos. 6,210,884 and 6,183,960, herein incorporated by reference in their entireties); NASBA (e.g., U.S. Pat. No. 5,409,818, herein incorporated by reference in its entirety); molecular beacon technology (e.g., U.S. Pat. No. 6,150,097, herein incorporated by reference in its entirety); E-sensor technology (Motorola, U.S. Pat. Nos. 6,248,229, 6,221,583, 6,013,170, and 6,063,573, herein incorporated by reference in their entireties); cycling probe technology (e.g., U.S. Pat. Nos. 5,403,711, 5,011,769, and 5,660,988, herein incorporated by reference in their entireties); Dade Behring signal amplification methods (e.g., U.S. Pat. Nos. 6,121,001, 6,110,677, 5,914,230, 5,882,867, and 5,792,614, herein incorporated by reference in their entireties); ligase chain reaction (Barnay Proc. Natl. Acad. Sci USA 88, 189-93 (1991)); and sandwich hybridization methods (e.g., U.S. Pat. No. 5,288,609, herein incorporated by reference in its entirety).

6. Mass Spectroscopy Assay

In some embodiments, a MassARRAY system (Sequenom, San Diego, CA.) is used to detect variant sequences (*See e.g.*, U.S. Patent Nos. 6,043,031; 5,777,324; and 5,605,798; each of which is herein incorporated by reference). DNA is isolated from blood samples using standard procedures. Next, specific DNA regions containing the mutation or SNP of interest, about 200 base pairs in length, are amplified by PCR. The amplified fragments are then attached by one strand to a solid surface and the non-immobilized strands are removed by standard denaturation and washing. The remaining immobilized single strand then serves as a template for automated enzymatic reactions that produce genotype specific diagnostic products.

Very small quantities of the enzymatic products, typically five to ten nanoliters, are then transferred to a SpectroCHIP array for subsequent automated analysis with the SpectroREADER mass spectrometer. Each spot is preloaded with light absorbing crystals that form a matrix with the dispensed diagnostic product. The MassARRAY system uses MALDI-TOF (Matrix Assisted Laser Desorption Ionization - Time of Flight) mass spectrometry. In a process known as desorption, the matrix is hit with a pulse from

a laser beam. Energy from the laser beam is transferred to the matrix and it is vaporized resulting in a small amount of the diagnostic product being expelled into a flight tube. As the diagnostic product is charged when an electrical field pulse is subsequently applied to the tube they are launched down the flight tube towards a detector. The time between
5 application of the electrical field pulse and collision of the diagnostic product with the detector is referred to as the time of flight. This is a very precise measure of the product's molecular weight, as a molecule's mass correlates directly with time of flight with smaller molecules flying faster than larger molecules. The entire assay is completed in less than one thousandth of a second, enabling samples to be analyzed in a total of 3-5 second
10 including repetitive data collection. The SpectroTYPER software then calculates, records, compares and reports the genotypes at the rate of three seconds per sample.

In some embodiments, the present invention provides an oligonucleotide comprising a DME related sequence, or a complement of a DME-related sequence. In preferred embodiments, an oligonucleotide of the present invention comprises a sequence
15 or a complement of a sequence selected from the group consisting SEQ ID NOs. 1-3360 and 3361-7669, or a substantially similar sequence.

In some embodiments, an oligonucleotide probe or oligonucleotide primer is created so the 5' terminus, 3' terminus or central base contains the genetic polymorphism site. In some preferred embodiments, an oligonucleotide is created comprising at least 13
20 contiguous bases of a sequence selected from SEQ ID NOs 1 through 3360 and 3361-7669, or the complement thereto, and further comprising the 21st nucleotide of the sequence selected from SEQ ID NOs 1 through 3360 and 3361-7669, or the complement thereto.

In some embodiments, an oligonucleotide of the present invention flanks or is
25 adjacent to a polymorphic site, such that the presence of the polymorphism can be detected by modification of the oligonucleotide in a manner dependent on the presence or absence of the polymorphism.

In some embodiments, the present invention provides kits comprising one or more of the components necessary for practicing the present invention. For example, the
30 present invention provides kits for storing or delivering the enzymes of the present

invention and/or the reaction components necessary to practice a cleavage assay (e.g., the INVADER assay). The kit may include any and all components necessary or desired for the enzymes or assays including, but not limited to, the reagents themselves, buffers, control reagents (e.g., tissue samples, positive and negative control target oligonucleotides, etc.), solid supports, labels, written and/or pictorial instructions and product information, inhibitors, labeling and/or detection reagents, package environmental controls (e.g., ice, desiccants, etc.), and the like. In some embodiments, the kits provide a sub-set of the required components, wherein it is expected that the user will supply the remaining components. In some embodiments, the kits comprise two or more separate containers wherein each container houses a subset of the components to be delivered. For example, a first container (e.g., box) may contain an enzyme (e.g., structure specific cleavage enzyme in a suitable storage buffer and container), while a second box may contain oligonucleotides (e.g., INVADER oligonucleotides, probe oligonucleotides, control target oligonucleotides, etc.). In some embodiments one or more the reaction components may be provided in a predispensed format (*i.e.*, pre-measured for use in a step of the procedure without re-measurement or re-dispensing). In some embodiments, selected reaction components are mixed and predispensed together. In preferred embodiments, predispensed reaction components are predispensed and are provided in a reaction vessel (including but not limited to a reaction tube or a well, as in, *e.g.*, a microtiter plate). In particularly preferred embodiments, predispensed reaction components are dried down (*e.g.*, desiccated or lyophilized) in a reaction vessel.

Examples of genetic polymorphism data (especially the SNP data) that can be used in the method of the present invention are shown in Table 1.

In Table 1, the name of the gene encoding the drug metabolizing enzyme is recorded in the gene name column. The base in capital letters is the SNP data in the sequence column. Two bases separated by a forward slash indicate the SNP of homo and hetero bases. For example, A/G indicates a homo allele A/A and G/G as well as a hetero allele A/G. The sequences in this table have 20 bases before and after the SNP. Here, the base in parentheses, for example the 26th (T) in ABCB4, indicates a polymorphism with an inserted base, and D, such as the 10th spot in NAT2, indicates a polymorphism

with a deleted base. In Sequence No. 674, n is VNTR and (cctgy)x, where x is an integer between 1 and 50, indicates a repeated sequence. The bases with numbers in parentheses indicate the number of times they are repeated. For example, "(T) 9-12" in Sequence No. 1552 (ABCB11 No. 55 in Table 1) indicates T is repeated 9 to 12 times.

5 Here, "position" indicates the position of the SNP genome. The position of SNPs in the 5' flanking region, intron region and 3' flanking region are intron base sequences counted as a single number starting at the exon-intron junction. The position of SNPs in the exon region are exon base sequences counted as a single number starting at the exon-intron junction. Also, (+) or no symbol indicates a number counted in the 3' upstream
10 direction and (-) indicates a number counted in the 5' downstream direction. The number in the "number" column indicates the position of the SNP in the gene maps of the various genes (FIG 9 through FIG 141 and FIG 144 through 312).

The sequence represented by the SEQ ID Nos. 1-3360 and 3361-7669 can readily be associated with the corresponding gene, chromosome, and chromosomal position.

15 Each of the genes shown in Table 1 correlates to a corresponding Figure in the present application. The Figures show a map of the gene with positional identifiers for each of the polymorphisms. The Figures also provide an accession number that correlates to public genome databases, allowing the genetic context of the polymorphism and the gene to be understood. Using the information in Table 1, the Figures, and public genome
20 databases, one skilled in the art is able to identify flanking sequences. This allows, for example, the development of PCR primers that flank the polymorphism. Considerations for PCR primer design are known in the art for both single PCR reactions and multiplex reactions (See e.g., Henegariu et al., BioTechniques 23:504-511 [1997] and PCR Applications, edited by Innis, Gelfand, and Sninsky, Academic Press, San Diego, CA
25 1999), each of which is herein incorporated by references in its entirety). Examples of primers that find use in the amplification of sequences containing polymorphisms, as well as amplification conditions, are found at the IMS-JST JSNP database website (See, submissions from Laboratory for Genotyping, The SNP Research Center, The Institute of Physical and Chemical Research (RIKEN)).

One example of information generated using SEQ ID Nos. 1-3360 and 3361-7669 and information in publicly available databases is provided in Figure 143. The first column in this figure shows that 3360 entries are made, corresponding to the first 3360 entries found in Table 1. The second column, entitled "GENE" provides a gene name abbreviation, while the next column provides a long gene name. The next columns show the chromosome (CHROM), a reference mRNA accession number (REF. MRNA), a locus link database accession number (L-LINK), an OMIM database accession number (OMIM_ID) which allows disease association information to be readily obtained, the exon count for the gene (EXONS), and the number of polymorphisms in the gene (NO GENE).

Creating an Oligonucleotide Probe or Oligonucleotide Primer

In some embodiments, an oligonucleotide used as a primer and/or probe in the detection method of the present invention serves as the template of the base sequences (Sequence No. 1 through 3360 and 3361 through 7669) shown in Table 1 if, for example, a SNP is to be detected. The primer/probe can be designed so it is synthesized as the base sequence itself or as a portion of the base sequence. In preferred embodiments, the SNP is included in the base sequence of the primer/probe (and denoted in capital letters in the base sequence column of Table 1). The primers/probes may also be complementary to the non-mutant sequence.

The SNP in the following example is designed so it is on the 3' or 5' end of the base sequence. It is designed to be within four bases of the 3' or 5' end, and ideally within two bases of the end. The SNP can also be in the center of the oligonucleotide base sequence. Here, "center" means the number of the bases from the SNP base to the 5' end is substantially equal to the number of bases from the SNP base to the 3' end. If there is an odd number of bases in the oligonucleotide, the central region should be essentially five bases in length, preferably three bases in length, and ideally one base in length. In a base sequence with 41 bases, for example, the central region should be bases 19 through 23, preferably bases 20 through 22, and ideally base 21. If there is an even number of bases, the central region should be four bases and ideally two bases. In a base sequence

of 40 bases, for example, the central region should be bases 19 through 22 and ideally base 20.

If the polymorphism consists of a plurality of bases, in some embodiments, the probe/primer is designed so the full polymorphism sequence is contained in the probe/primer. In some preferred embodiments, it is designed so one of the bases 1 through 4 on the 5' end or 3' end complementing the primer DNA corresponds to the base at the very end of the polymorphism bases. (This is called the "corresponding base"; ideally, it is the base at the 5' or 3' end). For example, in the INVADER assay, if a probe and INVADER oligonucleotide are prepared to detect a genetic polymorphism (CAGAGGCT) in No. 12 of NDUFA7 in Table 1 (Sequence No. 828), the position of the corresponding base in the probe in FIG 4a (a "T" base in the figure) is designed to become "C" at the far left of sequence CAGAGGCT, and the N base in the INVADER oligonucleotide shown in FIG 4b is designed to replace the "C" at the far left of CAGAGGCT with A, T, C or G). Conversely, if designed so the position of the corresponding base in the INVADER oligonucleotide is the far right "T" in CAGAGGCT, the "N" base is such that the corresponding base in the probe is "T." Further, the corresponding base of the INVADER oligonucleotide and the allele probe can be set anywhere in the CAGAGGCT sequence.

In preferred embodiments, the length of the base sequence is at least 13 bases, preferably between 13 and 60 bases, more preferably between 15 and 40 bases, and ideally between 18 and 30 bases. These oligonucleotide base sequences can be used as probes, as forward (sense) primers or as reverse (anti-sense) primers to detect target genes.

These oligonucleotides can link regions hybridized with genome DNA in tandem to unhybridized regions. The linking order can be upstream or downstream. The hybridized regions in these oligonucleotides can be designed from base sequence data containing the SNP described in Table 1, and created so the sequence containing the region hybridized with genome DNA closest to the 5' or 3' end is the SNP. These oligonucleotides can be used as probes to detect SNP using the INVADER assay.

The primer used in some embodiments of the present invention is designed to determine the functional change caused by the SNPs in the base sequences in Table 1, to determine whether the change is effective or ineffective, and to determine the existence of side effects. It is designed to include the SNP in the PCR-amplified base sequence. In some preferred embodiments, the primer should have at least 15 base sequences, preferably between 15 and 30 base sequences, and ideally between 18 and 24 base sequences. The template DNA regions in the primer base sequence should contain 500 bp or less amplified fragments, preferably between 100 and 300 bp fragments, and ideally between 100 and 150 bp fragments.

The oligonucleotide probes and primers designed in this manner can be synthesized chemically using any method commonly known in the art. For example, the oligonucleotides can be synthesized using a commercially available chemical synthesis device. The production of probes can be conducted automatically by adding fluorescent tags (e.g., FAM, VIC, Cy3) or other labels.

These oligonucleotides can be included in genetic polymorphism detection kits along with polymerase (e.g., Taq polymerase), a buffering solution (e.g., a Tris buffering solution), dNTP, fluorescent dyes (e.g., VIC, FAM), or other desired kit components.

Detection

In some embodiments, the oligonucleotides prepared in the examples above are used as primers/probes, and the genes or a portion thereof (template DNA) encoding the drug metabolizing enzyme is amplified using DNA polymerase. A primer/probe prepared in this manner can be hybridized with template DNA and used to detect DNA with the target genetic polymorphism. The DNA used as the template can be prepared using any method commonly known in the art. Examples include cesium chloride density gradient ultra centrifugation method, the SDS solvency method or the phenol chloroform extraction method.

1 Detection Using PCR

The amplification can be performed using a polymerase chain reaction (PCR). The DNA polymerase can be LA Taq DNA polymerase (Takara), Ex Taq polymerase (Takara), AMPLITAQ Gold polymerase (Applied Biosystems), AMPLITAQ (Applied Biosystems) or Pfu DNA polymerase (Stratagene), as well as other polymerases.

An illustrative example of amplification conditions is provided below. The present invention is not limited to the conditions provided in this example. In preferred embodiments, each cycle in the transforming phase should last between 10 and 40 seconds at 85°C to 105°C and preferably 20 and 30 seconds at 94°C, each cycle in the annealing phase should last 30 seconds to 1 minute at 50°C to 72°C and preferably 20 seconds to 1 minute at 60°C, and each cycle in the elongation phase should last 1 minute to 4 minutes between 65°C and 75°C and preferably 2 minutes to 3 minutes at 72°C. There should be 30 to 40 cycles, although fewer or more cycles are contemplated. In order to completely transform the template DNA and the primer, each cycle in the transforming phase should last 1 minute to 5 minutes at 95°C before the amplifying cycle. If AMPLITAQ GOLD polymerase manufactured by Applied Biosystems is used, it should last from 8 minutes to 15 minutes and ideally from 10 minutes to 12 minutes. In order to completely elongate the amplified DNA, the elongation phase should last between 1 minute and 10 minutes at 72°C after the amplification cycle. If the amplified product is not immediately detected, it should be processed again at 4°C to make sure the amplification was not irregular. In this way, the gene encoding the drug metabolizing enzyme is amplified.

After amplification, gel electrophoresis is performed on the amplified product, the amplified product is stained using ethidium bromide or SYBR Green, and one, two or three bands are detected in the amplified product (DNA fragments) to determine the portion (DNA fragment) of the drug metabolizing enzyme containing the genetic polymorphism in the gene encoding the drug metabolizing enzyme. Polyacrylamide gel electrophoresis or capillary electrophoresis can be performed instead of aerogel electrophoresis. PCR can be performed using a primer tagged with a fluorescent dye to detect the amplified product. A detection method that does not require electrophoresis

can also be used, such as bonding the amplified product in solid phase to a microplate and detecting the amplified product using a fluorescent or enzymatic reaction.

2. Detection Using the TAQMAN PCR Method

5 In the TAQMAN PCR method, the PCR reaction is performed using a fluorescent dye-tagged allele-specific oligo and Taq DNA polymerase. The allele-specific oligo used in the TAQMAN PCR method (TAQMAN probe) can be designed based on the SNP data. The 5' end of the TAQMAN probe is tagged using a fluorescent reporter dye R such as FAM or VIC, and the 3' end is tagged using a quencher Q (light-quenching
10 substance). (See FIG 1.). Here, the fluorescent light energy absorbed by the quencher is not detected. Because the 3' end of the TAQMAN probe is phosphorylated, there is no elongation reaction from the TAQMAN probe in the PCR reaction (FIG 1). However, a PCR reaction is performed on the TAQMAN probe with TaqDNA polymerase and a primer designed to amplify the region containing the SNP. The following reaction
15 occurs.

First, the TAQMAN probe is hybridized in a specific sequence of template DNA (FIG 2a) and an elongation reaction is simultaneously performed from the PCR primer (FIG 2b). Because the Taq DNA polymerase has 5' nuclease activity, the hybridized TAQMAN probe is severed as the PCR primer elongation reaction continues. When the
20 TAQMAN probe is severed, the quencher has no effect on the fluorescent dye, and the fluorescent light is detected (FIG 2c).

For example, suppose there is an A allele (Allele 1) and a G allele (Allele 2) at the SNP position as shown in FIG 3. Allele 1 is tagged by a specific TAQMAN probe with FAM and Allele 2 is tagged by a specific TAQMAN probe with VIC (see FIG 3). Two
25 different allele-specific oligos are added to the PCR drug, and TAQMAN PCR is performed on the detected template. The fluorescence detector then detects the fluorescent intensity of the FAM and VIC. When the SNP position in the allele and the position corresponding to the SNP in the TAQMAN probe are complementary, the probe is hybridized with the allele, the fluorescent dye in the probe is severed by the Taq

polymerase, the effect of the quencher is eliminated, and the intensity of the fluorescence is detected.

If the template is homozygous for Allele 1, strong FAM fluorescence is detected and hardly any VIC fluorescence is detected. If the template is heterozygous for Allele 1
5 and Allele 2, both FAM and VIC fluorescence are detected.

3. SNP Detection Using the INVADER assay

In the INVADER assay, an allele-specific oligo and the template are hybridized to detect the SNP. In the INVADER assay, two different non-tagged oligos and one
10 fluorescent dye-tagged oligo are used. One of the two non-tagged oligos is known as the probe. In some embodiments, the probe has a region hybridized to the genome DNA (template DNA) and a region (called a flap) that is not hybridized with the genome DNA, and that has a sequence unrelated to the sequence of the genomic DNA. The hybridized region has base sequences corresponding to the SNP (FIG 4a). The flap sequence is
15 complementary to a FRET probe (described below). The other of the two non-tagged oligos is called the INVADER oligonucleotide. This oligonucleotide is designed so that it is hybridized in complementary fashion from the SNP position towards the 3' end of the genome DNA (FIG 4b). In some preferred embodiments, the sequence corresponding to the SNP position can be any base (denoted by N in FIG 4b). When the template DNA
20 genome is hybridized with the two probes, the base (N) from the INVADER oligonucleotide is inserted in the SNP position (FIG 4c) forming a cleavage structure at the SNP position.

In some embodiments, the fluorescent dye-tagged oligonucleotide is a sequence completely unrelated to the alleles. This probe is a FRET (fluorescence resonance energy
25 transfer) probe (FIG 5). The fluorescent dye R tags the base (reporter) at the 5' end of the FRET probe. A quencher Q absorbs the fluorescence. Here, the quencher absorbs the fluorescent light and the light is not detected. A specific region (Region 1) is designed on the 5' end of the FRET probe (reporter base) to face the 3' end from Region 1 (This region is Region 2). As a result, Region 1 and Region 2 form a complementary duplex

(FIG 5). The 3'-region from the regions forming the complementary duplex can be hybridized with the flap of the allele probe to form a complementary chain (FIG 5).

In the INVADER assay, a cleavage agent (e.g., CLEAVASE enzyme, Third Wave Technologies, Madison, WI) is used, which is an enzyme (5' nuclease) with specific
5 endonuclease activity for identifying and cleaving a specific DNA structure. When the genome DNA, the probe and the INVADER oligonucleotide form a cleavage structure at the SNP position, the cleavage agent severs 3' of the SNP position on the allele probe. The section with three bases forming a flap with the 5' end is identified as shown in FIG 4c, and the flap is severed. The structure with the SNP position is identified by the
10 cleavage agent (FIG 6a), the probe is severed at the flap position, and the flap is separated (FIG 6b). Next, the released flap from the probe bonds with the FRET probe in complementary fashion to form a duplex (FIG 6c). The cleavage agent identifies this structure and cleaves the section with the fluorescent dye. The cleaved fluorescent dye is no longer affected by the quencher and fluorescent light becomes detectable (FIG 6d). If
15 the SNP position does not match the sequence corresponding to the SNP in the allele probe as shown in FIG 7, the specific DNA structure is not identified by the cleavage agent, the probe is not severed, and fluorescent light is not detected.

When the SNP is T/C, for example, a T INVADER oligonucleotide, a T probe, a FRET probe with FAM bonded to the reporter for the T SNP, a C INVADER
20 oligonucleotide, a C probe and a FRET probe with VIC bonded to the reporter for the C SNP are prepared. These are combined and SNP detection is performed. If there is a T/T homo, FAM fluorescence is generated. If there is a C/C homo, VIC fluorescence is detected. If there is a T/C hetero, both FAM and VIC fluorescence are detected. Because the FAM and VIC fluorescence wavelengths are different, both can be readily identified.

Detection Using the SniPer Method

In order to detect SNP using the SniPer method, an allele identifier is amplified using RCA. The genome DNA template is a straight chain, and a probe is hybridized with the genome DNA. When there is a complementary match between the probe
30 sequence and the genome DNA template sequence and a complementary chain forms, a

ligation reaction on the genome DNA forms a ring. As a result, RCA continues on cyclic DNA. If the end of the probe does not match the genome DNA, the RCA reaction does not occur because there is no ligation and no ring. In the SniPer method, therefore, a single chain probe is designed to anneal the genome DNA and create a ring. This single chain probe is called a padlock probe. The severed end of the padlock probe is the sequence corresponding to the target SNP. The padlock probe and the genome DNA mix and a ligation reaction occurs. If the severed end of the padlock probe and the SNP section of the genome DNA are complementary, the severed end of the padlock probe connects and forms a ring during the ligation reaction. If they are not complementary, a ring does not form. Therefore, only a padlock probe corresponding to the target SNP forms a ring and is amplified by the DNA polymerase. The presence of amplification is used to detect the SNP. A synthetic oligonucleotide with a hairpin structure and a fluorescent dye and quencher on both ends can be used in the detection process.

Detection Using the MALDI-TOF/MS Method

In the matrix assisted laser desorption-time of flight/mass spectroscopy (MALDI-TOF/MS) method, SNP typing is performed using a mass spectrometer. A preferred embodiment of this method has the following steps.

(i) PCR Amplification and Refinement of DNA Fragments Containing SNP

After making sure the base at the SNP location and the PCR primer do not overlap, the DNA fragment is amplified, exonuclease or alkali phosphatase processing is performed on the amplified product, the dNTP is removed, and the amplified fragment is refined.

(ii) Primer Extension Reaction (Thermal Cycle) and Refinement

A primer ten or more times the template in the region identified as the PCR product is added, a thermal cycle reaction is performed, and a primer elongation reaction is performed. The primer used here is designed so the 3' end is next to the base corresponding to the SNP position. The primer length should be 15 to 30 bases, ideally 20 to 25 bases. If there is a multiplex reaction, a sequence that is not complementary to

the template is added to the 5' end. There should be 20 to 30 (ideally 25) thermal cycles at two different temperatures. These should be 85 to 105°C (ideally 94°C) and 35 to 40°C (ideally 37°C).

The reaction product is then refined using a refining kit so it can be used in the mass spectrometer.

(iii) Mass Spectroscopy Using a Mass Spectrometer

The elongated and refined reaction product is applied to the mass spectrometer, and a quality of the target product is measured. In other words, the refined product is mixed with the matrix and 0.5 to 1.0 mL spots are formed on the MALDI plate. After drying the plate, the substance is irradiated by a laser beam and a spectrogram is produced.

Detection Using the Base Sequence Determining Method

In the present invention, a polymorphism can be detected using an elongation reaction on a single base. In other words, four different types of dideoxynucleotides identified by different fluorescent compounds are added to reaction systems including the gene to be detected and a single base elongation reaction is performed. Here, the base to be elongated is the polymorphism. Two reactions are performed; one to stop the DNA synthesis and another to identify the 3' end of the DNA molecule with fluorescence.

Electrophoresis is performed on four different reaction solutions with the same lanes and capillaries for the sequencing gel. The sequence is determined by detecting the differences in the fluorescent dyes identifying the DNA bands using a fluorescence detector. The oligonucleotides with one base elongated have the elongation confirmed using different types of fluorescent dyes in a fluorescence detector and mass spectrometer. Instead of fluorescent-tagged dideoxynucleotides, the primer can be identified using fluorescence used with non-tagged dideoxynucleotides.

Drug Evaluation

Using information obtained by the methods of the present invention, the efficacy and stability of the drug metabolized by the drug metabolizing enzyme can be evaluated.

For example, in some embodiments, the drug can be evaluated using a typing system. In other words, the frequency of expressed and unexpressed alleles (e.g., toxic alleles that cause undesired side effects) can be compared using any one of the detection methods mentioned above. Once they have been compared, markers can be selected to indicate, for example, a toxic expression where the allele frequency differs. In statistical analysis, this is usually set as x^2 . However, this is different in other methods such as the Fisher method. The active components (altered and metabolized drug components) in the drug will be reflected in blood and tissue concentrations. All of the genetic polymorphisms can be checked against the causes of the toxic effects to isolate specific correlating genetic polymorphisms. The substances corresponding to the probes or primers used to analyze all of the genetic polymorphisms are prepared beforehand on reaction plates, cards or glass plates, and unprepared human genome DNA is added and reacted to determine the allele pattern. If there are genetic polymorphisms correlating with toxicity or other phenotypes, then human side-effects can be expected or predicted. The same is true of drug effectiveness. Because the genetic polymorphisms correlating to effectiveness and side-effects differ depending on the drug, typing performed using genetic polymorphisms can be performed to anticipate effectiveness and side-effects.

Differences in allele frequency can be determined in certain instances by comparing the frequency of genetic polymorphisms to effectiveness/ineffectiveness or the presence/absence of side-effects. If, for example, an SNP analysis is performed on persons with a toxic reaction (side-effect) to Drug A, the results may show a 90% of the people have T/T (e.g., detected based on the intensity of fluorescent FAM light). The same results may show 10% of people with no toxic reaction have a T/T and 90% have a C/C. As a result of the SNP analysis, the evaluation may be not to administer Drug A to persons with T/T.

Drug Screening

In the present invention, the genetic polymorphism data obtained as described above is compared to genetic polymorphism data from genes encoding certain drug metabolizing enzymes to indicate the safety and effectiveness of drugs metabolized by

these drug metabolizing enzymes. Therefore, the genetic polymorphism data obtained using the method of the present invention can be used to determine the likely effectiveness of certain drug therapies and to select the appropriate drug.

The evaluation methods described above can be used. Genetic polymorphisms with correlations to side-effects and effectiveness are said to be influenced by the activation, transfer and translation of certain enzymes. The cause and effect relationship with the side-effect or effectiveness expression mechanism may be indirect. The metabolization of drugs is being studied by pharmaceutical companies in laboratory and clinical testing. If there are genetic polymorphisms in enzyme genes correlating with severe side-effects, they can be removed and used under different conditions. The same is true of effectiveness. Drugs can be screened, therefore, using side-effects and effectiveness data. A wide variety of conditions and diseases (See e.g., Physician's Desk Reference) benefit from analysis using the systems and methods of the present invention.

In some embodiments of the present invention, a sample is taken from a subject (e.g., by a drug company) and sent to a laboratory for analysis using a detection assay. The laboratory results (e.g., detection assay test result data) is returned to the party providing the sample such that an appropriate decision can be made, including, but not limited to, development or administration of a drug to a subject.

In clinical testing (Tests I through III), the frequency of the expression of genetic polymorphisms can be studied in volunteers exhibiting certain side-effects and volunteers not exhibiting the same side-effects to a drug. In this way, novel genetic polymorphisms correlating with side-effects and effectiveness can be detected. This information can be used to screen drugs. Exemplary drugs and drug-related data and other information that find use in or with the present invention, including but are not limited to the methods and databases described herein, are described in the PHYSICIANS' DESK REFERENCE (PDR). (e.g., 2002 Edition, Medical Economics Company, Inc., Montvale, NJ). The PDR is expressly incorporated by reference herein as if fully set forth.

EXPERIMENTAL EXAMPLES

The following examples are provided in order to demonstrate and further illustrate certain preferred embodiments and aspects of the present invention and are not to be construed as limiting the scope thereof.

5

Example 1 Obtaining SNP Data

(1) DNA Extraction

10 Blood was extracted from 48 unrelated people in the presence of EDTA. The DNA was extracted in the following way based on the method in the Genome Analysis Manual (Yusuke Nakamura ed., Springer-Verlag Tokyo).

Ten milliliters of blood was transferred to a 50 ml test tube and centrifuged for five minutes at room temperature and 3000 rpm. After the supernatant (blood serum) had
15 been removed using a pipette, 30 ml of RBC-dissolving buffer (10 mM NH_4HCO_3 , 144 mM NH_3Cl) was added. After mixing until there was no sediment, it was allowed to stand for 20 minutes at room temperature. After being centrifuged for five minutes at room temperature and 3000 rpm, the supernatant (blood serum) was again removed using a pipette to obtain white blood cells. Another 30 ml of RBC-dissolving buffer was added and the process was repeated twice. Then, 4 ml of proteinase K buffer [50 mM Tris-HCl (pH 7.4), 100 mM NaCl, 1 mM EDTA (pH 8.0)] was added to the white blood cells, 200 ml of SDS was added, 200 ml of 10 mg/ml proteinase K was added, and the solution was
20 tumble-mixed. The solution was then allowed to stand overnight at 37°C. The next day, 4 ml of phenol was added, and the solution was slowly tumble-mixed for four hours using a Taitec T-50 Rotator. After being centrifuged for 10 minutes at room temperature and 3000 rpm, the supernatant was removed using a new tube. Then, 4 ml of phenol-chloroform-isoamylalcohol (volume ratio 25:24:1) was added, the solution was tumble-mixed for two hours in the manner described above, and the solution was centrifuged. The supernatant was removed using a new tube, 4 ml of chloroform-isoamylalcohol
25 (volume ratio 24:1) was added, and the solution was tumble-mixed. Fibrous white
30

precipitate (DNA) was removed using a 2 ml tube, 1 ml of 70% ethanol was added, and the solution was tumble-mixed. The DNA was transferred to a new tube, dried and dissolved in 500 µl of TE solution [10 mM Tris-HCl (pH 4.7), 1 mM EDTA (pH 7.4)] to obtain a genome DNA sample.

(2) PCR

A genome sequence was obtained from the GenBank DNA Database. After removing the repeating sequences using the RepMask computer program, the PCR primer was set so there would be approximately 1 kb of PCR product. The genome DNA from 48 unrelated people was prepared at the same concentration. After mixing the same amount of DNA from three people in a single tube, 60 ng was used in the PCR. The PCR was Ex-Taq (Takara 2.5 U) and performed using the GeneAmp PCR System 9700 (PE Applied Biosystems). After reacting for two hours at 94°C, denaturing was performed for 30 seconds at 96°C, annealing was performed for 30 seconds at 55°C or 60°C, and elongation was performed for one minute at 72°C in each cycle. There were 35 cycles.

(3) Sequence

After refining the PCR product using ArrayIt (Telechem), the sequence reaction was performed using the BigDye Terminator RR Mix (PE Applied Biosystems). After reacting for two hours at 96°C, denaturing was performed for 20 seconds at 96°C, annealing was performed for 30 seconds at 50°C, and elongation was performed for 4 minutes at 60°C in each cycle using the GeneAmp PCR System 9700 (PE Applied Biosystems). There were 25 cycles. After the sequencing reaction, the sequencing was analyzed using the ABI Prism 3700 DNA Analyzer.

(4) SNP Detection

An analysis was performed on the SNP detection using the PolyPhred computer program (Nickerson et al., 1997, Nucleic Acid Res., 25, 2745-2751).

(5) Results

The SNP results shown in Table 1 were obtained. The analyzed drug metabolizing enzyme, the abbreviation of the enzyme, the databank (GenBank) accession number, the structure of the gene for the drug metabolizing enzyme, and the position of the SNPs are shown in FIG 9 through FIG 141 and FIG 144 through 312. In FIG 9

through FIG 141 and FIG 144 through 312, the exons are blank boxes or black lines in the genes denoted by the horizontal lines. The position of the SNPs is denoted above the genes with solid lines and numbers.

5

Example 2

Typing

Typing was performed on two different groups of patients using the INVADER assay. In FIG 142, the x-axis (Allele 1) indicates the intensity of the FAM fluorescent light corresponding to T, and the x-axis (Allele 2) indicates the intensity of the VIC fluorescent light corresponding to C. The slanted line indicates the SNP pattern for T/T, the black circles denote the pattern for C/C, and the white circles denote the pattern for T/C. The black squares indicate the background values. The x marks indicate where the detection failed. The group of patients in the graph for panel A (top) had many C/C SNP patterns and the group of patients in the graph for panel B (bottom) had many T/T SNP patterns.

15

Example 3

SNP Detection

20

Genome DNA was extracted from five unrelated people using the method described in Example 1, and the SNPs in three different drug metabolizing enzyme genes (EPHX1, ABCB2, AANAT) were detected using the INVADER assay method. The INVADER oligonucleotides and probes were designed using base sequence No. 3 (Sequence No. 49) and No. 17 (Sequence No. 63) in the case of EPHX1, base sequence No. 4 (Sequence No. 4) and No. 11 (Sequence No. 11) in the case of ABCB2, and base sequence No. 3 (Sequence No. 561) in the case of AANAT. The positions of the SNPs are shown in Table 1.

25

30 The results are shown in Table 2.

Table 2

Drug Metabolizing Enzyme Gene	EPHX1		ABCB2		AANAT
	No. 3	No. 17	No. 4	No. 11	No. 3
	Seq. No. 49	Seq. No. 63	Seq. No. 4	Seq. No. 11	Seq. No. 561
SNP	(T/G)	(A/G)	(G/T)	(G/A)	(T/A)
Subject I	T/T	A/G	T/T	G/A	T/T
Subject II	T/T	A/A	G/G	G/G	T/A
Subject III	T/G	A/A	G/G	A/A	T/T
Subject IV	G/G	A/G	G/T	G/G	T/T
Subject V	T/G	A/G	G/T	G/A	T/A

As shown in Table 2, the SNPs in the drug metabolizing genes of patients can be detected and the patterns determined using the method of the present invention.

Example 4

Correlation between SNP genotypes and optimal amounts of a medicament for treatment validity and safety

In this example, validity and safety of medicaments were investigated using SNP analysis.

Thiopurine S-methyltransferase (TPMT) is an enzyme that transfers a methyl group to a sulfur atom attached to a purine ring, and is one of the major enzymes for metabolizing drugs such as the anti-cancer agents 6-mercaptopurine and 6-thioguanine, and thiopurine derivatives such as the immunosuppressive agent azathioprine. This example shows a correlation between optimal amounts of azathioprine and various combinations of the alleles at the 868th SNP of intron 3 of TPMT (Seki, *et al.*, J Hum Genet 45(5):299 [2000], incorporated by reference herein in its entirety; Accession No. AB045146.1) (G or T alleles) and the 2682nd SNP of intron 3 (C or A alleles)(Table 3 and Table 4).

Table 3

868	2682	High	Low
TT	AA	2	0
TT	AT	3	0
TT	TT	1	0
GT	AA	0	2
GT	AT	1	7
GT	TT	4	1
GG	AA	1	0
GG	AT	0	1
GG	TT	1	0

Optimal amounts of azathioprine were determined by adopting suppression of rejection after renal transplantation as an index. A group of patients in which the validity of treatment with 100 mg/day of azathioprine was confirmed was designated as a high dose group, and a group of patients in which side effects developed with treatment of 100 mg/day, but in which validity was confirmed with a treatment of 50 mg/day was designated as a low dose group. Table 3 indicates the number of patients having each combination of alleles, with the columns labeled “High” and “Low” representing the numbers of patients of each genotype in the high dose and the low dose groups, respectively. Side effects include leukopenia, anthema, angiitis, nausea/vomiting, anorexia, diarrhea, malaise, myalgia, arthralgia, fever, chill, and dizziness. More serious side effects include, for example, blood disorders, shock-like symptoms, infectious diseases, and hepatic disorders, and renal disorders.

Investigation of a correlation between the high dose and low dose groups and the two types of SNPs indicated above revealed that when G is present in at least one allele at the 868th SNP of intron 3 (G/G homozygous or G/T heterozygous) and A is present in at least one allele at the 2682nd SNP of intron 3 (A/A homozygous or A/T heterozygous),

side effects were developed with 100 mg/day and 50 mg/day was an optimal amount for 10 out of 12 patients (low dose group), while 100 mg/day was an optimal amount for 11 out of 12 patients with other allele combinations (high dose group) (Table 4).

Investigation of this combination of two SNP loci in patients enables prediction of

- 5 optimal amounts of azathioprine for treatment prior to the administration of the drug, for improved validity and safety. These results indicate that the validity and safety of medicaments can be predicted using analysis of SNPs associated with medicament metabolic enzymes, *e.g.*, as described in this specification and including but not limited to the DME-associated SNPs listed in Table 1. As used in this example only, the term
- 10 "optimal amount" refers to the best dosage selected from the tested amounts of 50 mg/day or 100/mg per day. It will be appreciated by those skilled in the art that a study testing additional amounts of a medicament (*e.g.*, a study in which amounts are varied in smaller increments, such as 40, 50, 60, 70, 80, 90, etc. mg/day) would provide additional information regarding ranges of amounts giving optimal performance for patients having
- 15 a particular genotype, and that optimal amounts of this or any other medicament are not limited to the particular amounts of 50 or 100 mg/day tested in this example.

Table 4

Genotype	Optimal amount	
	100 mg/day	50 mg/day
G as the 868 th SNP and A as the 2682 nd	2	10
Other combinations	11	1

(Fisher exact test: p=0.0003)

Sequence Listing Free Text

- SEQ ID NO:39: n indicates t (Position 21).
- 5 SEQ ID NO:64: n indicates c (Position 21).
- SEQ ID NO:580: n indicates a or deletion (Position 21).
- SEQ ID NO:634: n indicates a or deletion (Position 21).
- SEQ ID NO:656: n indicates a or deletion (Position 21).
- SEQ ID NO:658: n indicates c or deletion (Position 21).
- 10 SEQ ID NO:671: n indicates a or deletion (Position 21).
- SEQ ID NO:672: n indicates g or deletion (Position 21).
- SEQ ID NO:673: n indicates c or deletion (Position 21).
- SEQ ID NO:674: n indicates (cctgy)x or deletion (Position 21).
- SEQ ID NO:676: n indicates gaa or deletion (Position 21).
- 15 SEQ ID NO:677: n indicates ag or deletion (Position 21).
- SEQ ID NO:785: n indicates ta. (Position 21).
- SEQ ID NO:797: n indicates acac. (Position 21).
- SEQ ID NO:806: n indicates gatttggtatccag. (Position 21).
- SEQ ID NO:808: n indicates ag or deletion (Position 21).
- 20 SEQ ID NO:809: n indicates ta or deletion (Position 21).
- SEQ ID NO:815: n indicates t (Position 21).
- SEQ ID NO:828: n indicates cagagct (Position 21).
- SEQ ID NO:830: n indicates ca or deletion (Position 21).
- SEQ ID NO:831: n indicates ag or deletion (Position 21).
- 25 SEQ ID NO:843: n indicates gtaaa (Position 21).
- SEQ ID NO:845: n indicates a (Position 21).
- SEQ ID NO:888: n indicates tc (Position 21).
- SEQ ID NO:890: n indicates t or deletion (Position 21).
- SEQ ID NO:913: n indicates t or deletion (Position 21).
- 30 SEQ ID NO:932: n indicates t or deletion (Position 21).

- SEQ ID NO:933: n indicates t or deletion (Position 21).
 SEQ ID NO:955: n indicates at or deletion (Position 21).
 SEQ ID NO:956: n indicates a or deletion (Position 21).
 SEQ ID NO:957: n indicates c or deletion (Position 21).
 5 SEQ ID NO:987: n indicates c (Position 21).
 SEQ ID NO:999: n indicates gtt or deletion (Position 21).
 SEQ ID NO:1164: n indicates at (Position 21).
 SEQ ID NO:1166: n indicates c or deletion (Position 21).
 SEQ ID NO:1167: n indicates t or deletion (Position 21).
 10 SEQ ID NO:1168: n indicates t or deletion (Position 21).
 SEQ ID NO:1169: n indicates g (Position 21).
 SEQ ID NO:1171 n indicates c (Position 21).
 SEQ ID NO:1173: n indicates t (Position 21).
 SEQ ID NO:1175: n indicates c or deletion (Position 21).
 15 SEQ ID NO:1200: n indicates a or deletion (Position 21).
 SEQ ID NO:1204: n indicates a (Position 21).
 SEQ ID NO:1207: n indicates tt (Position 21).
 SEQ ID NO:1210: n indicates at (Position 21).
 SEQ ID NO:1245: n indicates t (Position 21).
 20 SEQ ID NO:1248: n indicates t or deletion (Position 21).
 SEQ ID NO:1249: n indicates t (Position 21).
 SEQ ID NO:1251: n indicates a or deletion (Position 21).
 SEQ ID NO:1252: n indicates tgt or deletion (Position 21).
 SEQ ID NO:1260: n indicates t or deletion (Position 21).
 25 SEQ ID NO:1309: n indicates a or deletion (Position 21).
 SEQ ID NO:1389: n indicates g or deletion (Position 21).:
 SEQ ID NO:1411: n indicates a or deletion (Position 21).
 SEQ ID NO:1417: n indicates aaag (Position 21).
 SEQ ID NO:1424: n indicates gtg or deletion (Position 21).
 30 SEQ ID NO:1426: n indicates gg or tgggtgggtgga (Position 21).

SEQ ID NO:1436: n indicates a (Position 21).

SEQ ID NO:1453: n indicates c or deletion (Position 21).

SEQ ID NO:1456: n indicates gg (Position 21).

- 5 SEQ ID NO:1465: n indicates gtc or deletion (Position 21).

SEQ ID NO:1487: n indicates t or deletion (Position 21).

SEQ ID NO:1494: n indicates tt (Position 21).

SEQ ID NO:1497: n indicates t repeated 9 to 12 times (Position 21).

SEQ ID NO:1499: n indicates a or deletion (Position 21).

- 10 SEQ ID NO:1501: n indicates a repeated 10 to 13 times (Position 21).

SEQ ID NO:1504: n indicates ct or deletion (Position 21).

SEQ ID NO:1507: n indicates cagatcttcttcagctaatttagaaatgt (Position 21).

SEQ ID NO:1533: n indicates a or deletion (Position 21).

SEQ ID NO:1540: n indicates c (Position 21).

- 15 SEO ID NO:1545: n indicates t (Position 21).

SEQ ID NO:1552: n indicates t repeated 9 to 12 times (Position 21).

SEQ ID NO:1555: n indicates t (Position 21).

SEQ ID NO:1557: n indicates aaaaaaagaaaa (Position 21).

SEQ ID NO:1558: n indicates aaaaaaaaaaaaaa (Position 21).

- 20 SEQ ID NO:1559: n indicates aaaaaaaaaa (Position 21).

SEQ ID NO:1563: n indicates t or deletion (Position 21).

SEQ ID NO:1572: n indicates c (Position 21).

SEQ ID NO:1574: n indicates a or deletion (Position 21).

SEQ ID NO:1575: n indicates c or deletion (Position 21).

- 25 SEQ ID NO:1596: n indicates cct or deletion (Position 21).

SEQ ID NO:1598: n indicates tc (Position 21).

SEQ ID NO:1616: n indicates ca or deletion (Position 21).

SEQ ID NO:1638: n indicates g (Position 21).

SEQ ID NO:1661: n indicates t or deletion (Position 21).

- 30 SEQ ID NO:1690: n indicates gccag (Position 21).

- SEQ ID NO:1718: n indicates t (Position 21).
- SEQ ID NO:1723: n indicates c or deletion (Position 21).
- SEQ ID NO:1729: n indicates tc or deletion (Position 21).
- SEQ ID NO:1740: n indicates ct or deletion (Position 21).
- 5 SEQ ID NO:1771: n indicates a (Position 21).
- SEQ ID NO:1781: n indicates a or deletion (Position 21).
- SEQ ID NO:1787: n indicates t or deletion (Position 21).
- SEQ ID NO:1791: n indicates t or deletion (Position 21).
- SEQ ID NO:1792: n indicates g or deletion (Position 21).
- 10 SEQ ID NO:1800: n indicates t or deletion (Position 21).
- SEQ ID NO:1801: n indicates t or deletion (Position 21).
- SEQ ID NO:1802: n indicates a or deletion (Position 21).
- SEQ ID NO:1815: n indicates a or deletion (Position 21).
- SEQ ID NO:1819: n indicates ca or deletion (Position 21).
- 15 SEQ ID NO:1820: n indicates t or deletion (Position 21).
- SEQ ID NO:1824: n indicates t or deletion (Position 21).
- SEQ ID NO:1829: n indicates t or deletion (Position 21).
- SEQ ID NO:1830: n indicates c or deletion (Position 21).
- SEQ ID NO:1838: n indicates a or deletion (Position 21).
- 20 SEQ ID NO:1840: n indicates t or deletion (Position 21).
- SEQ ID NO:1847: n indicates gatt or deletion (Position 21).
- SEQ ID NO:1848: n indicates t (Position 21).
- SEQ ID NO:1853: n indicates t or deletion (Position 21).
- SEQ ID NO:1854: n indicates gt (Position 21).
- 25 SEQ ID NO:1857: n indicates a or deletion (Position 21).
- SEQ ID NO:1858: n indicates a or deletion (Position 21).
- SEQ ID NO:1862: n indicates t or deletion (Position 21).
- SEQ ID NO:1865: n indicates at or deletion (Position 21).
- SEQ ID NO:1871: n indicates a or deletion (Position 21).
- 30 SEQ ID NO:1874: n indicates t or deletion (Position 21).

- SEQ ID NO:1877: n indicates at or deletion (Position 21).
SEQ ID NO:1878: n indicates a or deletion (Position 21).
SEQ ID NO:1879: n indicates t repeated 12 to 14 times (Position 21).
SEQ ID NO:1882: n indicates t or deletion (Position 21).
- 5 SEQ ID NO:1884: n indicates cac or deletion (Position 21).
SEQ ID NO:1891: n indicates cca (Position 21).
SEQ ID NO:1919: n indicates t or deletion (Position 21).
SEQ ID NO:1949: n indicates c or deletion (Position 21).
SEQ ID NO:1957: n indicates aaaa or deletion (Position 21).
- 10 SEQ ID NO:1970: n indicates c or deletion (Position 21).
SEQ ID NO:1980: n indicates t repeated 7 to 9 times (Position 21).
SEQ ID NO:1981: n indicates a or deletion (Position 21).
SEQ ID NO:1993: n indicates taac or deletion (Position 21).
SEQ ID NO:1994: n indicates ctcttt (Position 21).
- 15 SEQ ID NO:1995: n indicates ct (Position 21).
SEQ ID NO:2002: n indicates a or deletion (Position 21).
SEQ ID NO:2005: n indicates t or deletion (Position 21).
SEQ ID NO:2008: n indicates g or deletion (Position 21).
SEQ ID NO:2011: n indicates aattagaa or deletion (Position 21).
- 20 SEQ ID NO:2012: n indicates tttaaaa or tttaa (Position 21).
SEQ ID NO:2015: n indicates t or deletion (Position 21).
SEQ ID NO:2020: n indicates t or deletion (Position 21).
SEQ ID NO:2024: n indicates g or deletion (Position 21).
SEQ ID NO:2025: n indicates t or deletion (Position 21).
- 25 SEQ ID NO:2030: n indicates aaa or deletion (Position 21).
SEQ ID NO:2031: n indicates a or deletion (Position 21).
SEQ ID NO:2042: n indicates c (Position 21).
SEQ ID NO:2072: n indicates a or deletion (Position 21).
SEQ ID NO:2074: n indicates a or deletion (Position 21).
- 30 SEQ ID NO:2243: n indicates tca repeated 14 to 16 times (Position 21).

- SEQ ID NO:2244: n indicates a repeated 8 to 10 times (Position 21).
SEQ ID NO:2245: n indicates cacagtcac or deletion (Position 21).
SEQ ID NO:2246: n indicates tt or deletion (Position 21).
SEQ ID NO:2247: n indicates a repeated 10 to 12 times (Position 21).
5 SEQ ID NO:2248: n indicates c or deletion (Position 21).
SEQ ID NO:2249: n indicates a repeated 16 to 18 times (Position 21).
SEQ ID NO:2250: n indicates g (Position 21).
SEQ ID NO:2252: n indicates c or deletion (Position 21).
SEQ ID NO:2253: n indicates t or deletion (Position 21).
10 SEQ ID NO:2254: n indicates a or deletion (Position 21).
SEQ ID NO:2255: n indicates tg (Position 21).
SEQ ID NO:2257: n indicates t repeated 10 to 13 (Position 21).
SEQ ID NO:2258: n indicates gt repeated 11 to 13 times (Position 21).
SEQ ID NO:2259: n indicates a or deletion (Position 21).
15 SEQ ID NO:2260: n indicates g or deletion (Position 21).
SEQ ID NO:2261: n indicates g or deletion (Position 21).
SEQ ID NO:2262: n indicates t repeated 9 to 11 times (Position 21).
SEQ ID NO:2263: n indicates g (Position 21).
SEQ ID NO:2265: n indicates tt or deletion (Position 21).
20 SEQ ID NO:2266: n indicates a repeated 7 to 9 times (Position 21).
SEQ ID NO:2267: n indicates t repeated 9 to 11 times (Position 21).
SEQ ID NO:2268: n indicates a repeated 9 to 10 times (Position 21).
SEQ ID NO:2269: n indicates gt or deletion (Position 21).
SEQ ID NO:2270: n indicates a or deletion (Position 21).
25 SEQ ID NO:2271: n indicates t (Position 21).
SEQ ID NO:2273: n indicates a or deletion (Position 21).
SEQ ID NO:2274: n indicates ct or deletion (Position 21).
SEQ ID NO:2275: n indicates g or deletion (Position 21).
SEQ ID NO:2276: n indicates a or deletion (Position 21).
30 SEQ ID NO:2277: n indicates a or deletion (Position 21).

SEQ ID NO:2279: n indicates c or deletion (Position 21).

SEQ ID NO:2280: n indicates aaag or deletion (Position 21).

SEQ ID NO:2348: n indicates t repeated 22 to 26 times (Position 21).

5 SEQ ID NO:2349: n indicates g repeated 8 to 10 times (Position 21).

SEQ ID NO:2350: n indicates c repeated 6 to 7 times (Position 21).

SEQ ID NO:2351: n indicates a repeated 12 to 14 times (Position 21).

SEQ ID NO:2427: n indicates caccaggcagcagactctgatgaggaggggagggg (Position 21).

SEQ ID NO:2429: n indicates g (Position 21).

10 SEQ ID NO:2474: n indicates tcac or deletion (Position 21).

SEQ ID NO:2475: n indicates t or deletion (Position 21).

SEQ ID NO:2476: n indicates t repeated 9 to 11 times (Position 21).

SEQ ID NO:2477: n indicates a repeated 7 to 8 times (Position 21).

SEQ ID NO:2495: n indicates t repeated 13 to 16 times (Position 21).

15 SEQ ID NO:2496: n indicates t repeated 9 to 10 times (Position 21).

SEQ ID NO:2497: n indicates t repeated 14 to 16 times (Position 21).

SEQ ID NO:2498: n indicates t repeated 13 to 17 times (Position 21).

SEQ ID NO:2499: n indicates t (Position 21).

SEQ ID NO:2501: n indicates a repeated 8 to 9 times (Position 21).

20 SEQ ID NO:2502: n indicates t repeated 8 to 9 times (Position 21).

SEQ ID NO:2503: n indicates gcagtattactgtagt or deletion (Position 21).

SEQ ID NO:2504: n indicates t repeated 13 to 14 times (Position 21).

SEQ ID NO:2505: n indicates t repeated 9 to 10 times (Position 21).

SEQ ID NO:2506: n indicates t repeated 10 to 11 times (Position 21).

25 SEQ ID NO:2524: n indicates t or deletion (Position 21).

SEQ ID NO:2525: n indicates t repeated 12 to 15 times (Position 21).

SEQ ID NO:2586: n indicates a or deletion (Position 21).

SEQ ID NO:2587: n indicates at or deletion (Position 21).

SEQ ID NO:2594: n indicates t or deletion (Position 21).

30 SEQ ID NO:2595: n indicates ttc or deletion (Position 21).

SEQ ID NO:2606: n indicates ctt (Position 21).

SEQ ID NO:2651: n indicates c repeated 9 to 11 times (Position 21).

SEQ ID NO:2652: n indicates a repeated 15 to 21 times (Position 21).

SEQ ID NO:2653: n indicates ggggtggcggggtggg or deletion (Position 21).

5 SEQ ID NO:2654: n indicates t or deletion (Position 21).

SEQ ID NO:2655: n indicates a (Position 21).

SEQ ID NO:2657: n indicates a or deletion (Position 21).

SEQ ID NO:2658: n indicates t repeated 10 to 12 times (Position 21).

SEQ ID NO:2659: n indicates tt (Position 21).

10 SEQ ID NO:2661: n indicates tccctccttgaagctgacgt or deletion (Position 21).

SEQ ID NO:2662: n indicates ca repeated 12 to 18 times (Position 21).

SEQ ID NO:2685: n indicates a repeated 18 to 20 times (Position 21).

SEQ ID NO:2686: n indicates aa (Position 21).

SEQ ID NO:2688: n indicates t or deletion (Position 21).

15 SEQ ID NO:2689: n indicates t repeated 9 to 13 times (Position 21).

SEQ ID NO:2690: n indicates aa or deletion (Position 21).

SEQ ID NO:2691: n indicates ttgaca or gtccaatat (Position 21).

SEQ ID NO:2692: n indicates cta or deletion (Position 21).

SEQ ID NO:2693: n indicates t repeated 9 to 10 times (Position 21).

20 SEQ ID NO:2694: n indicates gagatgttggtggctcat (Position 21).

SEQ ID NO:2696: n indicates cc or deletion (Position 21).

SEQ ID NO:2697: n indicates act or deletion (Position 21).

SEQ ID NO:2755: n indicates tat or deletion (Position 21).

SEQ ID NO:2756: n indicates ac repeated 14 to 17 times (Position 21).

25 SEQ ID NO:2757: n indicates a repeated 16 to 27 times (Position 21).

SEQ ID NO:2758: n indicates t or deletion (Position 21).

SEQ ID NO:2759: n indicates a repeated 8 to 10 times (Position 21).

SEQ ID NO:2760: n indicates gt repeated 9 to 11 times (Position 21).

SEQ ID NO:2761: n indicates aa or deletion (Position 21).

30 SEQ ID NO:2762: n indicates t or deletion (Position 21).

- SEQ ID NO:2763: n indicates ac repeated 8 to 12 times (Position 21).
 SEQ ID NO:2764: n indicates a or deletion (Position 21).
 SEQ ID NO:2810: n indicates a (Position 21).
 SEQ ID NO:2812: n indicates aa or deletion (Position 21).
 5 SEQ ID NO:2813: n indicates ca or deletion (Position 21).
 SEQ ID NO:2814: n indicates t or deletion (Position 21).
 SEQ ID NO:2815: n indicates tgtgtg or deletion (Position 21).
 SEQ ID NO:2912: n indicates a (Position 21).
 SEQ ID NO:2914: n indicates g (Position 21).
 10 SEQ ID NO:2916: n indicates actt or deletion (Position 21).
 SEQ ID NO:2917: n indicates ttta or deletion (Position 21).
 SEQ ID NO:2918: n indicates a repeated 11 to 13 times (Position 21).
 SEQ ID NO:2919: n indicates t repeated 8 to 10 times (Position 21).
 SEQ ID NO:2920: n indicates a repeated 12 to 14 times (Position 21).
 15 SEQ ID NO:2921: n indicates ctgta or deletion (Position 21).
 SEQ ID NO:2922: n indicates a repeated 9 to 10 times (Position 21).
 SEQ ID NO:2923: n indicates ctt or deletion (Position 21).
 SEQ ID NO:2924: n indicates ctt (Position 21).
 SEQ ID NO:2926: n indicates a or deletion (Position 21).
 20 SEQ ID NO:2927: n indicates a repeated 9 to 11 times (Position 21).
 SEQ ID NO:2928: n indicates tgt or deletion (Position 21).
 SEQ ID NO:2929: n indicates a repeated 24 to 27 times (Position 21).
 SEQ ID NO:2930: n indicates ta repeated 10 to 21 times (Position 21).
 SEQ ID NO:2931: n indicates a repeated 8 to 10 times (Position 21).
 25 SEQ ID NO:2932: n indicates a repeated 11 to 13 times (Position 21).
 SEQ ID NO:2933: n indicates a repeated 8 to 10 times (Position 21).
 SEQ ID NO:2999: n indicates tacc or deletion (Position 21).
 SEQ ID NO:3000: n indicates atattcacttggtatctg or deletion (Position 21).
 SEQ ID NO:3001: n indicates ttta or deletion (Position 21).
 30 SEQ ID NO:3002: n indicates t (Position 21).

- SEQ ID NO:3004: n indicates g or deletion (Position 21).
- SEQ ID NO:3005: n indicates a or deletion (Position 21).
- SEQ ID NO:3006: n indicates a repeated 9 to 11 times (Position 21).
- SEQ ID NO:3007: n indicates g or deletion (Position 21).
- 5 SEQ ID NO:3008: n indicates at repeated 4 to 5 times (Position 21).
- SEQ ID NO:3009: n indicates t repeated 7 to 8 times (Position 21).
- SEQ ID NO:3010: n indicates t repeated 19 to 23 times (Position 21).
- SEQ ID NO:3011: n indicates t or deletion (Position 21).
- SEQ ID NO:3012: n indicates tgat or deletion (Position 21).
- 10 SEQ ID NO:3013: n indicates t repeated 8 to 10 times (Position 21).
- SEQ ID NO:3014: n indicates a or deletion (Position 21).
- SEQ ID NO:3021: n indicates a repeated 13 to 15 times (Position 21).
- SEQ ID NO:3022: n indicates t repeated 12 to 15 times (Position 21).
- SEQ ID NO:3042: n indicates g (Position 21).
- 15 SEQ ID NO:3044: n indicates a or deletion (Position 21).
- SEQ ID NO:3046: n indicates g or deletion (Position 21).
- SEQ ID NO:3047: n indicates t repeated 11 to 13 times (Position 21).
- SEQ ID NO:3049: n indicates a or deletion (Position 21).
- SEQ ID NO:3051: n indicates t repeated 9 to 11 times (Position 21).
- 20 SEQ ID NO:3054: n indicates t or deletion (Position 21).
- SEQ ID NO:3056: n indicates t or deletion (Position 21).
- SEQ ID NO:3060: n indicates t or deletion (Position 21).
- SEQ ID NO:3065: n indicates aaga (Position 21).
- SEQ ID NO:3069: n indicates aaaa or deletion (Position 21).
- 25 SEQ ID NO:3073: n indicates t repeated 9 to 11 times (Position 21).
- SEQ ID NO:3081: n indicates a or deletion (Position 21).
- SEQ ID NO:3103: n indicates t repeated 11 to 13 times (Position 21).
- SEQ ID NO:3119: n indicates acta (Position 21).
- SEQ ID NO:3125: n indicates gtg or deletion (Position 21).
- 30 SEQ ID NO:3130: n indicates t repeated 11 to 12 times (Position 21).

- SEQ ID NO:3140: n indicates tta or deletion (Position 21).
- SEQ ID NO:3154: n indicates g (Position 21).
- SEQ ID NO:3156: n indicates a (Position 21).
- SEQ ID NO:3158: n indicates cct or deletion (Position 21).
- 5 SEQ ID NO:3169: n indicates gga or deletion (Position 21).
- SEQ ID NO:3179: n indicates t repeated 12 to 14 times (Position 21).
- SEQ ID NO:3184: n indicates t repeated 16 to 17 times (Position 21).
- SEQ ID NO:3196: n indicates g (Position 21).
- SEQ ID NO:3273: n indicates ag (Position 21).
- 10 SEQ ID NO:3306: n indicates g (Position 21).
- SEQ ID NO:3310: n indicates c (Position 21).
- SEQ ID NO:3315: n indicates ct or deletion (Position 21).
- SEQ ID NO:3317: n indicates gc or deletion (Position 21).
- SEQ ID NO:3352: n indicates t repeated 9 to 11 times (Position 21).
- 15 SEQ ID NO:3355: n indicates a (Position 21).
- SEQ ID NO:3358: n indicates t or deletion (Position 21).
- SEQ ID NO: 3510² n represents at or deletion (Location 21).
- SEQ ID NO: 3512² n represents c or deletion (Location 21).
- SEQ ID NO: 3513² n represents t or deletion (Location 21).
- 20 SEQ ID NO:3514² n represents t or deletion (Location 21).
- SEQ ID NO:3515² n represents g or deletion (Location 21).
- SEQ ID NO:3517² n represents c or deletion (Location 21).
- SEQ ID NO:3519² n represents t or deletion (Location 21).
- SEQ ID NO:3521² n represents c or deletion (Location 21).
- 25 SEQ ID NO:3649² n represents 14 to 16 repeats of tca (from Location 21).
- SEQ ID NO:3650² n represents 8 to 10 repeats of a (from Location 21).
- SEQ ID NO:3651² n represents cacagtcac or deletion (Location 21).
- SEQ ID NO:3652² n represents tt or deletion (Location 21).
- SEQ ID NO:3653² n represents 10 to 12 repeats of a (from Location 21).

- SEQ ID NO:3654² n represents c or deletion (Location 21).
- SEQ ID NO:3655² n represents 16 to 18 repeats of a (from Location 21).
- SEQ ID NO:3656² n represents g or deletion (Location 21).
- SEQ ID NO:3658² n represents c or deletion (Location 21).
- 5 SEQ ID NO:3659² n represents t or deletion (Location 21).
- SEQ ID NO:3660² n represents a or deletion (Location 21).
- SEQ ID NO:3661² n represents tg or deletion (Location 21).
- SEQ ID NO:3663² n represents 10 to 13 repeats of t (from Location 21).
- SEQ ID NO:3664² n represents 11 to 13 repeats of gt (from Location 21).
- 10 SEQ ID NO:3665² n represents a or deletion (Location 21).
- SEQ ID NO:3666² n represents g or deletion (Location 21).
- SEQ ID NO:3667² n represents g or deletion (Location 21).
- SEQ ID NO:3668² n represents 9 to 11 repeats of t (from Location 21).
- SEQ ID NO:3669² n represents g or deletion (Location 21).
- 15 SEQ ID NO:3671² n represents tt or deletion (Location 21).
- SEQ ID NO:3672² n represents 7 to 9 repeats of a (from Location 21).
- SEQ ID NO:3673² n represents 9 to 11 repeats of t (from Location 21).
- SEQ ID NO:3674² n represents 9 to 10 repeats of a (from Location 21).
- SEQ ID NO:3675² n represents gt or deletion (Location 21).
- 20 SEQ ID NO:3676² n represents a or deletion (Location 21).
- SEQ ID NO:3677² n represents t or deletion (Location 21).
- SEQ ID NO:3679² n represents a or deletion (Location 21).
- SEQ ID NO:3680² n represents ct or deletion (Location 21).
- SEQ ID NO:3681² n represents g or deletion (Location 21).
- 25 SEQ ID NO:3682² n represents a or deletion (Location 21).
- SEQ ID NO:3683² n represents a or deletion (Location 21).
- SEQ ID NO:3684² n represents a or deletion (Location 21).

SEQ ID NO:3685 ^b n represents c or deletion (Location 21).

SEQ ID NO:3686 ²¹n represents aaag or deletion (Location 21).

SEQ ID NO:3751 ^a n represents 22 to 26 repeats of t (from Location 21).

SEQ ID NO:3752 ²n represents 8 to 10 repeats of g (from Location 21).

5 SEQ ID NO:3753 ^b n represents 6 to 7 repeats of c (from Location 21).

SEQ ID NO:3754 ²n represents 12 to 14 repeats of a (from Location 21).

SEQ ID NO:3833 ン represents tt or deletion (Location 21).

SEQ ID NO:3834 ²n represents 9 to 11 repeats of a (from Location 21).

SEQ ID NO:3835 n represents 8 to 12 repeats of a (from Location 21).

10 SEQ ID NO:3836 n represents t or deletion (Location 21).

SEQ ID NO:3837 ²¹n represents t or deletion (Location 21).

SEQ ID NO:3838 ²n represents t or deletion (Location 21).

SEQ ID NO:3839 n represents a or deletion (Location 21).

SEQ ID NO:3840 ²n represents t or deletion (Location 21).

15 SEQ ID NO:3841 Δ n represents t or deletion (Location 21).

SEQ ID NO:3842 ⁿ represents 11 to 15 repeats of t (from Location 21).

SEQ ID NO:3843 ⁵ n represents cat or deletion (Location 21).

SEO ID NO:3844 where n represents t or deletion (Location 21).

SEQ ID NO:3845 ン represents a or deletion (Location 21).

20 SEQ ID NO:3846 n represents a or deletion (Location 21).

SEQ ID NO:3847 ^{*} n represents t or deletion (Location 21).

SEQ ID NO:3848 ²n represents a or deletion (Location 21).

SEQ ID NO:3857 ²n represents g or deletion (Location 21).

SEQ ID NO:3879 n represents a or deletion (Location 21).

25 SEQ ID NO:3885 n represents aaag or deletion (Location 21).

SEQ ID NO:3915 ⁵ n represents t or deletion (Location 21).

SEQ ID NO:3918 n represents a or deletion (Location 21).

- SEQ ID NO:4089 n represents 10 to 12 repeats of a (from Location 21).
- SEQ ID NO:4092 n represents c or deletion (Location 21).
- SEQ ID NO:4102 n represents ca or deletion (Location 21).
- SEQ ID NO:4109 n represents at or deletion (Location 21).
- 5 SEQ ID NO:4113 n represents ctt or deletion (Location 21).
- SEQ ID NO:4115 n represents g or deletion (Location 21).
- SEQ ID NO:4117 n represents ggggct or deletion (Location 21).
- SEQ ID NO:4121 n represents 19 to 22 repeats of t (from Location 21).
- SEQ ID NO:4126 n represents 6 to 7 repeats of t (from Location 21).
- 10 SEQ ID NO:4129 n represents 11 to 13 repeats of t (from Location 21).
- SEQ ID NO:4173 n represents 7 to 8 repeats of c (from Location 21).
- SEQ ID NO:4175 n represents 10 to 12 repeats of a (from Location 21).
- SEQ ID NO:4183 n represents c or deletion (Location 21).
- SEQ ID NO:4188 n represents aaga or deletion (Location 21).
- 15 SEQ ID NO:4190 n represents 9 to 11 repeats of a (from Location 21).
- SEQ ID NO:4193 n represents ct or deletion (Location 21).
- SEQ ID NO:4198 n represents 8 to 9 repeats of t (from Location 21).
- SEQ ID NO:4218 n represents g or deletion (Location 21).
- SEQ ID NO:4224 n represents cttt or deletion (Location 21).
- 20 SEQ ID NO:4229 n represents t or deletion (Location 21).
- SEQ ID NO:4234 n represents c or deletion (Location 21).
- SEQ ID NO:4235 n represents a or deletion (Location 21).
- SEQ ID NO:4238 n represents gtt or deletion (Location 21).
- SEQ ID NO:4239 n represents t or deletion (Location 21).
- 25 SEQ ID NO:4259 n represents at or deletion (Location 21).
- SEQ ID NO:4273 n represents g or deletion (Location 21).
- SEQ ID NO:4280 n represents 15 to 17 repeats of a (from Location 21).

- SEQ ID NO:4294 n represents t or deletion (Location 21).
- SEQ ID NO:4298 n represents t or deletion (Location 21).
- SEQ ID NO:4310 n represents t or deletion (Location 21).
- SEQ ID NO:4314 n represents a or deletion (Location 21).
- 5 SEQ ID NO:4315 n represents 13 to 15 repeats of t (from Location 21).
- SEQ ID NO:4316 n represents 12 to 13 repeats of a (from Location 21).
- SEQ ID NO:4317 n represents t or deletion (Location 21).
- SEQ ID NO:4319 n represents t or deletion (Location 21).
- SEQ ID NO:4320 n represents 13 to 15 repeats of a (from Location 21).
- 10 SEQ ID NO:4325 n represents a or deletion (Location 21).
- SEQ ID NO:4331 n represents 5 to 11 repeats of t (from Location 21).
- SEQ ID NO:4333 n represents 8 to 9 repeats of t (from Location 21).
- SEQ ID NO:4334 n represents t or deletion (Location 21).
- SEQ ID NO:4345 n represents 9 to 10 repeats of t (from Location 21).
- 15 SEQ ID NO:4348 n represents 10 to 11 repeats of a (from Location 21).
- SEQ ID NO:4354 n represents a or deletion (Location 21).
- SEQ ID NO:4361 n represents a or deletion (Location 21).
- SEQ ID NO:4372 n represents ct or deletion (Location 21).
- SEQ ID NO:4391 n represents t or deletion (Location 21).
- 20 SEQ ID NO:4397 n represents a or deletion (Location 21).
- SEQ ID NO:4398 n represents at or deletion (Location 21).
- SEQ ID NO:4408 n represents tgtcaaaggaaggacacg or deletion (Location 21).
- SEQ ID NO:4414 n represents 6 to 8 repeats of tc (from Location 21).
- SEQ ID NO:4416 n represents c or deletion (Location 21).
- 25 SEQ ID NO:4419 n represents t or deletion (Location 21).
- SEQ ID NO:4424 n represents t or deletion (Location 21).
- SEQ ID NO:4425 n represents c or deletion (Location 21).

- SEQ ID NO:4433² n represents a or deletion (Location 21).
- SEQ ID NO:4435² n represents t or deletion (Location 21).
- SEQ ID NO:4442² n represents 6 to 7 repeats of gatt (from Location 21).
- SEQ ID NO:4443² n represents t or deletion (Location 21).
- 5 SEQ ID NO:4448² n represents t or deletion (Location 21).
- SEQ ID NO:4449² n represents gt or deletion (Location 21).
- SEQ ID NO:4452² n represents a or deletion (Location 21).
- SEQ ID NO:4453² n represents a or deletion (Location 21).
- SEQ ID NO:4457² n represents t or deletion (Location 21).
- 10 SEQ ID NO:4460² n represents at or deletion (Location 21).
- SEQ ID NO:4466² n represents a or deletion (Location 21).
- SEQ ID NO:4469² n represents t or deletion (Location 21).
- SEQ ID NO:4472² n represents at or deletion (Location 21).
- SEQ ID NO:4473² n represents a or deletion (Location 21).
- 15 SEQ ID NO:4474² n represents 12 to 14 repeats of t (from Location 21).
- SEQ ID NO:4477² n represents t or deletion (Location 21).
- SEQ ID NO:4479² n represents cac or deletion (Location 21).
- SEQ ID NO:4486² n represents cca or deletion (Location 21).
- SEQ ID NO:4514² n represents t or deletion (Location 21).
- 20 SEQ ID NO:4544² n represents c or deletion (Location 21).
- SEQ ID NO:4552² n represents aaaa or deletion (Location 21).
- SEQ ID NO:4565² n represents c or deletion (Location 21).
- SEQ ID NO:4575² n represents 8 to 9 repeats of t (from Location 21).
- SEQ ID NO:4576² n represents a or deletion (Location 21).
- 25 SEQ ID NO:4588² n represents taac or deletion (Location 21).
- SEQ ID NO:4589² n represents ctcttt or deletion (Location 21).
- SEQ ID NO:4590² n represents ct or deletion (Location 21).

- SEQ ID NO:4597 n represents a or deletion (Location 21).
- SEQ ID NO:4600 n represents t or deletion (Location 21).
- SEQ ID NO:4603 n represents g or deletion (Location 21).
- SEQ ID NO:4606 n represents aattagaa or deletion (Location 21).
- 5 SEQ ID NO:4607 n represents tttaaaa or ttttaa (Location 21).
- SEQ ID NO:4610 n represents t or deletion (Location 21).
- SEQ ID NO:4615 n represents t or deletion (Location 21).
- SEQ ID NO:4627 n represents c or deletion (Location 21).
- SEQ ID NO:4652 n represents 11 to 14 repeats of t (from Location 21).
- 10 SEQ ID NO:4653 n represents t or deletion (Location 21).
- SEQ ID NO:4654 n represents 10 to 13 repeats of t (from Location 21).
- SEQ ID NO:4655 n represents t or deletion (Location 21).
- SEQ ID NO:4657 n represents t or deletion (Location 21).
- SEQ ID NO:4658 n represents ta or deletion (Location 21).
- 15 SEQ ID NO:4660 n represents 13 to 15 repeats of t (from Location 21).
- SEQ ID NO:4661 n represents c or deletion (Location 21).
- SEQ ID NO:4662 n represents 17 to 20 repeats of a (from Location 21).
- SEQ ID NO:4663 n represents 11 to 13 repeats of t (from Location 21).
- SEQ ID NO:4664 n represents 8 to 9 repeats of t (from Location 21).
- 20 SEQ ID NO:4665 n represents 10 to 11 repeats of a (from Location 21).
- SEQ ID NO:4666 n represents 16 to 19 repeats of a (from Location 21).
- SEQ ID NO:4758 n represents g or deletion (Location 21).
- SEQ ID NO:4760 n represents 6 to 7 repeats of a (from Location 21).
- SEQ ID NO:4761 n represents c or deletion (Location 21).
- 25 SEQ ID NO:4763 n represents tcctcaggg or deletion (Location 21).
- SEQ ID NO:4764 n represents 8 to 10 repeats of cgc (from Location 21).
- SEQ ID NO:4765 n represents 10 to 12 repeats of a (from Location 21).

SEQ ID NO:4766 n represents caccaggcagcagactctgatgaggaggggaggggg or
deletion (Location 21).

SEQ ID NO:4768 n represents g or deletion (Location 21).

SEQ ID NO:4808 n represents tcac or deletion (Location 21).

5 SEQ ID NO:4809 n represents t or deletion (Location 21).

SEQ ID NO:4810 n represents 9 to 11 repeats of t (from Location 21).

SEQ ID NO:4811 n represents 7 to 8 repeats of a (from Location 21).

SEQ ID NO:4847 n represents agg or deletion (Location 21).

SEQ ID NO:4848 n represents taacatt or deletion (Location 21).

10 SEQ ID NO:4849 n represents 10 to 12 repeats of a (from Location 21).

SEQ ID NO:4850 n represents 15 to 17 repeats of t (from Location 21).

SEQ ID NO:4851 n represents 11 to 13 repeats of a (from Location 21).

SEQ ID NO:4877 n represents 11 to 13 repeats of t (from Location 21).

SEQ ID NO:4878 n represents t or deletion (Location 21).

15 SEQ ID NO:4879 n represents t or deletion (Location 21).

SEQ ID NO:4880 n represents 10 to 12 repeats of a (from Location 21).

SEQ ID NO:4881 n represents t or deletion (Location 21)

SEQ ID NO:4883 n represents 7 to 9 repeats of c (from Location 21).

SEQ ID NO:4884 n represents a or deletion (Location 21)

20 SEQ ID NO:4891 n represents 13 to 16 repeats of t (from Location 21).

SEQ ID NO:4892 n represents 9 to 10 repeats of t (from Location 21).

SEQ ID NO:4893 n represents 14 to 16 repeats of t (from Location 21).

SEQ ID NO:4894 n represents 13 to 17 repeats of t (from Location 21).

SEQ ID NO:4895 n represents t or deletion (Location 21).

25 SEQ ID NO:4897 n represents 8 to 9 repeats of a (from Location 21).

SEQ ID NO:4898 n represents 8 to 9 repeats of t (from Location 21).

SEQ ID NO:4899 n represents gcagtattactgtagt or deletion (Location 21).

SEQ ID NO:4901 ⁵ n represents 9 to 10 repeats of t (from Location 21).

SEQ ID NO:4902 E_n represents 10 to 11 repeats of t (from Location 21).

SEQ ID NO:4907 ϵ_n represents 10 to 14 repeats of a (from Location 21).

SEQ ID NO:4908 E_n represents 13 to 15 repeats of a (from Location 21).

SEQ ID NO:4909 n represents a or deletion (Location 21).

SEQ ID NO:4910 ²n represents t or deletion (Location 21).

SEQ ID NO:4918 ²n represents 13 to 15 repeats of a (from Location 21).

SEQ ID NO:4919 ²¹n represents 12 to 15 repeats of a (from Location 21).

10

SEQ ID NO:4936 ²n represents g or deletion (Location 21).

SEQ ID NO:4938 n represents aa or deletion (Location 21).

SEQ ID NO:4983 ⁵ n represents a or deletion (Location 21).

SEQ ID NO:4985 n represents aa or deletion (Location 21).

SEQ ID NO:4986 ²n represents ca or deletion (Location 21).

15

SEQ ID NO:4987 ⁵ n represents t or deletion (Location 21).

SEQ ID NO:4988 ^h n represents tgtgtg or deletion (Location 21).

SEQ ID NO:5076 n represents a or deletion (Location 21).

SEQ ID NO:5078² n represents g or deletion (Location 21).

SEQ ID NO:5080 ²n represents actt or deletion (Location 21).

20

SEQ ID NO:5081 ϵ_n represents tttta or deletion (Location 21).

SEQ ID NO:5082 E_n represents 11 to 13 repeats of a (from Location 21).

SEQ ID NO:5083 ²n represents 8 to 10 repeats of t (from Location 21).

SEQ ID NO:5084 n represents 12 to 14 repeats of a (from Location 21).

SEQ ID NO:5085 ⁵n represents cttgta or deletion (Location 21).

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SEQ ID NO:5086 n represents 9 to 10 repeats of a (from Location 21).

SEQ ID NO:5087² n represents ctt or deletion (Location 21).

SEQ ID NO:5088 ²n represents ctt or deletion (Location 21).

SEQ ID NO:5210 E^n represents 11 to 13 repeats of t (from Location 21).

- SEQ ID NO:5212⁵ n represents 15 to 18 repeats of ac (from Location 21).
- SEQ ID NO:5218⁵ n represents 18 to 26 repeats of t (from Location 21).
- SEQ ID NO:5227⁵ n represents tc or deletion (Location 21).
- SEQ ID NO:5231⁵ n represents 16 to 18 repeats of t (from Location 21).
- 5 SEQ ID NO:5246⁵ n represents 18 to 20 repeats of t (from Location 21).
- SEQ ID NO:5247⁵ n represents tggtagt or deletion (Location 21).
- SEQ ID NO:5249⁵ n represents t or deletion (Location 21).
- SEQ ID NO:5255⁵ n represents g or deletion (Location 21).
- SEQ ID NO:5256⁵ n represents g or deletion (Location 21).
- 10 SEQ ID NO:5257⁵ n represents c or deletion (Location 21).
- SEQ ID NO:5258⁵ n represents ctct or deletion (Location 21).
- SEQ ID NO:5261⁵ n represents a or deletion (Location 21).
- SEQ ID NO:5264⁵ n represents t or deletion (Location 21).
- SEQ ID NO:5271⁵ n represents 14 to 17 repeats of t (from Location 21).
- 15 SEQ ID NO:5276⁵ n represents 12 to 15 repeats of t (from Location 21).
- SEQ ID NO:5277⁵ n represents 10 to 13 repeats of a (from Location 21).
- SEQ ID NO:5278⁵ n represents 25 to 27 repeats of a (from Location 21).
- SEQ ID NO:5299⁵ n represents c or deletion (Location 21).
- SEQ ID NO:5308⁵ n represents 20 to 24 repeats of t (from Location 21).
- 20 SEQ ID NO:5311⁵ n represents t or deletion (Location 21).
- SEQ ID NO:5312⁵ n represents t or deletion (Location 21).
- SEQ ID NO:5314⁵ n represents g or deletion (Location 21).
- SEQ ID NO:5320⁵ n represents 18 to 23 repeats of t (from Location 21).
- SEQ ID NO:5340⁵ n represents c or deletion (Location 21).
- 25 SEQ ID NO:5400⁵ n represents a or deletion (Location 21).
- SEQ ID NO:5404⁵ n represents a or deletion (Location 21).
- SEQ ID NO:5407⁵ n represents tt or deletion (Location 21).

- SEQ ID NO:5410⁵ n represents at or deletion (Location 21).
- SEQ ID NO:5436⁵ n represents tgt or deletion (Location 21).
- SEQ ID NO:5445⁵ n represents t or deletion (Location 21).
- SEQ ID NO:5550⁵ n represents t or deletion (Location 21).
- 5 SEQ ID NO:5556⁵ n represents g or deletion (Location 21).
- SEQ ID NO:5557⁵ n represents 11 to 13 repeats of t (from Location 21).
- SEQ ID NO:5559⁵ n represents a or deletion (Location 21).
- SEQ ID NO:5561⁵ n represents 9 to 11 repeats of t (from Location 21).
- SEQ ID NO:5564⁵ n represents t or deletion (Location 21).
- 10 SEQ ID NO:5566⁵ n represents t or deletion (Location 21).
- SEQ ID NO:5570⁵ n represents t or deletion (Location 21).
- SEQ ID NO:5575⁵ n represents aaga or deletion (Location 21).
- SEQ ID NO:5579⁵ n represents aaaa or deletion (Location 21).
- SEQ ID NO:5583⁵ n represents 9 to 11 repeats of t (from Location 21).
- 15 SEQ ID NO:5591⁵ n represents a or deletion (Location 21).
- SEQ ID NO:5614⁵ n represents 11 to 13 repeats of t (from Location 21).
- SEQ ID NO:5630⁵ n represents acta or deletion (Location 21).
- SEQ ID NO:5636⁵ n represents gtg or deletion (Location 21).
- SEQ ID NO:5641⁵ n represents 11 to 12 repeats of t (from Location 21).
- 20 SEQ ID NO:5651⁵ n represents tta or deletion (Location 21).
- SEQ ID NO:5665⁵ n represents g or deletion (Location 21).
- SEQ ID NO:5667⁵ n represents a or deletion (Location 21).
- SEQ ID NO:5669⁵ n represents cct or deletion (Location 21).
- SEQ ID NO:5680⁵ n represents gga or deletion (Location 21).
- 25 SEQ ID NO:5690⁵ n represents 12 to 14 repeats of t (from Location 21).
- SEQ ID NO:5695⁵ n represents 16 to 17 repeats of t (from Location 21).
- SEQ ID NO:5707⁵ n represents g or deletion (Location 21).

SEQ ID NO:5800 n represents ag or deletion (Location 21).

SEQ ID NO:5806 ⁿ represents g or deletion (Location 21).

SEQ ID NO:5807 ⁿ represents a or deletion (Location 21).

5 SEQ ID NO:5835 n represents g or deletion (Location 21).

SEQ ID NO:5839 n represents c or deletion (Location 21).

SEQ ID NO:5844 ²n represents ct or deletion (Location 21).

SEQ ID NO:5846 wherein n represents gc or deletion (Location 21).

SEQ ID NO:5849 n represents c or deletion (Location 21).

10 SEQ ID NO:5884 wherein n represents c or deletion (Location 21).

SEQ ID NO:5890 ⁵ n represents tc or deletion (Location 21).

SEQ ID NO:5902 Δ n represents c or deletion (Location 21).

SEQ ID NO:5904 n represents g or deletion (Location 21).

SEQ ID NO:5917 ^{*} n represents a or deletion (Location 21).

15 SEQ ID NO:5921 ²n represents ca or deletion (Location 21).

SEQ ID NO:5922 ^{*}n represents t or deletion (Location 21).

SEQ ID NO:5934² n represents ct or deletion (Location 21).

SEQ ID NO:5965² n represents a or deletion (Location 21).

SEQ ID NO:5980 n represents t or deletion (Location 21).

20 SEQ ID NO:5981 Δ n represents t or deletion (Location 21).

SEQ ID NO:5981 E_n represents 11 to 13 repeats of t (from Location 21).

SEQ ID NO:5987 ²n represents t or deletion (Location 21).

SEQ ID NO:5989 n represents 16 to 18 repeats of t (from Location 21).

SEQ ID NO:5991 ²n represents cttta or deletion (Location 21).

25 SEQ ID NO:5992 n represents c or deletion (Location 21).

SEQ ID NO:5994 n represents 10 to 12 repeats of a (from Location 21).

SEQ ID NO:5995 ⁵n represents gt or deletion (Location 21).

- SEQ ID NO:6181 n represents 8 to 12 repeats of ac (from Location 21).
- SEQ ID NO:6182 n represents a or deletion (Location 21).
- SEQ ID NO:6202 n represents agg or deletion (Location 21).
- SEQ ID NO:6204 n represents 11 to 15 repeats of a (from Location 21).
- 5 SEQ ID NO:6205 n represents 11 to 14 repeats of a (from Location 21).
- SEQ ID NO:6208 n represents gt or deletion (Location 21).
- SEQ ID NO:6224 n represents ta or deletion (Location 21).
- SEQ ID NO:6307 n represents 16 to 19 repeats of a (from Location 21).
- SEQ ID NO:6308 n represents aa or deletion (Location 21).
- 10 SEQ ID NO:6310 n represents t or deletion (Location 21).
- SEQ ID NO:6311 n represents 10 to 12 repeats of t (from Location 21).
- SEQ ID NO:6312 n represents aa or deletion (Location 21).
- SEQ ID NO:6313 n represents ttgacagtccaatat, ttgaca, gtccaatat or deletion (Location 21).
- 15 SEQ ID NO:6314 n represents cta or deletion (Location 21).
- SEQ ID NO:6315 n represents a or deletion (Location 21).
- SEQ ID NO:6317 n represents 9 to 11 repeats of t (From Location 21).
- SEQ ID NO:6318 n represents c or deletion (Location 21).
- SEQ ID NO:6320 n represents gagatgtgtggctcacat or deletion (Location 21).
- 20 SEQ ID NO:6322 n represents cc or deletion (Location 21).
- SEQ ID NO:6323 n represents act or deletion (Location 21).
- SEQ ID NO:6405 n represents a or deletion (Location 21).
- SEQ ID NO:6415 n represents 8 to 11 repeats of t (from Location 21).
- SEQ ID NO:6416 n represents 10 to 13 repeats of t (from Location 21).
- 25 SEQ ID NO:6472 n represents g or deletion (Location 21).
- SEQ ID NO:6473 n represents c or deletion (Location 21).
- SEQ ID NO:6554 n represents t or deletion (Location 21).

SEQ ID NO:6555 n represents 12 to 15 repeats of t (from Location 21).

SEQ ID NO:6609 n represents a or deletion (Location 21).

SEQ ID NO:6610 n represents at or deletion (Location 21).

SEQ ID NO:6725 n represents 16 repeats of cctgc or 16 repeats of cctgt (from

5 Location 21).

SEQ ID NO:6726 n represents t or deletion (Location 21).

SEQ ID NO:6728 n represents c or deletion (Location 21).

SEQ ID NO:6739 n represents acac or deletion (Location 21).

SEQ ID NO:6748 n represents gatttggtatccag or deletion (Location 21).

10 SEQ ID NO:6750 n represents ag or deletion (Location 21).

SEQ ID NO:6751 n represents ta or deletion (Location 21).

SEQ ID NO:6757 n represents t or deletion (Location 21).

SEQ ID NO:6759 n represents 12 to 14 repeats of gt from Location 21).

SEQ ID NO:6771 n represents cagagct or deletion (Location 21).

15 SEQ ID NO:6772 n represents ct or deletion (Location 21).

SEQ ID NO:6773 n represents ag or deletion (Location 21).

SEQ ID NO:6785 n represents gtaaa or deletion (Location 21).

SEQ ID NO:6786 n represents aaaaa or deletion (Location 21).

SEQ ID NO:6787 n represents a or deletion (Location 21).

20 SEQ ID NO:6828 n represents tc or deletion (Location 21).

SEQ ID NO:6830 n represents t or deletion (Location 21).

SEQ ID NO:6831 n represents t or deletion (Location 21).

SEQ ID NO:6832 n represents gaagaaactgtgacagttt or deletion (Location 21).

SEQ ID NO:6833 n represents cct or deletion (Location 21).

25 SEQ ID NO:6834 n represents ttcc or deletion (Location 21).

SEQ ID NO:6835 n represents ttcttttaaaattg or deletion (Location 21).

SEQ ID NO:6837 n represents tcaggccttt or deletion (Location 21).

- SEQ ID NO:6839 n represents ggctg or deletion (Location 21).
- SEQ ID NO:6841 n represents a or deletion (Location 21).
- SEQ ID NO:6870 n represents 9 to 11 repeats of c (from Location 21).
- SEQ ID NO:6871 n represents 15 to 21 repeats of a (from Location 21).
- 5 SEQ ID NO:6872 n represents ggggtggcggggtggg or deletion (Location 21).
- SEQ ID NO:6873 n represents t or deletion (Location 21).
- SEQ ID NO:6874 n represents a or deletion (Location 21).
- SEQ ID NO:6876 n represents a or deletion (Location 21).
- SEQ ID NO:6877 n represents 10 to 12 repeats of t (from Location 21).
- 10 SEQ ID NO:6878 n represents tt or deletion (Location 21).
- SEQ ID NO:6880 n represents tcctcctgaagctgacgt or deletion (Location 21).
- SEQ ID NO:6881 n represents 12 to 18 repeats of ca (from Location 21).
- SEQ ID NO:6894 n represents gtt or deletion (Location 21).
- SEQ ID NO:6897 n represents ga or deletion (Location 21).
- 15 SEQ ID NO:6921 n represents t or deletion (Location 21).
- SEQ ID NO:6940 n represents t or deletion (Location 21).
- SEQ ID NO:6941 n represents t or deletion (Location 21).
- SEQ ID NO:6942 n represents t or deletion (Location 21).
- SEQ ID NO:6965 n represents at or deletion (Location 21).
- 20 SEQ ID NO:6966 n represents a or deletion (Location 21).
- SEQ ID NO:6967 n represents c or deletion (Location 21).
- SEQ ID NO:6997 n represents c or deletion (Location 21).
- SEQ ID NO:7005 n represents t or deletion (Location 21).
- SEQ ID NO:7006 n represents ttc or deletion (Location 21).
- 25 SEQ ID NO:7017 n represents ctt or deletion (Location 21).
- SEQ ID NO:7049 n represents 8 to 9 repeats of a (from Location 21).
- SEQ ID NO:7053 n represents 10 to 12 repeats of t (from Location 21).

- SEQ ID NO:7209 n represents t or deletion (Location 21).
- SEQ ID NO:7238 n represents gccag or deletion (Location 21).
- SEQ ID NO:7278 n represents a or deletion (Location 21).
- SEQ ID NO:7281 n represents g or deletion (Location 21).
- 5 SEQ ID NO:7282 n represents t or deletion (Location 21).
- SEQ ID NO:7287 n represents aaa or deletion (Location 21).
- SEQ ID NO:7288 n represents a or deletion (Location 21).
- SEQ ID NO:7299 n represents c or deletion (Location 21).
- SEQ ID NO:7329 n represents 17 to 19 repeats of a (from Location 21).
- 10 SEQ ID NO:7332 n represents 16 to 18 repeats of a (from Location 21).
- SEQ ID NO:7333 n represents 4 to 6 repeats of ga (from Location 21).
- SEQ ID NO:7346 n represents a or deletion (Location 21).
- SEQ ID NO:7375 n represents 2 to 3 repeats of tc (from Location 21).
- SEQ ID NO:7381 n represents 6 to 7 repeats of a (from Location 21).
- 15 SEQ ID NO:7383 n represents 13 to 15 repeats of a (from Location 21).
- SEQ ID NO:7385 n represents 9 to 10 repeats of t (from Location 21).
- SEQ ID NO:7387 n represents 11 to 14 repeats of a (from Location 21).
- SEQ ID NO:7389 n represents 14 to 17 repeats of t (from Location 21).
- SEQ ID NO:7390 n represents 8 to 9 repeats of a (from Location 21).
- 20 SEQ ID NO:7397 n represents g or deletion (Location 21).
- SEQ ID NO:7417 n represents 14 to 17 repeats of t (from Location 21).
- SEQ ID NO:7421 n represents 7 to 9 repeats of g (from Location 21).
- SEQ ID NO:7426 n represents 9 to 10 repeats of a (from Location 21).
- SEQ ID NO:7434 n represents 9 to 10 repeats of a (from Location 21).
- 25 SEQ ID NO:7436 n represents 6 to 7 repeats of g (from Location 21).
- SEQ ID NO:7443 n represents g or deletion (Location 21).
- SEQ ID NO:7458 n represents 8 to 9 repeats of a (from Location 21).

SEQ ID NO:7461 n represents 4 to 6 repeats of c (from Location 21).

SEQ ID NO:7483 n represents ggcgaggcggcgcgc or deletion (Location 21).

SEQ ID NO:7485 n represents ata or deletion (Location 21).

SEQ ID NO:7488 n represents 11 to 12 repeats of t (from Location 21).

5 SEQ ID NO:7489 n represents 12 to 14 repeats of t (from Location 21).

SEQ ID NO:7493 n represents 9 to 10 repeats of t (from Location 21).

SEQ ID NO:7495 n represents 6 to 7 repeats of ta (from Location 21).

SEQ ID NO:7497 n represents tgtatagctatacatagctatacatatatacatagctatata or deletion (Location 21).

10 SEQ ID NO:7503 n represents attt or deletion (Location 21).

SEQ ID NO:7510 n represents cct or deletion (Location 21).

SEQ ID NO:7519 n represents tggt or deletion (Location 21).

SEQ ID NO:7520 n represents a or deletion (Location 21).

SEQ ID NO:7531 n represents 9 to 10 repeats of t (from Location 21).

15 SEQ ID NO:7538 n represents a or deletion (Location 21).

SEQ ID NO:7566 n represents a or deletion (Location 21).

SEQ ID NO:7615 n represents a or deletion (Location 21).

SEQ ID NO:7649 n represents gtg or deletion (Location 21).

SEQ ID NO:7651 n represents gg or tgggtgggtgga (Location 21).

20 SEQ ID NO:7667 n represents ct or deletion (Location 21).

All publications and patents mentioned in the above specification are herein incorporated by reference. Various modifications and variations of the described method and system of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific

embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in the relevant fields are intended to be within the scope of the following claims.